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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow is described. Also described are single exon nucleic acid probes expressed in the bone marrow and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_BONE_MARROW.txt,
25 created 24 January 2001, having 26,421,347 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

bone marrow and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert *et al.*, *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick *et al.*, *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches — and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species — there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.
Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality.
20 Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia
25 - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the bone marrow, particularly those diseases with polygenic etiology.

30

Summary of the Invention

 The present invention solves these and other problems in the art by providing methods and apparatus for
35 predicting, confirming, and displaying functional

information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

5 In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions
10 and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention,
15 there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs:
20 1 - 13,114 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

25 In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably
30 isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

35 In yet another embodiment, said set of single

exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,012 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include

polymethylacrylic, polyethylene, polypropylene,
polyacrylate, polymethylmethacrylate, polyvinylchloride,
polytetrafluoroethylene, polystyrene, polycarbonate,
polyacetal, polysulfone, celluloseacetate,
5 cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

10 In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is
15 packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression
20 analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 13,115 - 26,012, wherein the fragment hybridizes at high stringency to an expressed human gene.
25 In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,114.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from
30 human bone marrow which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone
35 marrow.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,013 - 38,628 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid

probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer; wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human bone marrow, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human bone marrow; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from

genomic sequence of said eukaryote; and then
detecting specific hybridization of detectably
labeled nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are
5 derived from mRNA from the bone marrow of said eukaryote,
said probe is a single exon probe having a fragment
identical in sequence to, or complementary in sequence to,
said predicted exon, said probe is included within a single
exon microarray in accordance with the first aspect of the
10 invention, and said fragment is selectively hybridizable at
high stringency.

In a eighth aspect of the invention, there is
provided a method of assigning exons to a single gene,
comprising:
15 identifying a plurality of exons from genomic
sequence in accordance with the seventh aspect of the
invention; and then
measuring the expression of each of said exons in
a plurality of tissues and/or cell types using
20 hybridization to single exon microarrays having a probe
with said exon,
wherein a common pattern of expression of said
exons in said plurality of tissues and/or cell types
indicates that the exons should be assigned to a single
25 gene.

In an ninth aspect of the invention, there is
provided a nucleic acid sequence as set out in any of SEQ
ID NOS: 1 - 26,012 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is
30 provided a peptide encoded by a sequence comprising a
sequence as set out in any of SEQ ID NOS: 13,115 - 26,012,
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
encoded by a sequence comprising a sequence set out in any
35 of SEQ ID NOS.: 1 - 13,114.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 26,013 - 38,628.

5 Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,013 - 38,628, or fragment thereof.

In another aspect, the invention provides means
10 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated
15 sequence.

Detailed Description of the Invention

20 Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately
25 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach
30 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the
35 term "microarray" and phrase "nucleic acid microarray"

further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner
5 *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid
10 microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution
15 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the
20 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop
30 codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

35 As used herein the term "exon" refers to the

consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

5 As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons
10 encoding the peptide are wholly contained within the exon.

 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a
15 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present
20 within a target mRNA.

 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is
25 meant that it is homologous to the given sequence.

 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 ,
30 preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

 As used herein with respect to the visual display
35 of annotated genomic sequence, the term "rectangle" means

any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

5 As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and
15 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in
20 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

25 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length
30 shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color
35 hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

5 FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured
10 tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

15 FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a
20 BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

 FIG. 9 presents a Mondrian of BAC AC008172 (bases
25 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

 FIG. 10 is a Mondrian of BAC A049839.

30 Methods and Apparatus for Predicting, Confirming,
 Annotating, and Displaying Functional Regions From Genomic
 Sequence Data

 FIG. 1 is a flow chart illustrating in broad
35 outline a process for predicting functional regions from

genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original
5 sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence
10 data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will
15 typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will
20 minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically
25 be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below.
30 Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly
35 include several divisions thereof, including the

htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).

5 Databases of genomic sequence from species other than human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

10 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,

15 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing

20 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which

25 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

30 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic

35 assay. Where the subsequent experimental assay is

bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

5 The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

10 Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by
15 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for
20 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

25 The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output
30 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational
35 substrates for, and performance of subsequent assay, of

functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

5 Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to
10 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be
15 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction
20 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of
25 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend
30 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the
35 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in
5 subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently
10 long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment
15 length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal
20 number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes
25 (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate
30 a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been
35 described above as if genomic sequence database 100 were

static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query

20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or

codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified

within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after
5 transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X
10 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment,
15 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described
20 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene
25 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and
30 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For
35 the newly accessioned human genomic sequence input in

Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with
5 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase
10 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

15 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to
20 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report
25 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7%
30 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

35 Furthermore, consensus can be required among

different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process
5 can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence,
10 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done
15 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
300 for identification of a subset thereof for functional
20 assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental
25 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the
30 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

35 Where such subsequent gene expression assay uses

amplified nucleic acid, considerations such as desired
amplicon length, primer synthesis requirements, putative
exon length, sequence GC content, existence of possible
secondary structure, and the like can be used to identify
5 and select those ORFs that appear most likely successfully
to amplify. Where subsequent gene expression assay relies
upon nucleic acid hybridization, whether or not using
amplified product, further considerations involving
hybridization stringency can be applied to identify that
10 subset of sequences that will most readily permit sequence-
specific discrimination at a chosen hybridization and wash
stringency. One particular such consideration is avoidance
of putative exons that span repetitive sequence; such
sequence can hybridize spuriously to nonspecific message,
15 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer
constraints on the sequences that can be tested
experimentally, and in this latter case therefore process
300 can output the entirety of the input sequence.

20 The subset of sequences identified by process 300
as suitable for use in assay is then used in process 400 to
create the physical and/or informational substrate for
experimental verification of the predictions made in
process 200, and thereafter to assay those substrates.

25 As mentioned, the methods of the present
invention are particularly useful for identifying potential
coding regions within genomic sequence. In a preferred
embodiment of process 400, therefore, the expression of the
sequences predicted to encode protein is verified. The
30 combination of the predictive and experimental methods
provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
provides methods and apparatus for verifying the expression
of putative genes identified within genomic sequence. In
35 particular, the invention provides a novel method of

verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

5 Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is
10 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)
15 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500
20 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more
25 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400
30 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs
35 predicted from human genomic sequence according to the

methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
5 amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are
10 thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no
15 more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit
25 further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all
30 amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not
35 exceed about 25 nt in length. The "universal" priming

sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

5 Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 10 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 15 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

 The amplified nucleic acids can be attached 20 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

25 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 30 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

 As is well known in the art, microarrays 35 typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 5 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural 10 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the 15 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, 20 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed 25 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using 30 nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid 35 probe than can be achieved with spotting or lithography

techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such

microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the

desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST
5 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

10 As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a
15 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
20 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T,
25 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical
30 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the
35 probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include

artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even
5 smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning
10 artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide
15 greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the
20 optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the
25 range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often
30 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of
35 human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95

(1999)"; predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from
5 algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-
10 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure
15 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

20 Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons
25 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic
30 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn
35 from noncoding regions. As discussed above, the additional

presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

5 The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

10 Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization
15 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

 In contrast, the longer probe length of the
20 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or
25 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

30 A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound
35 noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence

drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, *Reviewed in Schena et al.*, and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-

transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is

disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation
5 information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in
10 international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should
15 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and
20 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic
25 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected
30 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,
35 SAGE ("serial analysis of gene expression") databases, and

more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -
5 including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200,
10 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such
15 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or
20 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

25 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the
30 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively
35 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the

sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the

number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

5 However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-
10 selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted
15 functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the
20 results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function
25 by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is
30 protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe
35 immobilized on the support surface of the microarray. As

noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

5 Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in
10 process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically
15 need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

 Rectangle 87 as shown in FIG. 3 includes smaller
20 rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880
25 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

30 Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

 For example, where the function assayed and displayed is protein coding, the degree of shading of
35 rectangles 880 can be used to represent the degree of

sequence similarity found upon query of expression
databases. The number of levels of discrimination can be
as few as two (identity, and similarity, where similarity
has a user-selectable lower threshold). Alternatively, as
5 many different levels of discrimination can be indicated as
can visually be discriminated.

Where display 80 is used as a graphical user
interface, rectangles 880 can additionally provide links
directly to the sequences identified by the query of
10 expression databases, and/or statistical summaries thereof.
As with each of the precedingly-discussed uses of display
80 as a graphical user interface, it should be understood
that the information accessed via display 80 need not be
resident on the computer presenting such display, which
15 often will be serving as a client, with the linked
information resident on one or more remotely located
servers.

Rectangle 85 displays the results of physical
assay of the sequence delimited by its left and right
20 borders.

Rectangle 85 can consist of a single rectangle,
thus indicating a single assay, or alternatively, and
increasingly typically, will consist of a series of
rectangles (85a, 85b, 85c) indicating separate physical
25 assays of the same sequence.

Where the function assayed is gene expression,
and where gene expression is assayed as herein described
using simultaneous two-color fluorescent detection of
hybridization to genome-derived single exon microarrays,
30 individual rectangles 85 can be colored to indicate the
degree of expression relative to control. Conveniently,
shades of green can be used to depict expression in the
sample over control values, and shades of red used to
depict expression less than control, corresponding to the
35 spectra of the Cy3 and Cy5 dyes conventionally used for

respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such
5 relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further
10 information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

15 FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to
20 rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return
25 identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

30 Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

35 Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,114 of these ORFs in bone marrow.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in bone marrow is currently available for use in measuring the level of its ORF's expression in bone marrow.

Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations

in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies.

5 For example, cancers that originate in the bone marrow and lymphatic tissues such as the lymphomas, leukemias, and myeloma have been recognized as a major health concern. An estimated 632,000 Americans are presently living with lymphoma, leukemia or myeloma, and
10 over 110,000 new cases are anticipated each year. The new cases alone account for 11% of all cancer cases reported in the United States.

 Lymphoma is a general term for a group of cancers of lymphocytes that manifest in the tissues of the
15 lymphatic system. Eventually, monoclonal proliferation crowds out healthy cells and creates tumors which enlarge lymph nodes. Approximately 450,000 members of the U.S. population are living with lymphoma: 160,000 with Hodgkin disease (HD) and 290,000 with non-Hodgkin lymphoma.

20 Hodgkin disease (HD) is a specialized form of lymphoma, and represent about 8% of all lymphomas. HD can be distinguish in tissues by the presence of an abnormal cell called the Reed-Sternberg cell. Incidence rates of HD are higher in adolescents and young adults, but HD is
25 considered to be one of the most curable forms of cancer. Symptoms of HD include painless swelling of lymph glands, fatigue, recurrent high fever, sweating at night, skin irritations and loss of weight.

 Although an infectious etiology has been proposed
30 to account for the disproportionate incidence of HD among siblings reared together - particularly an association with Epstein Barr Virus (EBV) - multiple genetic contributions have also been suggested.

 As early as 1986, linkage to HLA was suggested,
35 with Klitz et al., Am. J. Hum. Genet. 54: 497-505 (1994)

reporting an overall association of the nodular sclerosing (NSHD) group with the HLA class II region. Results of the study suggested that susceptibility to NSHD is influenced by more than 1 locus within the class II region. Through a literature search, Shugart and Collins (2000), *Europ. J. Hum. Genet.* 8: 460-463 (2000), performed a combined segregation and linkage analysis on 59 nuclear families with HD and concluded that HD is most likely determined by both an HLA-associated major gene and other non-HLA genetic factors, in conjunction with environmental effects.

Non-Hodgkin lymphoma (NHL) is a malignant monoclonal proliferation of the lymphoid cells in the immune system, including bone marrow, spleen, liver and GI tract. The pathologic classification of NHL continues to evolve, reflecting new insights into the cells of origin and the biologic bases of these heterogeneous diseases. The course of NHL varies from indolent and initially well tolerated to rapidly fatal. Furthermore, common clinical symptoms of NHL, but rare in HD, are congestion and edema of the face and neck and ureteral compression.

Non-Hodgkin lymphoma (NHL) has been linked to a variety of specific genetic defects, including 26 mutated genes and at least 9 identified chromosomal translocations. Among the mutated genes are: ALK (2p23); API2 (MIHC, cIAP2) (11q22-q23); API4 (survivin, SVV) (17q25(?)); ATM (ATA, ATC) (11q22.3); BCL1 (11q13.3); BCL10 (CLAP, CIPER) (1p22); BCL2 (18q21.3); BCL6 (LAZ3, ZNF51) (3q27); BLYM (1p32); BMI1 (10p13); CCND1 (D11S287E, Cyclin D, PRAD1) (11q13); CD44 (MDU3, HA, MDU2) (11pter-p13); FRAT1 (10q23-q24(?)); FRAT2 (GBP) (10(?)); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LCP1 (PLS2) (13q14.1-q14.3); MALT1 (MLT) (18q21); MUC1 (PUM, PEM) (1q21); MYBL1 (AMYB, A-MYB) (8q22); MYC (CMYC, C-MYC) (8q24.12-q24.13); NBS1 (8q21); NPM1 (B23) (5q35); PCNA (20p12); TIAM1 (21q22.1); and TP53 (p53, P53) (17q13.1).

Among the chromosomal abnormalities are: t(1;14)

(p22;q32); t(14;18)(q32;q21); t(3;14)(q27;q32);
t(6;14)(p25;q32); t(11;18)(q21;q21); t(1;14)(q21;q32);
t(2;5)(p23;q35); add(14q32) / dup(14p32); and
t(11;14)(q13;q32).

5 Additional genetic loci, as yet undiscovered, are believed to account for other occurrences of NHL.

As another example, acute leukemia is a malignant disease of blood-forming tissues such as the bone marrow. It is characterized by the uncontrolled growth of white
10 blood cells. As a result, immature myeloid cells (in acute myelogenous leukemia (AML)) or lymphoid cells (in acute lymphocytic leukemia (ALL)) rapidly accumulate and progressively replace the bone marrow; diminished production of normal red cells, white cells, and platelets
15 ensues. This loss of normal marrow function in turn gives rise to the typical clinical complications of leukemia: anemia, infection, and bleeding.

If untreated, ALL is rapidly fatal; most patients die within several months of diagnosis. With appropriate
20 therapy, many patients can be cured. The survival rate for patients diagnosed with AML or ALL is 14% and 58% respectively. However, the incidences of AML is expected to be greater than ALL: an estimated 10,000 new cases of AML, predominantly in older adults, is anticipated in the
25 U.S. alone, whereas 3,100 new cases of ALL are expected, with 1,500 of these new cases occurring among children.

The etiology of acute leukemia is not known. Although human T-cell lymphotropic virus type I (HTLV-I), a causative agent of adult T-cell leukemia, and HTLV-II,
30 obtained from several patients with a syndrome resembling hairy cell leukemia, have been isolated, the etiologic link between HTLV and malignancy is uncertain. There is, however, evidence which suggests a genetic predisposition to incidences of acute leukemia.

35 For example, genetic disorders such as Fanconi

anemia and Down syndrome appear to increase risk of acute leukemia, specifically, AML. Evidence supporting a chromosome 21 locus for acute myelogenous leukemia (AML) includes the finding of linkage to 21q22.1-q22.2 in a family with a platelet disorder and propensity to develop AML (Ho et al., Blood 87: 5218-5224 (1996), an increased incidence of leukemia in Down syndrome, and frequent somatic translocation in leukemia involving the CBFA gene on 21q22.3. In addition, Horwitz et al., Am. J. Hum. Genet. 61:873-881 (1997), suggest that a gene on 16q22 may be a second cause of acute myelogenous leukemia. Nonparametric linkage analysis gave a P-value of 0.00098 for the conditional probability of linkage. Mutational analysis excluded expansion of the AT-rich minisatellite repeat FRA16B fragile site and the CAG trinucleotide repeat in the E2F-4 transcription factor. Large CAG repeat expansion was excluded as a cause of leukemia in this family.

Similarly, acute lymphoblastic leukemia (ALL) has been suggested to have a genetic predisposition. In particular, linkage to chromosome 9p has been reported by a number of groups. Chilcote et al., New Eng. J. Med. 313: 286-291 (1985), found that 6 of 8 patients with clinical features of lymphomatous ALL (LALL), a distinct category of ALL of T-cell lineage, had karyotypic abnormalities leading to loss of bands 9p22-p21. The mechanisms varied and included deletions, unbalanced translocations, and loss of the entire chromosome; only 1 of 57 patients without LALL had an abnormality of chromosome 9 at diagnosis. Kowalczyk et al., Cancer Genet. Cytogenet. 9:383-385 (1981), had earlier found changes in 9p in a subgroup of ALL cases. Chilcote et al. (1985) pointed out that there is a fragile site at 9p21 and raised the question of familial predisposition on this basis. This fragile site is the breakpoint in the translocation t(9;11)(p21-22;q23), which

is associated with acute nonlymphocytic leukemia with monocytic features, ANLL-AMoL-M5a. In a large series, Murphy et al., New Eng. J. Med. 313:1611 (1985), confirmed an abnormality of 9p in 10 to 11% of cases (33 out of more
5 than 300) of acute lymphoblastic leukemia. The breakpoints in 9p clustered in the p22-p21 region. They could not, however, corroborate the specific association with T-cell origin or so-called lymphomatous clinical features. In addition, Taki et al., Proc. Natl. Acad. Sci. USA 96:14535
10 (1999), recently identified AF5q31, a new AF4-related gene, fused to MLL in infant ALL with ins(5;11)(q31;q13q23), and suspects that AF5q31 and AF4 might define a new family particularly involved in the pathogenesis of 11q23-associated-ALL.

15 As yet a further example of a disease affecting bone marrow with likely polygenic etiology is multiple myeloma (MM).

MM is a cancer of plasma cells, the final differentiated stage of B lymphocyte maturation. The
20 malignant clone proliferates in the bone marrow and frequently invades the adjacent bone, producing extensive skeletal destruction that results in bone pain and fractures. Anemia, hypercalcemia, and renal failure are some clinical manifestations associated with MM.

25 MM causes 1% of all cancer deaths in Western countries. A genetic component to its etiology is suggested by disparate incidence among various groups in the country. Its incidence is higher in men than in women, in people of African descent relative to the U.S.
30 population at large, and in older adults as compared to the young. It has been estimated that 14,000 new cases of myeloma will be diagnosed in the U.S., and over 11,000 persons will die from MM within the year.

Although, Kaposi's sarcoma-associated herpes
35 virus has been associated with MM (Retig et al., Science

276:1851 (1997)), there is evidence that chromosomal abnormalities, such as the deletion of 13q14 and rearrangements of 14q increase the proliferation of myeloma cells.

5 Up to 30% of patients who suffer with MM have a balanced translocation, t(4;14)(p16.3;q32), that places the fibroblast growth factor receptor 3 (FGFR3) gene under the control of IgH promoter elements (Chesi et al., Nat. Genet. 16:260 (1997)). This results in increased expression of
10 FGFR3, a member of a family of tyrosine kinase receptors implicated in control of cellular proliferation.

According to Zoger et al., Blood 95:1925 (2000), monoallelic deletions of the retinoblastoma-1 (rb-1) gene and the D13S319 locus were observed in 48 of 104 patients
15 (46.2%) and in 28 of 72 (38.9%) patients, respectively, with newly diagnosed MM. Fluorescence in situ hybridization (FISH) studies found that 13q14 was deleted in all 17 patients with karyotypic evidence of monosomy 13 or deletion of 13q but also in 9 of 19 patients with
20 apparently normal karyotypes. Patients with a 13q14 deletion were more likely to have higher serum levels of beta(2)-microglobulin (P=0.059) and a higher percentage of bone marrow plasma cells (P=0.085) than patients with a normal 13q14 status on FISH analysis. In patients with a
25 deletion of 13q14, myeloma cell proliferation was markedly increased. The presence of a 13q14 deletion on FISH analysis was associated with a significantly lower rate of response to conventional-dose chemotherapy (40.8% compared with 78.6%; P =.009) and a shorter overall
30 survival (24.2 months compared with > 60 months; P <.005) than in patients without the deletion.

There are numerous other mutated genes and chromosomal abnormalities that may predispose to MM. Examples of such genes are: B2M (15q21-q22); CCND1
35 (D11S287E, Cyclin D, PRAD1)(11q13); CD19 (16p11.2); HGF

(HPTA) (7q21.1); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LTA (TNFB, LT) (6p21.3); SDC1 (2p24.1); and TNF (TNFA, TNFSF2, DIF) (6p21.3). Examples of chromosomal abnormalities include: t(6;14)(p25;q32) and
5 t(11;14)(q13;q32).

Other significant diseases or disorders of the bone marrow are also believed, or likely to have, a genetic, typically polygenic, etiologic component. These diseases include, for example, chronic myeloid leukemia,
10 chronic lymphoid leukemia, polycythemia vera, myelofibrosis, primary thrombocythemia, myelodysplastic syndromes, Wiskott-Aldrich, lymphoproliferative syndrome, aplastic anemia, Fanconi anemia, Down syndrome, sickle cell disease, thalassemia, granulocyte disorders, Kostmann
15 syndrome, chronic granulomatous disease, Chediak-Higashi syndrome, platelet disorders, Glanzmann thrombasthenia, Bernard-Soulier syndrome, metabolic storage diseases, osteoporosis, congenital hemophagocytic syndrome.

The human genome-derived single exon nucleic acid
20 probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human bone marrow, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed
25 at detectable levels in human bone marrow, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging
30 of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given bone marrow disease, or to specific grades or stages thereof.

35 In one embodiment, the patient gene expression

profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's bone marrow (or cells cultured therefrom) to the genome-derived single exon microarray of the present
5 invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the bone marrow of individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the
10 function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be
15 used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of diseases of bone marrow to be assessed through the massively parallel determination of altered copy number, deletion, or mutation
20 in the patient's genome of exons known to be expressed in human bone marrow. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

25 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of expression of message specifically containing that ORF.

30 It should be appreciated, however, that the probes of the present invention, for which expression in the bone marrow has been demonstrated are useful for both measurement in the bone marrow and for survey of expression in other tissues.

35 Significant among such advantages is the presence

of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
5 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
10 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
15 databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
20 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
25 for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. Nature 405,
30 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
35 Programs Regulating Lung Inflammation and Fibrosis," *Proc.*

- Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
5 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
10 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).
- 15 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl.*
20 *Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell
25 Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for
30 example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer

Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in bone marrow. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity

sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable

of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are
5 required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,115 - 26,012, respectively, for probe SEQ ID
10 NOS. 1 - 13,114. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,115 - 26,012 individually
15 by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency
20 conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20
25 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as
30 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes
35 of the present invention is dictated by the proximity of

other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one
5 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more
10 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand
15 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art
20 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to
25 provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic
30 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

35 And when intended for use in solution

hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent
5 labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates
10 thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

15 The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived
20 single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96
25 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3'
30 primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon
35 probes can usefully include a plurality of probes chosen

for the common attribute of expression in the human bone marrow.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be
5 chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be
10 used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

15 It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

20 The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human bone marrow. In preferred embodiments, the present invention provides human genome-derived single exon microarrays
25 comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 13,114.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived
30 single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression
35 measurements. Alternatively, at a given probe density, the

same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,114 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,115 - 26,012, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,114 can be used, or that portion thereof in SEQ ID NOS. 13,115 - 26,012 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverly, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Emoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis

(Oxford Chemistry Primers, No 7) , Oxford Univ. Press
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles
of Peptide Synthesis (Springer Laboratory), Springer Verlag
(December 1993) (ISBN: 0387564314).

5 It is, therefore, another aspect of the invention
to provide peptides comprising an amino acid sequence
translated from SEQ ID NOS.: 13,115 - 26,012. Such amino
acid sequences are set out in SEQ ID NOS: 26,013 - 38,628.
Any such recombinantly-expressed or synthesized peptide of
10 at least 8, and preferably at least about 15, amino acids,
can be conjugated to a carrier protein and used to generate
antibody that recognizes the peptide. Thus, it is a
further aspect of the invention to provide peptides that
have at least 8, preferably at least 15, consecutive amino
15 acids.

The following examples are offered by way of
illustration and not by way of limitation.

20 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
in Human Genomic Sequence

Bioinformatics Results

25 All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

30 After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
35 GRAIL uses a neural network, GENEFINDER uses a hidden

Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
5 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
10 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
15 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs
20 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single
25 gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not
30 span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments
35 fewer than 250 bp in length do not bind well to the amino-

modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

5 Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first
10 additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing
15 the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

 The ORFs were then PCR amplified from genomic
20 DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

 Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard
25 techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
30 amplification was classified as successful if a single band appeared.

 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)
35 length and distribution of amplified PCR products, with ORF

length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
5 size of 150 bp (n=9498). With an average amplicon size of 475 \pm 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

10 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
15 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
20 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

 Some genomic clones (BACs) yielded very poor PCR
25 and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

 Although the intronic and intergenic material
30 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
35 similarly found not to affect differential expression

ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-
5 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally
10 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt
15 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe
20 sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

25 All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are
30 presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis
--

Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1)
 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message

pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

5 Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
10 and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
15 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup
20 column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a
25 Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C
30 overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

35 Slides were scanned using a Molecular Dynamics

Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

5 Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of
10 at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

15 Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

 The relative expression signal for these probes
20 was then plotted as function of tissue or cell type, and is presented in FIG. 6.

 FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not
25 expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

 Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed"
30 products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were
35 expressed in all 10 tissues. The next most common class

(15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data – that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested

tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 5 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

10

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 15 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") 20 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 25 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being 30 found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' 35 or 5' end of a gene, many of these high expression genes

will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the

observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous

				system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to

				the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
15 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed

down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in

choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm
Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

10

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

20 EXAMPLE 3

Representation of Sequence and Expression Data as a
"Mondrian"

For each genomic clone processed for microarray
5 as above-described, a plethora of information was
accumulated, including full clone sequence, probe sequence
within the clone, results of each of the three gene finding
programs, EST information associated with the probe
sequences, and microarray signal and expression for
10 multiple tissues, challenging our ability to display the
information.

Accordingly, we devised a new tool for visual
display of the sequence with its attendant annotation
which, in deference to its visual similarity to the
15 paintings of Piet Mondrian, is hereinafter termed a
"Mondrian". FIGS. 3 and 4 present the key to the
information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases
25,000 to 130,000 shown), containing the carbamyl phosphate
20 synthetase gene (AF154830.1). Purple background within the
region shown as field 81 in FIG. 3 indicates all 37 known
exons for this gene.

As can be seen, GRAIL II successfully identified
27 of the known exons (73%), GENEFINDER successfully
25 identified 37 of the known exons (100%), while DICTION
identified 7 of the known exons (19%).

Seven of the predicted exons were selected for
physical assay, of which 5 successfully amplified by PCR
and were sequenced. These five exons were all found to be
30 from the same gene, the carbamyl phosphate synthetase gene
(AF154830.1).

The five exons were arrayed, and gene expression
measured across 10 tissues. As is readily seen in the
Mondrian, the five chip sequences on the array show
35 identical expression patterns, elegantly demonstrating the

reproducibility of the system..

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in bone marrow tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical

structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
5 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,114 single exon probes, each fragment corresponding to an extension product from one of
10 the two amplification primers.)

The structures of the 13,114 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,114 . The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
15 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,115 - 26,012, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
20 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
25 expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give
30 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the
35 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining
5 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)
10 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
15 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
20 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human bone marrow and thus
25 presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human bone marrow tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,115 - 26,012 was individually
30 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were
35 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs

in an exhaustive process based on the following criteria:
1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
5 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
10 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
15 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
20 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ — which is probative evidence that the query sequence has previously
25 been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
30 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
35 a proper subset of the data present within the attached

sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,114) and probe exon (SEQ ID NOs.: 13,115 - 26,012, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

- 5 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;
- (b) the most similar sequence provided by BLAST
10 query of the EST database, with accession number and BLAST E value for the "hit";
- (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
- 15 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

20 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring
Expression of Genes in Human Bone marrow

Table 4 (546 pages) presents expression, homology, and
25 functional information for the genome-derived single exon probes that are expressed significantly in human bone marrow.

30

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human bone marrow comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,114 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,115 - 26,012.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human bone marrow.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
10 of SEQ ID NOs.: 26,013 - 38,628, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.

15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human bone marrow, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human bone marrow; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
 wherein said detectably labeled nucleic acids are derived
20 from mRNA from the bone marrow of said eukaryote, said
 probe is a single exon probe having a fragment identical in
 sequence to, or complementary in sequence to, said
 predicted exon, said probe is included within a microarray
 according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 26,012 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 26,012.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,013 - 38,628.

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
450	13523	26455	4.57			
890	13945	26903	10.46			
1046	14092		3.88			
1305	14341	27305	7.19			
1618	14650	27628	4.21			
1642	14674	27647	6.05			
1738	14768	27753	2.88			
1764	14793	27778	1.27			
1770	14798	27788	9.04			
1808	14833	27828	1.24			
1888	15016	28023	2.44			
2175	15191	28212	2.92			
2287	15300	28324	2.97			
3200	16255	29175	3.13			
3464	16510	29431	1.32			
3527	16573	29496	10.05			
3574	16619		0.86			
3688	17008		1.15			
4225	17254	30141	1.66			
4280	17319	30188	6.25			
4310	17339	30218	0.83			
4310	17339	30219	0.83			
4364	17381		1.03			
4420	17447	30338	0.63			
4874	17891	30780	1.27			
4959	17874	30865	0.74			
5083	18083	30969	5.85			
5095	18105	30980	1.42			
5329	18435	31187	1.78			
5329	18435	31188	1.78			
5498	18696		4.07			
5678	18773		7.77			
5782	18988		3.48			
5824	18914	32097	0.65			

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
5830	18920	32103	3.19			
6138	25655	32443	1.58			
6167	19242	32473	2.11			
6556	19816		1.24			
6700	19757	33034	0.89			
6700	19757	33035	0.89			
7332	20303	33647	1.52			
7332	20303	33648	1.52			
7642	20602	33968	1.45			
7642	20602	33967	1.45			
8114	21051		0.81			
8396	21365	34774	1.55			
8830	21797	35218	1.21			
9212	22178	35608	0.57			
9212	22178	35609	0.57			
9892	22845	36302	5.61			
10124	23050	36529	0.69			
10241	23169	36653	1.44			
10383	23305	36782	0.81			
10675	23597	37093	0.49			
10675	23597	37094	0.49			
10794	23715	37216	0.6			
10794	23715	37217	0.6			
11043	24007		2.14			
11366	24314		1.81			
11687	24653	38232	1.82			
11829	24712		1.84			
12600	25302		1.5			
12888	25476	31730	1.34			
6170	19245	32477	15.3	9.9E+00	AJ239028.1	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8339	21308	34723	1.75	9.8E+00	U32716.1	Haemophilus influenzae Rd section 31 of 163 of the complete genome
10100	23028	36502	0.47	9.8E+00	Y18930.1	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
10100	23026	36503	0.47	9.8E+00	Y18930.1	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
7194	20218	33549	0.68	9.6E+00	AF065630.1	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7194	20218	33550	0.66	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10787	23708	37209	1.19	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor I1H polypeptide 2 (Gtf2h2) genes, complete cds
10787	23708	37210	1.19	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor I1H polypeptide 2 (Gtf2h2) genes, complete cds
2835	15993	28913	3.21	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
6457	19522	32773	0.54	9.4E+00	P75130	SWISSPROT	HYPOTHETICAL PROTEIN MG447 HOMOLOG
11911	24792	36381	2.45	9.4E+00	O99825	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
11911	24792	36382	2.45	9.4E+00	O99825	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
8435	21404	34817	0.86	9.3E+00	AF130990.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9356	22321	35748	3.15	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5369	18474	31346	2.66	9.1E+00	AF095809.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5369	18474	31347	2.66	9.1E+00	AF095809.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9785	22726	32456	0.95	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6152	19227	32456	5.62	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934562 3'
6517	19580	32837	2.21	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6517	19580	32838	2.21	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
440	13514	28445	1.03	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9810	21133	34536	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11504	24446		1.54	8.0E+00	P41920	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8491	21459		0.82	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7589	20532		2.17	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8704	21672	35095	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8704	21672	35096	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5898	19985	32176	3.63	7.4E+00	BE700517.1	EST_HUMAN	602128876F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4285506 5'
9106	22072	35498	2.72	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
9106	22072	35499	2.72	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2990	16048	28968	4.7	7.2E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
2990	16048	28969	4.7	7.2E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
7230	20252	33586	1.12	7.2E+00	BE179030.1	EST_HUMAN	RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA
7356	20326	33673	1.1	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7356	20326	33674	1.1	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9957	22884		6.86	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11715	24678	38256	2.98	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
							MET17 PROTEIN [INCLUDES: O-ACETYLHOMOSERINE SULFHYDRYLASE (OAH SULFHYDRYLASE); O-ACETYL SERINE SULFHYDRYLASE (OAS SULFHYDRYLASE)]
11909	24760	38379	4.81	7.1E+00	P06106	SWISSPROT	ARGININE KINASE (AK)
10341	23265	38744	3.43	7.0E+00	P48610	SWISSPROT	WD-40 REPEAT PROTEIN MSI3
11580	24518	38074	1.7	7.0E+00	Q22469	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
8626	21594	35014	3.94	6.9E+00	P35679	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10716	23638	37131	1.32	6.9E+00	P44834	SWISSPROT	SKT5 PROTEIN
10734	23656	37149	0.44	6.9E+00	P34226	SWISSPROT	
8240	21209	34613	1.31	6.8E+00	W03412.1	EST_HUMAN	z007c11.1 Scores melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:291860 5'
8240	21209	34614	1.31	6.8E+00	W03412.1	EST_HUMAN	z007c11.1 Scores melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:291860 5'
							OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP6 AND VP8]
9498	22452		1.35	6.8E+00	P36307	SWISSPROT	
10569	23491	36983	3.31	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5356	18481		0.74	6.6E+00	Q99028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6695	19762	33029	0.72	6.6E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
10434	23366	36842	1.87	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10434	23366	36843	1.87	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11463	24406		2.49	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9535	22498	35946	7.17	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10667	23599	37086	0.47	6.5E+00	BE866001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3860969 5'
10089	23025	36501	1.17	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
10927	23847	37362	0.65	6.2E+00	6754621	NT	Mus musculus marnosidase 2, alpha B1 (Man2b1), mRNA
7236	20237	33591	1.35	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10175	23100	36580	0.46	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1169001-1485000 nt. position (677)
10890	23800	37302	0.63	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10890	23800	37303	0.63	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
							Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
6870	19727	33003	6.7	5.9E+00	AF165142.1	NT	complete cds
3536	16582		0.88	5.8E+00	7681567	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7369	20339	33690	0.65	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7369	20339	33691	0.65	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7819	20768		1.5	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLII)
11805	23960	37485	2.98	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE

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6380	19448	32889	0.78	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10138	23064		0.47	5.5E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11803	23958	37482	2.35	5.5E+00	P11890	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7115	20049	33351	1.1	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7115	20049	33352	1.1	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7552	20515		0.84	5.4E+00	Q99435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8143	21080	34480	0.6	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
							VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
							LIPOVITELLIN LV-2)
8202	21172		1.72	5.4E+00	Q91082	SWISSPROT	
9151	22117	35543	0.73	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9151	22117	35544	0.73	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10396	23318	36799	1.41	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
10396	23318	36800	1.41	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4824	17841	30739	1.22	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6635	19693		0.6	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8415	21384		3.9	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
9335	22300		0.53	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11950	24929	38425	1.84	5.3E+00	Q27805	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
12093	24984	38559	2.34	5.3E+00	Z72963.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL141w
12093	24984	38560	2.34	5.3E+00	Z72963.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL141w
5539	18636		1.22	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-186409 HT0691 Homo sapiens cDNA
10738	23660		0.78	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11527	24468		1.46	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
9313	22278	36709	0.85	5.1E+00	O16005	SWISSPROT	RHODOPSIN
10184	23109	36592	1.07	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
11617	24555	38117	3.01	5.1E+00	P55200	SWISSPROT	ZINC FINGER PROTEIN HPX (ALL-1)
6418	19485	32734	0.65	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4124114 5'
10554	23476		0.65	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10796	23717	37219	3.79	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11622	24560	38122	6.39	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10592	23514		0.63	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4090	17124		9.81	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds

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8494	21462	34878	0.53	4.8E+00	BF387909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8996	21852		5.16	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
289	13384	26311	2.03	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
290	13384	26311	1.69	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
3287	16341	29260	1.68	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8084	21001	34397	0.55	4.6E+00	U67569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9551	22513	35963	1.12	4.6E+00	BE646437.1	EST_HUMAN	7e88g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN. ; contains element PTR5 repetitive element ;
9551	22513	35964	1.12	4.6E+00	BE646437.1	EST_HUMAN	7e88g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN. ; contains element PTR5 repetitive element ;
10755	23677		0.6	4.6E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8047	20984		0.61	4.5E+00	AF126177.1	NT	Isosaccharin orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
11830	24811	39406	2.19	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
12055	24928	39526	1.67	4.5E+00	BF688841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3053	16110	29024	0.76	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3053	16110	29025	0.76	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
6326	19396		1.69	4.4E+00	X13414.1	NT	Murine I gene for MHC class II(a) associated invariant chain
6394	19482	32709	0.59	4.4E+00	AF156696.1	NT	Nicotiana tabacum inorganic phosphate transporter (PT1) mRNA, complete cds
6240	19313		0.71	4.3E+00	AF059678.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7672	20630	33994	3.53	4.3E+00	Y13402.1	NT	Plasmodium falciparum R23R+var1 gene, exon 1
7874	20818	34196	0.81	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
11210	24164	37694	7.01	4.3E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11279	24230		1.93	4.3E+00	11526311	NT	Homo sapiens DiGeorge syndrome critical region gene 2 (DGCR2), mRNA
5595	18691		3.57	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDF) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5675	18770	31842	1.35	4.2E+00	P61826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
5854	18945		0.58	4.2E+00	O27830	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
6938	20162	33483	1.69	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6938	20162	33484	1.69	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9371	22276	35708	5.1	4.2E+00	A1809013.1	EST_HUMAN	wf67g03.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2360692 3'
10218	23203	36688	1.1	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10508	23430		0.53	4.2E+00	P40886	SWISSPROT	HEXOSE TRANSPORTER HXT8

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6046	25652	32334	0.64	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
6046	25652	32335	0.64	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7319	20290	33633	0.76	4.1E+00	BE253688.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7420	20387	33738	0.55	4.1E+00	BF247939.1	EST_HUMAN	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069758 5'
7923	20866	34254	7.87	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
8061	20988		0.64	4.1E+00	AB041523.1	NT	Pallinoplecten yessoensis mRNA for calcineurin A, complete cds
8066	21002	34398	3.95	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8065	21002	34399	3.95	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8249	21218	34628	2.5	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9898	22851	36310	0.52	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
10031	22958	36426	2.43	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10669	23591		0.45	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10981	23901	37414	0.47	4.1E+00	O84242	SWISSPROT	3-OXOACYL-ACYL-CARRIER-PROTEIN[SYNTHASE III] (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
11231	24184		2.3	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVL1
11317	24287		13.22	4.1E+00	BE885880.1	EST_HUMAN	601607510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
3556	16602		0.7	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5534	20057	33361	0.94	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
5534	20057	33362	0.94	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7123	20057	33361	1.01	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7123	20057	33362	1.01	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7395	20363	33715	1.47	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9225	22191	35621	0.44	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10303	23228	38711	0.43	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10526	23448	35946	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10620	23542	37041	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10620	23542	37042	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11802	23957	37481	1.67	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11875	24757	38340	2.68	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN E); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11875	24757	38341	2.68	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3513	18559	28483	4.66	3.9E+00	XG4518.1	NT	N.tabacum chitinase gene 50 for class I chitinase C
4349	17376		0.96	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5741	18835	32015	2.98	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-105 BN0070 Homo sapiens cDNA
5741	18835	32016	2.98	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-105 BN0070 Homo sapiens cDNA
6791	19845	33129	0.95	3.9E+00	AF298209.1	NT	Dicystostellum discoides non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6848	19901	33195	0.87	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7057	20079	33388	4.24	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSP INTERGENIC REGION
7597	20548	33908	4.15	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8660	21628	35049	2.34	3.9E+00	XG5865.1	NT	X.laavis mRNA for M4 muscarinic receptor
11720	23917	37434	2.93	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11742	24827	38206	1.89	3.9E+00	AA681489.1	EST_HUMAN	nr18a12.s1 NC1_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416
2637	15636		1.27	3.8E+00	AE001592.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); Helicobacter pylori, strain J99 section 123 of the complete genome
6630	19693	32854	0.93	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
6937	20161	33482	0.59	3.8E+00	A1493549.1	EST_HUMAN	qz51f07.x1 NC1_CGAP_K111 Homo sapiens cDNA clone IMAGE:2030437 3'
8775	21742	35164	1.03	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
10154	23079		0.59	3.8E+00	AJ390061.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
12119	24989		15.21	3.8E+00	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
4049	17086	29982	9.75	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7372	20342		0.9	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9056	22022		0.49	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
8532	22495	35943	0.92	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11760	24698	39269	1.73	3.7E+00	BF69279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11760	24698	39270	1.73	3.7E+00	BF69279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
12266	25082		2.5	3.7E+00	AB013746.3	NT	Gallus gallus factor-1 alpha, complete cds
595	13692	28575	4.04	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5286	18292	31183	0.63	3.6E+00	Z89109.1	NT	Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940
5327	18433	31185	0.73	3.6E+00	BF316318.1	EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131018 5'
8897	21863	35285	0.93	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8897	21863	35286	0.93	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8892	21958	35383	4.21	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8892	21958	35384	4.21	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
10022	22949	36416	0.44	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
10022	22949	36417	0.44	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11200	24155		3.18	3.6E+00	M86795.1	NT	Escherichia coli glycerophosphate dehydrogenase (gipD) gene, partial cds; and the translation start site has been verified (gipe), the translation start site has been verified (gipG), and repressor protein (gipR) genes, complete cds
6115	18183		1.1	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6337	19408	32847	0.98	3.5E+00	R19745.1	EST_HUMAN	y40c08.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:34940 5'
8087	21023	34422	0.6	3.5E+00	P97608	SWISSPROT	6-OXOPROLINASE (6-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE)
8094	21030	34428	0.54	3.5E+00	AA982102.1	EST_HUMAN	d37f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618987 3' similar to gb:J04213
8124	21061	34459	0.56	3.5E+00	4505264	NT	CELLULAR RETINALDEHYDE-BINDING PROTEIN (HUMAN);
8829	21796		0.6	3.5E+00	P24557	SWISSPROT	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R) mRNA
9387	22352	35782	0.91	3.5E+00	AA190998.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9387	22352	35783	0.91	3.5E+00	AA190998.1	EST_HUMAN	z86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
9850	22788	36240	0.96	3.5E+00	AL161553.2	NT	z86b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
1514	14546	27517	5.3	3.4E+00	AF254577.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
6893	19945	33241	0.49	3.4E+00	U77617.1	NT	Brassica napus RP85d mRNA, complete cds
7586	20547	33907	2.99	3.4E+00	P04052	SWISSPROT	Chloranil-Aster yellows phytoplasma acetate kinase gene, complete cds
7668	20907	34298	0.9	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9025	21991		0.68	3.4E+00	U65408.1	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9428	22392	35831	0.73	3.4E+00	AJ229042.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNU1) gene, complete cds
9487	22431	35889	0.55	3.4E+00	AJ250567.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
10827	23549	37049	2.59	3.4E+00	AF013167.1	NT	Homo sapiens partial TMASf2 gene for tetraepanin protein, exon 6
							Saccharomyces cerevisiae MSS1 gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11861	24743	38327	2.86	3.4E+00	L77570.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
6186	19261	32496	1.03	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6186	19261	32497	1.03	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8225	21194	34601	0.9	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit ii gene, complete cds, and unknown genes
10830	23761	37250	0.9	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10830	23761	37251	0.9	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
501	13573	26495	1.85	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4056	13573	26495	0.89	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4759	17779	30874	1.35	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5648	18744	31910	1.2	3.2E+00	P64924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5648	18744	31911	1.2	3.2E+00	P64924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5683	18778	31950	2.79	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5683	18778	31951	2.79	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6439	19504	32754	1.66	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6439	19504	32755	1.66	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7863	20807	34185	0.71	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8052	20989	34388	2.47	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes
8052	20989	34387	2.47	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps8, ycf4, ycf3, rps18 genes
9385	22350		4.78	3.2E+00	P13061	SWISSPROT	PERIPLASMIC (NIFE) HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
8888	22841	36298	1.87	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (ILV1) gene, complete cds
10500	23422	36921	2	3.2E+00	AB015081.2	NT	Oryza latipes OIGC6 gene for guanylyl cyclase C, complete cds
12217	25055		2.84	3.2E+00	L33838.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5975	10060	32261	2.25	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7618	20578	33941	0.9	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7899	20938		1	3.1E+00	AF303226.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
8424	21393	34804	0.43	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8949	21915	35338	4.37	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE 1 5-DEIODINASE) (DIO1) (TYPE 1 D1) (5D1)
8949	21915	35339	4.37	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE 1 5-DEIODINASE) (DIO1) (TYPE 1 D1) (5D1)
							GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9814	22618		3.9	3.1E+00	Q14957	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9880	22633	36089	0.48	3.1E+00	Q01149	SWISSPROT	Chlorella vulgaris chloroplast, complete genome
10256	23181	36968	0.86	3.1E+00	7524759	NT	HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10347	23271		0.61	3.1E+00	Q10125	SWISSPROT	

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10700	23622	37118	5.2	3.1E+00	P49365	SWISSPROT	DEOXYHYPUISINE SYNTHASE (DHS)
11791	23946		1.95	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11811	24698		2.76	3.1E+00	S66860.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
2849	18909	28833	1.5	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5411	18514	31392	1.33	3.0E+00	X53056.1	NT	S.aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
6708	19764	33043	0.79	3.0E+00	X66037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6708	19764	33044	0.79	3.0E+00	X66037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7363	20333		9.66	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7402	20370		0.89	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9258	22224		1.21	3.0E+00	X67838.1	NT	B.napus DNA for myosinase
10667	23679	37076	0.54	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYL TRANSFERASE) (ADOMET SYNTHETASE)
11008	23973	37497	1.65	3.0E+00	Q16181	SWISSPROT	CDC10 PROTEIN HOMOLOG
11351	24301	37827	4.64	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
11351	24301	37828	4.64	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
2028	15046	28059	2.33	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 94 of the complete genome
6192	19268		0.6	2.9E+00	AB028033.1	NT	Bonapartia pediculus mitochondrial DNA for 16S ribosomal RNA
7094	20028	33332	1.97	2.9E+00	Z36879.1	NT	F.pirngel gdcSP gene for P-protein of the glycine cleavage system
7418	20385	33734	5.15	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7418	20385	33735	5.15	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7689	20647	34011	5.32	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN) STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2;
8200	21170	34580	0.61	2.9E+00	P05844	SWISSPROT	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8200	21170	34581	0.61	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2;
8434	21403	34816	0.82	2.9E+00	BF344171.1	EST HUMAN	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
1451	14484	27460	4.16	2.8E+00	AF186398.1	NT	602017413F1 NCL_OGAP_Brm64 Homo sapiens cDNA clone IMAGE:4153059 5'
							Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product

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1637	14669		2.57	2.8E+00	AL161652.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7529	20492	33854	4.93	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9972	22899		0.56	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC 63 Homo sapiens cDNA clone IMAGE:3684807 5'
11048	20492	33854	1.73	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
233	13333	26256	13.36	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
233	13333	26257	13.36	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
5631	18727	31888	1.11	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8485	21453		0.66	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
9319	22284		1.69	2.7E+00	AL119459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9787	21110	34510	0.64	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.x1 NCL_OGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17793
10866	23788		1.69	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4701	17722	30815	6.29	2.6E+00	AF068749.1	NT	CMD-BT0281-031199-087-P04 BT0281 Homo sapiens cDNA
5627	18723	31883	2.06	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5627	18723	31884	2.06	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5925	19011		3.9	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7603	26002		0.7	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7603	26002		0.7	2.6E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-5 genes
7987	20906		32.15	2.6E+00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8394	21363	34770	1.12	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
8394	21363	34771	1.12	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
10015	22842	36408	3.12	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10720	23642		1.61	2.6E+00	9055193	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12841	25877		2.58	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1460	14493	27466	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1460	14493	27467	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5911	18997	32186	2.32	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5911	18997	32187	2.32	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6001	18997	32186	1.49	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6001	18997	32187	1.49	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6992	19944	33240	0.66	2.5E+00	D30052.1	NT	Vibrio cholerae cba gene and cba8 gene for cholera toxins, complete cds
7960	20901	34293	0.55	2.5E+00	P17588	SWISSPROT	LATENCY-RELATED PROTEIN 1
8035	20972	34366	0.97	2.5E+00	AW094158.1	EST_HUMAN	QV4-FT0005-110500-205-q07 FT0005 Homo sapiens cDNA
8095	21031	34429	0.51	2.5E+00	4502802	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9459	22423	35861	1.49	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10211	23136	36523	0.73	2.5E+00	BE297766.1	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631090 5'
12214	25053		2.5	2.5E+00	AF289665.1	NT	Mus musculus E1F4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3026	16083	29006	1.1	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4944	17860	30851	5.31	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
6128	19204	32427	3.62	2.4E+00	P02843	SWISSPROT	VITELLOGENIN1 PRECURSOR (YOLK PROTEIN 1)
7606	20567	33927	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7608	20567	33928	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
8479	21448	34864	2.08	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8479	21448	34865	2.08	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8554	21522		2.92	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8998	21964		1.46	2.4E+00	AW875128.1	EST_HUMAN	RC2-PT0004-031299-011-005 PT0004 Homo sapiens cDNA
9180	22146	35573	9.52	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10398	23320	36803	2.34	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10398	23320	36804	2.34	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10466	23388	36882	2.1	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10604	23526		6.1	2.4E+00	P09090	SWISSPROT	XYLOLULOSE KINASE (XYLOLULOKINASE)
10685	23607	37100	1.87	2.4E+00	BE326702.1	EST_HUMAN	hr63106.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10685	23607	37101	1.67	2.4E+00	BE326702.1	EST_HUMAN	hr63106.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10955	23875	37389	1.14	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN N1RQ
11415	24359	37894	2.2	2.4E+00	Y14078.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFD operon and downstream
11517	24458		1.66	2.4E+00	AF096872.1	NT	Capra hircus alphaS2-casein type C gene, intron 15
11686	24652	38231	2.14	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1258	14283	27257	11.33	2.3E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4147	17178		1.45	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5934	19020		0.99	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYCABOXYPEPTIDASE
7687	20645	34009	2.42	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7653	26003		2.79	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
8059	20996	34392	1.12	2.3E+00	X60285.1	NT	M. mazel dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9465	22429	35868	0.54	2.3E+00	5833317	NT	Polyporus ornatiopsis mitochondrion, complete genome
9525	22488	36936	2.03	2.3E+00	Q11127	SWISSPROT	ALPHA(1-3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10958	23878	37390	0.45	2.3E+00	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
11153	24113	37638	7.84	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11897	24778	38364	1.59	2.3E+00	P45931	SWISSPROT	HYPOTHETICAL 171.0 KD PROTEIN IN SPOIIIC-CWLA INTERGENIC REGION
12072	24945	38539	2.34	2.3E+00	BF541987.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12072	24945	38540	2.34	2.3E+00	BF541987.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12443	25205	31828	6.31	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
13077	25609		1.3	2.3E+00	AF281862.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4046	17084	29981	1.42	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4342	17369	30251	3.8	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4342	17369	30252	3.8	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5415	18518	31395	11.02	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5415	18518	31398	11.02	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5953	19038	32234	1.83	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
5953	19038	32235	1.83	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
6180	19255	32488	8.78	2.2E+00	BE250383.1	EST_HUMAN	600843401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6489	19554	32804	3.91	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6750	19804	33085	3.14	2.2E+00	P51489	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7149	18381		3.5	2.2E+00	AA594574.1	EST_HUMAN	NI95b02 s1 NCL CGAP_C010 Homo sapiens cDNA clone IMAGE:566143 5'
7539	20502	33861	0.95	2.2E+00	AA137027.1	EST_HUMAN	NI95b02 s1 NCL CGAP_C010 Homo sapiens cDNA clone IMAGE:566143 5'
7865	20809	34187	18.24	2.2E+00	AA449012.1	EST_HUMAN	zn18704.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:786634 5'
7953	20894	34287	0.68	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8439	21408	34820	0.69	2.2E+00	BE301580.1	EST_HUMAN	b617h12x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8439	21408	34921	0.69	2.2E+00	BE301580.1	EST_HUMAN	b617h12x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9697	22650		11.22	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9927	25698		2.53	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413	23335	36819	1.57	2.2E+00	A1280373.1	EST_HUMAN	q9n9b03.x1 Soares_placenta_8tc9weeks_2Nb1P8b9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10413	23335	36820	1.57	2.2E+00	A1290373.1	EST_HUMAN	q9n9b03.x1 Soares_placenta_8tc9weeks_2Nb1P8b9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10456	23378	36871	2.22	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10822	23743	37244	3.06	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11768	23923	37442	3.23	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11937	24818	38415	6.31	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
571	15844	26555	12.39	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3601	16646		0.83	2.1E+00	AW449368.1	EST_HUMAN	UI-H-B18-akt-e-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6255	19328		0.86	2.1E+00	P76367	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6980	20203	33532	3.45	2.1E+00	O70159	SWISSPROT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7225	20247	33581	0.61	2.1E+00	4503430	NT	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7246	19981	33276	5.97	2.1E+00	N28575.1	EST_HUMAN	Y08a10.g1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
8842	21809		1.82	2.1E+00	AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1201	14240	27197	1.39	2.0E+00	AF180627.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1201	14240	27198	1.39	2.0E+00	AF180627.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1338	14372	27342	1.19	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
1578	14611		3.42	2.0E+00	P25882	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2159	15175	28195	4.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2159	15176	28196	4.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4127	17180	30048	2.24	2.0E+00	AW684496.1	EST_HUMAN	h13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
4127	17180	30049	2.24	2.0E+00	AW684496.1	EST_HUMAN	h13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7798	20750		0.85	2.0E+00	P07668	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
8358	21327	34738	3.84	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8358	21327	34739	3.84	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8358	21327	34740	3.84	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
9274	22240	35668	3.22	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
12766	28836	31427	4.52	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4829	17846	30746	0.98	1.9E+00	AF209488.1	NT	Danio rerio Rh50-like protein mRNA, complete cds
5679	18774	31945	4.52	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (ltp1), mRNA
5679	18774	31946	4.52	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (ltp1), mRNA
6219	19293	32527	1.05	1.9E+00	BE98695.1	EST_HUMAN	601879366F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6810	19884		1.19	1.9E+00	AW845689.1	EST_HUMAN	MRO-CT0063-071089-002-g02 CT0063 Homo sapiens cDNA
6912	19964		2.37	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8802	21769	35193	1.72	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8802	21769	35194	1.72	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8006	21972		3.6	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
9245	22211		1.52	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9988	22915	36380	0.53	1.9E+00	AA669125.1	EST_HUMAN	ab94804.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu
10928	23849	37364	0.63	1.9E+00	AF248289.1	NT	repetitive element/contains element L1 L1 repetitive element ;
3109	16166	29077	1.5	1.8E+00	P21004	SWISSPROT	Homo sapiens gag-pro-poi precursor protein gene, partial cds
3137	16194	29103	10.81	1.8E+00	U04356.1	NT	PROTEIN B8 PRECURSOR
3137	16194	29104	10.81	1.8E+00	U04356.1	NT	Synechococcus sp. FCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5987	19032		1.84	1.8E+00	P18502	SWISSPROT	Synechococcus sp. FCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6224	19298	32532	2.2	1.8E+00	BF31989.1	EST_HUMAN	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6538	19600		1.19	1.8E+00	BF683327.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6904	19956	33253	1.02	1.8E+00	BF305652.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
7260	19995	33292	1.07	1.8E+00	P21249	SWISSPROT	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7476	20442		0.7	1.8E+00	P27127	SWISSPROT	MAJOR ANTIGEN
8454	21423	34838	0.9	1.8E+00	P11369	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE- (GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8454	21423	34839	0.9	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8812	21779	35204	0.46	1.8E+00	P48634	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRIMIDIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8812	21779	35205	0.46	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35206	0.46	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9206	22172	35603	2.21	1.8E+00	O43281	SWISSPROT	EMBRONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9530	22493	35941	0.66	1.8E+00	R31042.1	EST_HUMAN	Yn72c08.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9617	22561	36009	0.64	1.8E+00	AW880004.1	EST_HUMAN	QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
10208	23133	36620	0.93	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10846	23568		2.88	1.8E+00	AF111849.1	NT	Homo sapiens PRO0830 mRNA, complete cds
10919	23839		0.75	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12563	25808		8.17	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12642	25328		5.63	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Atpclb), mRNA
1110	14154	27104	2.43	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2278	15292	28317	3.08	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2382	15390	28415	1.67	1.7E+00	AI141067.1	EST_HUMAN	oz43h03.x1 Sceres_NhiMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4487	17512	30400	0.8	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5694	18789	31980	1.66	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171299-127-c05 BT0282 Homo sapiens cDNA
5694	18789	31860	1.66	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171299-127-c05 BT0282 Homo sapiens cDNA
5955	19040	32238	0.49	1.7E+00	R58748.1	EST_HUMAN	G4846 Fetal heart Homo sapiens cDNA clone G4846 5' end
6133	19210	32436	3.14	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6703	19759	33038	0.59	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)
7428	20395	33746	1.01	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7428	20395	33747	1.01	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8187	21157	34566	0.81	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8367	21336	34748	1.21	1.7E+00	6755715	NT	Mus musculus T cell acute lymphocytic leukemia 1 (Tal1), mRNA
8397	21366	34775	0.54	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214669 5'
8887	21853	35273	0.45	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8974	21840		1.92	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
9052	22018	35442	0.51	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9052	22018	35443	0.51	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9166	22132	35558	0.43	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9504	25687	35909	2.37	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9504	25697	35910	2.37	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9665	22892		1.4	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10532	23454		0.5	1.7E+00	AW953681.1	EST_HUMAN	EST365751 MAOE resequences, MAGC Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12518	25249	31803	1.78	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.1
2049	15088	28088	14.89	1.6E+00	AF199339.1	NT	MSR1 repetitive element;
2059	15078	28097	3.29	1.6E+00	AF077374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2065	15083	28102	1.62	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2292	15304		1.33	1.6E+00	X98373.1	NT	Mus musculus ST6GalNAcII gene, exon 2
							B. napus gene encoding endo-polygalacturonase
2972	18030	28953	1.88	1.6E+00	W58428.1	EST_HUMAN	z25f01.1 Soares_fetal_heart_NH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
4063	17099		7.07	1.6E+00	BF570077.1	EST_HUMAN	gb:D28805 N-ACETYL-LACTOSAMINE SYNTHASE (HUMAN);
4378	17407	30287	1.29	1.6E+00	AF155827.1	NT	602186085T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4378	17407	30288	1.29	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5120	18130	31006	2.98	1.6E+00	Y11344.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5120	18130	31007	2.98	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5928	19012	32204	2.21	1.6E+00	L04908.1	NT	Mus musculus ST6GalNAcII gene, exon 2
6020	19103	32305	0.82	1.6E+00	AF005631.1	NT	Brachydanio rerio MHC class II DA-beta-2'01 gene, 3' end
6614	19872	32950	0.83	1.6E+00	BF380703.1	EST_HUMAN	Homo sapiens transglutaminase type I (Tgase) gene, promoter region
6888	19921	33217	0.97	1.6E+00	AW294881.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
7456	20422	33777	2.47	1.6E+00	BE697287.1	EST_HUMAN	UH-B12-ahr-B-04-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
8364	21333		1.1	1.6E+00	Q46378	SWISSPROT	RC0-CT0415-200700-032-ct10 CT0415 Homo sapiens cDNA
8722	21690	35117	3.42	1.6E+00	AJ297131.1	NT	VIRULENCE FACTOR MVIN HOMOLOG
9251	22217	35647	0.9	1.6E+00		NT	Mus musculus SIL, MAP_17, CYP_a, SOL & CYP_b genes
9251	22217	35648	0.9	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9815	25695	34540	1.54	1.6E+00	X52046.1	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9815	25695	34541	1.54	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9945	22872		0.48	1.6E+00	AF043466.1	NT	M.musculus COL3A1 gene for collagen alpha-1
10081	23017	36493	1.23	1.6E+00	T41290.1	EST_HUMAN	Thermoplasma ethanolicus D-xylose-binding protein (xyf) gene, complete cds
10506	23428	36925	0.48	1.6E+00	AF121361.1	NT	ph066_19/1TV Outward Alu-primed hcdNA library Homo sapiens cDNA clone ph066_19/1TV
10545	23467	36961	1.12	1.6E+00	AW835644.1	EST_HUMAN	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
10545	23467	36962	1.12	1.6E+00	AW835644.1	EST_HUMAN	QV4-L10016-090200-100-407 L10016 Homo sapiens cDNA
10709	23631	37126	0.78	1.6E+00	AF037352.1	NT	QV4-L10016-090200-100-407 L10016 Homo sapiens cDNA
11123	24083	37609	1.73	1.6E+00	P54817	SWISSPROT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11192	19103	32305	5.78	1.6E+00	AF005631.1	NT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
12017	24894	38491	2.83	1.6E+00	AF104313.1	NT	Homo sapiens transglutaminase type I (Tgase) gene, promoter region
						NT	Homo sapiens unknown mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
35	13155	26056	3.54	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
234	13334	26268	2.63	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome
622	13687		2.04	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2420	15427	26450	3.2	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2522	15525	26547	2.17	1.5E+00	6378350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3155	15427	26450	2.96	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3366	16435	26362	0.92	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5817	18907	32090	0.82	1.5E+00	AI655301.1	EST_HUMAN	HKF-1.;
5817	18907	32091	0.82	1.5E+00	AI655301.1	EST_HUMAN	HKF-1.;
6546	19607	32869	2.71	1.5E+00	R17879.1	EST_HUMAN	Y910602.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
7335	20306		1.48	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7368	20338	33688	16.72	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7368	20338	33689	16.72	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7568	20531	33890	0.6	1.5E+00	AA889289.1	EST_HUMAN	ak2610.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7850	20796	34172	0.73	1.5E+00	AI003254.1	EST_HUMAN	an07b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:595936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8144	21081		0.67	1.5E+00	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8459	21428	34945	0.91	1.5E+00	BE887446.1	EST_HUMAN	601505556F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8514	21482	34996	0.48	1.5E+00	AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8991	21957	35382	1.08	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
9370	22335		0.47	1.5E+00	AB038516.1	NT	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9489	22453	35693	0.55	1.5E+00	BF217818.1	EST_HUMAN	601862662F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4095135 5'
9838	22774	36229	0.91	1.5E+00	R81928.1	EST_HUMAN	y03h01.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9993	22920	36387	1.09	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-281099-008-d09 CT0192 Homo sapiens cDNA
10219	23144	36833	6.14	1.5E+00	BF376754.1	EST_HUMAN	RCO-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10412	23334		1.42	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCI_CGAP_Brr64 Homo sapiens cDNA clone IMAGE:4183865 5'
10556	23478	36972	2.92	1.5E+00	AA017693.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10556	23478	36973	2.92	1.5E+00	AA017693.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11727	24613	38190	5.98	1.5E+00	AL134197.1	EST_HUMAN	DKFZp647P243_s1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P243 3'
11869	24751		6.39	1.5E+00	X07380.1	NT	Malze mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
12112	24982	36583	1.53	1.5E+00	BE257562.1	EST_HUMAN	601109621F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350477 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12362	25151		1.87	1.5E+00	8753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
12510	25999	31420	1.51	1.5E+00	D63480.1	NT	Human mRNA for KIAA0148 gene, partial cds
12723	25376		4.94	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
12821	25443		1.33	1.5E+00		NT	Rattus norvegicus 5 - Lipoxigenase (Alox5), mRNA
32	13152	26052	1.41	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
32	13152	26053	1.41	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2285	15298		0.9	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (ghaA) gene, complete cds
2341	15351		8.77	1.4E+00	U67622.1	NT	Ovis aries prion protein gene, complete cds
2677	15673	28693	1.83	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2784	15776	28794	2.75	1.4E+00	AF064554.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2784	15776	28795	2.75	1.4E+00	AF064554.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3345	16396		0.63	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4284	17313	30191	1.38	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4284	17313	30192	1.38	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4590	16144	29056	0.92	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
4590	16144	29057	0.92	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
4615	17636		1.71	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5446	18648	31461	1.58	1.4E+00	AW054976.1	EST_HUMAN	wt45g07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5609	18702		5.52	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6410	19478	32725	3.06	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6427	25996		4.2	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6552	19813	32875	2.65	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6552	19813	32876	2.65	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6781	19836	33119	0.56	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
6781	19836	33120	0.56	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
6996	20122	33438	0.86	1.4E+00	AW693057.1	EST_HUMAN	CM3-NN0008-300300-132-b12 NN0008 Homo sapiens cDNA
7503	20468	33829	2.02	1.4E+00	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7521	20486	33848	1.15	1.4E+00	AW467760.1	EST_HUMAN	he23705.x1 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element;
7582	20544	33904	0.58	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7582	20544	33905	0.58	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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7611	20571	33935	0.66	1.4E+00	Q80905	SWISSPROT	MINOR CAPSID PROTEIN L2
8078	21646		0.6	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9146	22112		4.6	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9449	22413	35849	1.56	1.4E+00	R20459.1	EST_HUMAN	Y933F12.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5'
9552	22514	35965	3.46	1.4E+00	BE064667.1	EST_HUMAN	RC1-8T0313-301299-012-103 B10313 Homo sapiens cDNA
9587	22549	36000	0.45	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10568	23400	36982	0.89	1.4E+00	BF675545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10613	23535	37032	0.69	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10613	23535	37033	0.69	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10822	23812	37319	0.92	1.4E+00	D63441.1	NT	Pandorina clematis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10892	23812	37320	0.92	1.4E+00	D63441.1	NT	Pandorina clematis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11559	24499	38055	4.43	1.4E+00	AB006882.1	NT	Homo sapiens APOC2 mRNA for AIRE-1, complete cds
11733	24619	38196	2.83	1.4E+00	BE962107.2	EST_HUMAN	60165184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11733	24619	38197	2.83	1.4E+00	BE962107.2	EST_HUMAN	60165184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11756	24684	38263	2.16	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11756	24684	38264	2.16	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12360	25827		1.7	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
13068	25602		1.4	1.4E+00	7657624	NT	Homo sapiens slaufen (Drosophila, RNA-binding protein) homolog 2 (STAU2), mRNA
572	13641		1.66	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
903	13968	26915	3.12	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1131	14174		32.4	1.3E+00	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
1300	14336	27299	19.22	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1300	14336	27300	19.22	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1358	14393		0.89	1.3E+00	U61730.2	NT	Coix lacryma-jobi dihydroadipicinate synthase (dapA) gene, complete cds
1614	14646		2.69	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 86 of 85 of the complete genome
2255	15299		1.22	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2416	15422	28445	1.03	1.3E+00	P25391	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2567	15559		2.6	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916945 3'
2950	16007	28931	0.67	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3611	18656	29574	1.02	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P66), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5284	18290	31152	0.9	1.3E+00	AJ390500.1	NT	Candida albicans partial mRNA for ribonucleotide reductase large subunit (mr1 gene)
5592	18688	31657	1.08	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5794	18886	32067	0.52	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6063	19144	32355	0.54	1.3E+00	BF663825.1	EST_HUMAN	602145264F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309085 5'
6134	19211	32437	8.25	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-08 CT0289 Homo sapiens cDNA
6134	19211	32438	8.25	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-08 CT0289 Homo sapiens cDNA
6557	19617	32882	1.14	1.3E+00	M33496.1	NT	D melanogaster no-on-transient A gene product, complete cds
6914	19966		0.69	1.3E+00	Q00159	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6956	20181		0.54	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
7014	20140	33457	0.81	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7124	25673	33363	0.52	1.3E+00	AW821580.1	EST_HUMAN	IL2-ST0311-020200-040-G12 ST0311 Homo sapiens cDNA
7141	20117	33430	1.04	1.3E+00	BE536819.1	EST_HUMAN	6010617420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
							TCBAP-ID0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylon-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7307	20278	33616	0.8	1.3E+00	BE243571.1	EST_HUMAN	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
7691	20849	34013	0.72	1.3E+00	P24540	SWISSPROT	Sus scrofa plp gene
8041	21609	35032	1.09	1.3E+00	AJ009912.1	NT	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
8790	21757	35178	2.29	1.3E+00	BE963379.2	EST_HUMAN	601650250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3960592 3'
8907	21873	35289	0.87	1.3E+00	BE974280.1	EST_HUMAN	Homo sapiens GL004 protein (GL004), mRNA
9059	22025		1.68	1.3E+00	6910247	NT	wo85607.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9142	22108	35534	0.92	1.3E+00	A1927629.1	EST_HUMAN	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9873	22828		4.88	1.3E+00	AF042084.1	NT	S.alba phr-1 mRNA for photolase
9882	22835	36288	2.2	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolase
9882	22835	36289	2.2	1.3E+00	X72019.1	NT	Homo sapiens lipoygenase (ALOX12B) mRNA, complete cds
9882	22909	36374	1.02	1.3E+00	AF059250.1	NT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
10029	22956	36424	1.57	1.3E+00	Q00754	SWISSPROT	ALPHA-MANNOSIDASE (LAMAN)
10108	23034	36511	1.32	1.3E+00	A1827629.1	EST_HUMAN	wo85607.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
10185	23110	36593	0.83	1.3E+00	AJ223982.1	NT	Lactobacillus lactis cremoris NCDO-hv1 chromosomal inversion junction DNA
10185	23110	36594	0.83	1.3E+00	AJ223982.1	NT	Lactobacillus lactis cremoris NCDO-hv1 chromosomal inversion junction DNA
10235	23450	36689	3.75	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10286	23211			0.64	1.3E+00	EST_HUMAN	ig77at12.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb.X14723
10509	23431	36927	0.45	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10509	23431	36928	0.45	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10574	23498	36989	1.24	1.3E+00	AE004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10591	23513	37006	1.53	1.3E+00	M29953.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10948	23868		0.85	1.3E+00	AL163302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10975	23895	37409	0.49	1.3E+00	AI990846.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
10987	23907		0.43	1.3E+00	8923637	NT	ws32a10.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN
11052	24015		3.63	1.3E+00	Q14117	SWISSPROT	Q16881 THIOREDUXIN REDUCTASE
11252	24205	37727	2.35	1.3E+00	P25299	SWISSPROT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
11273	24225	37751	1.71	1.3E+00	Z18892.2	NT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11667	24749	38331	2.61	1.3E+00	D42042.1	NT	MRNA 3'-END PROCESSING PROTEIN RNA15
11945	24925	38420	2.1	1.3E+00	Z98692.1	NT	Mus musculus desmin gene
12001	24878		1.55	1.3E+00	L31891.1	NT	Human mRNA for KIAA0085 gene, partial cds
12498	25239		3.37	1.3E+00	AF187873.1	NT	Bacillus subtilis genomic DNA 23.9kB fragment
12669	25344	31762	6.47	1.3E+00	BF348043.1	EST_HUMAN	Arabidopsis thaliana 3-ketacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12679	25724		3.24	1.3E+00	P33464	SWISSPROT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12765	25407		1.68	1.3E+00	AF187035.1	NT	602023185F1 NCI CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158452 5'
651	13717	26639	13.29	1.2E+00	AA676246.1	EST_HUMAN	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
824	13882	26833	1.37	1.2E+00	P06228	SWISSPROT	Stumma illium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
824	13882	26834	1.37	1.2E+00	P05228	SWISSPROT	z22d08.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
824	13882	26835	1.37	1.2E+00	P06228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
879	13934		0.95	1.2E+00	8924234	NT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
1166	14206	27160	7.4	1.2E+00	AF080245.2	NT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
1210	14248	27206	1.43	1.2E+00	AJ252242.1	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1210	14248	27207	1.43	1.2E+00	AJ252242.1	NT	Homo sapiens sesquiterpene synthase mRNA, complete cds
2025	15045	28058	1.06	1.2E+00	AF140631.1	NT	pea seed-borne mosaic virus complete genome
3127	16194	28063	0.99	1.2E+00	AB020681.1	NT	pea seed-borne mosaic virus complete genome
3179	16234	28151	6.14	1.2E+00	AL161563.2	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16234	28152	6.14	1.2E+00	AL161563.2	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3299	16352		3.07	1.2E+00	P54910	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3357	16417	28343	0.78	1.2E+00	AF188740.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
							CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
							Homo sapiens LHX3 gene, intron 2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3725	16767	29878	8.46	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4012	17051	29957	1.76	1.2E+00	BF373570.1	EST_HUMAN	MRQ-F10175-050900-203-q06_1 F10175 Homo sapiens cDNA
4327	16417	29343	1.09	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, Intron 2
4498	17523		2.12	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4551	17574	30464	1.33	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4592	17613	30507	2.1	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4619	17640		6.6	1.2E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
5052	18064	30942	2.36	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5052	18064	30943	2.36	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5052	18064	30944	2.36	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5512	18612	31544	1.06	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5634	18730	31892	1.89	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5894	18982		0.57	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
5974	19059	32260	0.78	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6276	19348	32590	2.39	1.2E+00	X74895.1	NT	D.hydryl repeat cluster DNA, fragment D
6338	19407	32848	4.12	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0080-270400-190-a03 BN0080 Homo sapiens cDNA
6423	19490	32741	1.41	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
6423	19490	32742	1.41	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
6467	19532	32780	38.6	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.e1 Soeres_testis_NHT Homo sapiens cDNA clone 1322374 3'
6575	19635	32901	0.6	1.2E+00	N33295.1	EST_HUMAN	y39b12.e1 Soeres_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273599 3' similar to gb U87935 HUMAAALU472 Human carcinoma cell-derived Alu RNA transcript, (fRNA); gb J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6650	19708	32984	0.71	1.2E+00	P17671	SWISSPROT	ECYSONE-INDUCIBLE PROTEIN E75-A
6654	19711	32988	2.01	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7100	20034	33337	1.17	1.2E+00	AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7113	20047	33349	2.68	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7465	20431		0.64	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7670	25685	33934	1.64	1.2E+00	AV734595.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
7912	20855	34243	2.6	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
8122	21059	34457	0.53	1.2E+00	BE767646.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8915	21881	35307	3.24	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
9010	21976	35396	0.65	1.2E+00	P38427	SWISSPROT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9228	22104		0.58	1.2E+00	7708271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
9380	22345	35777	1.88	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-c07 CT0222 Homo sapiens cDNA
9594	22556	36008	0.47	1.2E+00	H48599.1	EST_HUMAN	yc60a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202066 5'
9753	22694	36150	3.63	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9954	22891	36353	1.71	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
10291	23216	36700	3.52	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10689	23611		0.73	1.2E+00	AB009666.1	NT	Homo sapiens klotho gene, exon 1
11674	24640	38219	1.89	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
11713	24676		7.68	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11785	23940	37462	2.59	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12466	25799	31524	18.09	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12487	25232		2.7	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
464	13537	26463	1.43	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1777	14808	27782	1.97	1.1E+00	AW095393.1	EST_HUMAN	QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1915	14939	27938	1.08	1.1E+00	AW575889.1	EST_HUMAN	UJHF-BR0p-ajk-f02-Q-U1.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3341	16392	29313	7.34	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3341	16392	29314	7.34	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3498	16545	29471	0.79	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3593	16638	29558					wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1;
3731	16773	29584	3.34	1.1E+00	AI808360.1	EST_HUMAN	
3731	16773	29584	1.52	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3731	16773	29585	1.52	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3831	16871		0.86	1.1E+00	X85374.1	NT	H. parahaemolyticus hphM(A), hphM(C), hphR and menB genes
3964	17004	28918	0.87	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4050	17087	29083	1.02	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4243	17272		6.78	1.1E+00	5935331	NT	R. unicornis complete mitochondrial genome
5028	18042	30925	3.15	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5085	18095	30971	3.91	1.1E+00	U34740.1	NT	Emeticella nidulans sterigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcE), (stcF), (stcI), (stcJ), (stcK), (stcL), (stcO), (stcQ), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds
5109	18119	30893	1.04	1.1E+00	X78425.1	NT	E. faecalis pbp5 gene
5259	18276	31139	0.9	1.1E+00	6680080	NT	Homo sapiens putative GR6 protein (GR6), mRNA
5380	18484	31359	1.53	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5695	18790	31961	13.39	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5715	18809	31087	0.99	1.1E+00	AI138582.1	EST_HUMAN	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6211	19285	32517	1.93	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6405	19473	32721	0.94	1.1E+00	AF197661.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6547	19608	32870	0.83	1.1E+00	R06037.1	EST_HUMAN	ye89c03.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
6876	19929	33226	1.21	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7468	20434		0.68	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7514	20479	33840	0.82	1.1E+00	X55981.1	NT	Maize mRNA for enolase (2-phospho-D-glycerate hydratase)
7732	20687	34050	1.83	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7732	20687	34051	1.83	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7754	20707	34076	8.13	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7833	25691	34158	0.84	1.1E+00	11967960	NT	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8470	21439	34857	2.95	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8563	21531	34951	0.73	1.1E+00	AI476339.1	EST_HUMAN	hm39h11.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
9089	22055	35479	0.63	1.1E+00	AB003088.1	NT	Acetabularia calliculus mitochondrial COXI-like gene
9167	22133	35559	1.42	1.1E+00	S80750.1	NT	VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
9278	22244	35673	0.45	1.1E+00	AI079946.1	EST_HUMAN	oz34f05.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9792	22115		0.84	1.1E+00	BE384976.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9886	22913	36378	0.95	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
10040	22967		0.69	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
10130	23056	36534	0.95	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaf, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10192	23117	36601	1.38	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
10287	23222	36706	5.56	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10357	23281	36757	20.52	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10867	23787	37287	1.09	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10959	23909	37422	0.63	1.1E+00	BF343644.1	EST_HUMAN	602014488F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150508 5'
10989	23909	37423	0.63	1.1E+00	BF343644.1	EST_HUMAN	602014488F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150508 5'
11012	23977	37502	2.03	1.1E+00	11087364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
11094	24027		3.83	1.1E+00	AF068942.1	NT	Klebsormidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11435	18340		4.65	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11439	24382	37921	3.12	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11439	24382	37922	3.12	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11683	24849	38227	3.44	1.1E+00	AB006599.1	EST_HUMAN	wf76e11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2361648 3'
12439	25202		3.12	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12539	25263	31807	1.55	1.1E+00	AF216696.1	NT	Taenia solium immunogenic protein Ta78 mRNA, partial cds
12661	25798		2.26	1.1E+00	AF234169.1	NT	Dicystosellum discoideum isopenicillin N pyrophosphate isomerase (Dipi) mRNA, complete cds
98	13215		1.55	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	13224	28148	1.68	1.0E+00	D89425.1	NT	Cavia cobaya mRNA for cerine/threonine kinase, complete cds
418	13491		3.03	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
578	13647	28560	2.22	1.0E+00	AJ251660.1	NT	Giardia liguria mRNA for homeodomain transcription factor (so gene)
678	13741	28688	6.74	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
679	13742		1.35	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1386	15868		3.53	1.0E+00	X80416.1	NT	V. carter Algal-CAM mRNA
1771	14800	27786	0.97	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, complete cds
2493	15496	28521	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2493	15496	28522	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2887	15946	28861	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2887	15946	28862	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2978	16038		0.81	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3212	16287	29190	1.08	1.0E+00	AA628453.1	EST_HUMAN	af28g08.s1 Soares_tetris_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3613	13215		0.93	1.0E+00	U23808.1	NT	WP:C42D8.3 CE04204 ; contains element MER22 MER22 repetitive element ;
3693	16736	29649	1.33	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
4097	17131	30024	1.16	1.0E+00	AF223391.1	NT	Agaricus bisporus mRNA for tyrosinase
4304	17333		0.73	1.0E+00	8922245	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4843	17890	30755	1.54	1.0E+00	AL163247.2	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5083	18085		0.9	1.0E+00	D10852.1	NT	Homo sapiens chromosome 21 segment HS21C047
							Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5354	18459	31328	3.23	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5949	19035	32228	5.05	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5949	19035	32229	5.05	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6057	19148	32360	1.44	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6238	19309	32541	4.52	1.0E+00	P04501	SWISSPROT	FIBRIN PROTEIN
6243	19318	32546	1.77	1.0E+00	AW452782.1	EST_HUMAN	U1H-B19-4b-4-09-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6637	19895	32972	2.12	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6691	19748	33025	0.68	1.0E+00	AF104869.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6786	19841		0.98	1.0E+00	P46506	SWISSPROT	SRB-11 PROTEIN
6813	19867	33155	0.71	1.0E+00	BE797718.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6813	19867	33156	0.71	1.0E+00	BE797718.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6944	20168	33491	1.17	1.0E+00	Y11204.1	NT	V. carteri gene encoding volvoxopsin
7033	18365	31252	0.64	1.0E+00	U63721.1	NT	Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds
7345	20316	33661	1	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7719	20876		8.7	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7979	20918	34309	1.52	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7997	20936	34330	6.07	1.0E+00	AA775191.1	EST_HUMAN	ac78b08.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:868791 3'
8165	21103		0.57	1.0E+00	BF679213.1	EST_HUMAN	602153792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8294	21263	34673	1.49	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8294	21263	34674	1.49	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8481	18065		1.22	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8693	21661	35084	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8693	21661	35085	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8821	21788		0.83	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8855	21822	35242	0.44	1.0E+00	Q9V5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8855	21822	35243	0.44	1.0E+00	Q9V5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8883	25696		2.37	1.0E+00	BE147931.1	EST_HUMAN	RC1-H10229-181099-011-006 HT0228 Homo sapiens cDNA
8923	21889	35316	0.89	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
9076	22041	35464	1.55	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9626	22570	36019	2.14	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9838	22772	36227	1.25	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9838	22772	36228	1.25	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9969	22896	36359	1.94	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK Homo sapiens cDNA clone GKCCYA11 5'
9974	22901	36364	1.23	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9974	22901	36365	1.23	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
10212	23137	36624	0.56	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10212	23137	36625	0.56	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10471	23393	36889	0.72	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10471	23393	36890	0.72	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10564	23486	36980	0.68	1.0E+00	A1077920.1	EST_HUMAN	cy15d07.a1 Soares_senescent_fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10690	23612	37106	3.7	1.0E+00	AV758925.1	EST_HUMAN	AV758925 BM Homo sapiens cDNA clone BMFAW C04 5'
10842	23762	37262	20.08	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.f1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10842	23762	37263	20.08	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.f1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10876	23766	37297	1.18	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
12048	18459	31328	1.66	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
12327	25129		3.28	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12650	25333		2.49	1.0E+00	AW976184.1	EST_HUMAN	EST388293 IMAGE resouces, MAGN Homo sapiens cDNA
1575	14608	27580	3.22	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1575	14608	27581	3.22	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2645	15842	28666	1	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3619	16663		1.1	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5717	18811	31690	8.92	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5869	19054	32254	0.79	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9916	22560		1.4	9.9E-01	U66667.1	NT	Lycopodium esculentum putative Mit copy 1 nematode-resistance gene
9913	22734		3.02	9.9E-01	Q26642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
11069	24032	37556	1.48	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
524	13595	26513	1.12	9.9E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL-GLUTAMATE SYNTHASE) (AGS) (NAGS)
2305	15317		1.28	9.8E-01	AJ003108.1	NT	Caillitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2813	15805		1.29	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
7406	20374	33725	4.12	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7406	20374	33726	4.12	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7907	20850	34236	0.99	9.8E-01	BF034016.1	EST_HUMAN	601458337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
7907	20850	34237	0.99	9.8E-01	BF034016.1	EST_HUMAN	601458337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
9069	22035	35458	0.88	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10804	23725		0.53	9.8E-01	AA925565.1	EST_HUMAN	cd55d04.a1 NCJ CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11339	24289	37813	2.06	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11339	24289	37814	2.06	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12545	26268		1.41	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cez2/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDH1 protein (CDM), adrenoleukodystrophy protein >
7368	20336	33686	2.3	9.7E-01	U28716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8948	21816	35235	1.81	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8854	21821	35241	1.33	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
11505	24447	38589	3.87	9.7E-01	BF511209.1	EST_HUMAN	U1H-B14-ec1-e-07-Q-UJ.st NCJ CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3085140 3'
12117	24987	38589	2.29	9.7E-01	U87514.1	NT	Dictyostellum discoideum CAR3 gene, promoter region
4486	17511	30399	1.68	9.6E-01	AW769674.1	EST_HUMAN	PM2-JM0053-240300-005-112 JM0053 Homo sapiens cDNA
5179	18168	31065	0.9	9.6E-01	7662375	NT	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
5847	18937	32121	3.85	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5847	18937	32122	3.85	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6910	19902	33259	0.57	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6
8735	21703		1.21	9.6E-01	X93275.1	NT	Pfalcepanium complete gene map of plastid-like DNA (IR-A)
9203	22169	35599	0.51	9.6E-01	U81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9446	22410	35847	0.44	9.6E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
11848	24731	38317	3.04	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NP2 Homo sapiens cDNA clone NPDBAG08 5'
11848	24731	38318	3.04	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NP2 Homo sapiens cDNA clone NPDBAG08 5'
12223	25060		2.19	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12839	25874	31416	3.03	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2484	15488	28512	1.03	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3796	16836	29741	2.39	9.5E-01	BE902340.1	EST_HUMAN	601875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3796	16836	29742	2.39	9.5E-01	BE902340.1	EST_HUMAN	601875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8354	22319	35745	0.68	9.5E-01	AI190162.1	EST_HUMAN	qd57d07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
8481	22425	35853	1.1	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 CT0295 Homo sapiens cDNA
11674	24512	38089	1.5	9.5E-01	BF218771.1	EST_HUMAN	601985163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11780	23935	37456	1.52	9.5E-01	AW293799.1	EST_HUMAN	UI-H-B12-ahp-f-03-0-J1-s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3214	16289		3.77	9.4E-01	AF165990.1	NT	Barionella claridgeae RNA polymerase beta subunit (rpbB) gene, partial cds
3231	16286		1.93	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9217	22183	35616	0.69	9.4E-01	M90724.1	NT	Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4
12480	25235		2.09	9.4E-01	BE781251.1	EST_HUMAN	601468703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'
12838	25790		1.93	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1745	14774		1.34	9.3E-01	AF242382.1	NT	Homo sapiens phyenoyl-CoA hydroxylase (PHYH) gene, exon 5
2641	15639	28663	1.01	9.3E-01	BE071172.1	EST_HUMAN	RC9-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4066	17102	29993	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4066	17102	29994	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5873	18768	31940	1.47	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5761	18854	32034	3.92	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7554	20517		0.76	9.3E-01	AF270648.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8402	21371	34779	1.75	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1365357
9165	22131		0.95	9.3E-01	AF091981.1	NT	Xenopus laevis CCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9289	22255	35685	0.91	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12853	25528	31713	1.34	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12665	25634		3.20	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3253	16307	29231	3.14	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5808	18898		1.73	9.2E-01	7106410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6101	19180	32389	4.04	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
6789	19843	33127	0.51	9.2E-01	M64703.1	NT	N.crassa vef1A-mRNA synthetase (cyt-20/un-3) gene
10018	22945	36412	0.77	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
10105	23031	36509	1.21	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10628	23550	37050	3.42	9.2E-01	11430863	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10780	23701	37199	1.84	9.2E-01	BF683251.1	EST_HUMAN	7c58e06.x1 NCI_CGAP_KK111 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
12031	24907	38501	1.54	9.2E-01	BF132402.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
1628	14662	27638	2.31	9.1E-01	T98875.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
2134	15151		2.06	9.1E-01	8823056	NT	ye52701.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2582	15583	28602	1.12	9.1E-01	AF062919.1	NT	Alu repetitive element;
3218	16273	29195	1.11	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3218	16273	29196	1.11	9.1E-01	T26418.1	EST_HUMAN	Pseudomonas fluorescens DNA polymerase III (dnaE) gene, complete cds
6291	18363	32602	1.68	9.1E-01	L36033.1	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6555	19712	32989	2.94	9.1E-01	Q61704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7827	20775	34152	16.4	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
8011	20949	34342	2.68	9.1E-01	U72695.1	NT	gb71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
10336	23458	36955	0.45	9.1E-01	P38432	SWISSPROT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12580	25987		10.31	9.1E-01	AF050113.1	NT	P80-COILIN
4406	17434	30319	1.77	9.0E-01	AF099810.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
7622	20582	33946	0.65	9.0E-01	L42547.1	NT	Homo sapiens neurexin II-alpha gene, partial cds
7652	20612		1.32	9.0E-01	D38621.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
9704	22657	36112	0.55	9.0E-01	AF086761.1	NT	Xenopus laevis gene for aldolase, complete cds
10189	23114	36598	0.44	9.0E-01	U39702.1	NT	Danio rerio semaphorin Z1a mRNA, complete cds
						NT	Mycoplasma genitalium section 24 of 51 of the complete genome
5781	18873	32054	2.37	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
6377	19445		1.28	8.9E-01	XG0986.1	NT	Rabbit MHC fragment RLA-DF DNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6605	25663	32837	0.69	8.9E-01	BF217839.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6605	25663	32838	0.69	8.9E-01	BF217839.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
7408	20375		0.54	8.9E-01	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
8563	21521		0.43	8.9E-01	AF260228.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8769	21736	35157	1.09	8.9E-01	AF259667.1	NT	Oithona nana cytochrome-c oxidase subunit 1 (cox) gene, partial cds; mitochondrial gene for mitochondrial product
12074	24946	38541	2.99	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12420	25190		5.46	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4573	17595	30489	1.58	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5238	18246	31118	0.9	8.8E-01	L41684.1	NT	Trypanosoma brucei microtubule-associated protein (MAP16) mRNA, 3' end of cds
5447	18549	31462	0.7	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
11418	24362	37897	2.31	8.8E-01	Z28337.1	NT	Maeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12082	24954	38549	6.51	8.8E-01	AA808055.1	EST_HUMAN	cc38h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element; contains element MER22 repetitive element
12237	25952		2.3	8.8E-01	D90911.1	NT	Synochocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
465	13538	26464	1.78	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2411	15418	28442	0.91	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2885	15944	28859	5.42	8.7E-01	AA595863.1	EST_HUMAN	nn08f11.s1 NCL_CGAP_P74.1 Homo sapiens cDNA clone IMAGE:1076877
5043	18056		2.78	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and pulp
5247	18265	31125	0.97	8.7E-01	BF219306.1	EST_HUMAN	601883175F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065378 5'
8374	21343	34754	0.65	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9282	22248	35677	0.71	8.7E-01	A1239456.1	EST_HUMAN	qh35e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9282	22248	35678	0.71	8.7E-01	A1239456.1	EST_HUMAN	qh35e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
10065	23021	36496	1.32	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
11181	24137	37669	4.66	8.7E-01	BF363970.1	EST_HUMAN	QVQ-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12042	24917	38512	3.97	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12042	24917	38513	3.97	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
475	13547		2.65	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
859	13915	26874	4.32	8.6E-01	W69089.1	EST_HUMAN	zd44e03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2278	15291	28316	1	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3635	16678	29592	0.87	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3813	18853	29760	1.38	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5207	18218	31091	2.6	8.6E-01	BE147609.1	EST_HUMAN	RC1-HT0228-160300-019-c05 HT0228 Homo sapiens cDNA
6001	19084	32283	7.79	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6001	19084	32284	7.79	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6515	25661	32835	0.54	8.6E-01	S76772.1	NT	polyprotein [Coxsackie B4 virus CB4, host=mouse, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6867	19020	33215	1.7	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6867	19020	33216	1.7	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7770	20723		0.81	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8260	21229		1.29	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 121/4
8377	21346	34787	0.51	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
10044	22971		0.46	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12798	25717		1.44	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6888	19840	33236	1.5	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7768	20721	34093	2.49	8.5E-01	BE542812.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8323	21292	34708	0.42	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8761	21728	35150	0.93	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8761	21728	35151	0.93	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8849	21816	35236	0.57	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10715	23637	37129	1.35	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10715	23637	37130	1.35	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12565	25869		2.25	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP1), mRNA
12572	26283		1.37	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4782	17802	30893	0.85	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome
5571	25641	31827	2.68	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5571	25641	31828	2.68	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
6107	21044	34443	0.51	8.4E-01	AF051142.1	NT	Manes brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10317	23241		3.25	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
12005	24882	30478	1.54	8.4E-01	M55884.1	NT	Human collagenase type IV (Cl.G4) gene, exon 4
743	13804	26743	3.01	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3111	16188	28078	3.15	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3823	16803	29767	0.83	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4040	17078	29978	3.15	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5341	18446	31199	2.42	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10028	22955		4.53	8.3E-01	A1791952.1	EST_HUMAN	nm011212.y5 NCL CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
10469	23391	36886	1.1	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10579	23501	36983	3.97	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
11033	23997	37524	2.97	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
11050	24013		1.92	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11634	24571	38135	2.22	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2068	15085	28103	2.24	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2101	15118		1.08	8.2E-01	AF145880.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2688	15684		1.06	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
3918	16958	29871	0.75	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
3940	16980	29895	0.92	8.2E-01	AF063417.1	NT	Tanystylum orbiculare elongation factor 1-alpha mRNA, partial cds
6900	19854	33139	0.57	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrat-1 protein
6900	19854	33140	0.57	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrat-1 protein
6941	20165	33488	0.85	8.2E-01	AJ010142.1	NT	Ananias muscaria mRNA for SCII25 protein
7082	20103	33414	3.69	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7484	25682	33807	4.38	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8787	21754	35176	0.68	8.2E-01	BE263145.1	EST_HUMAN	801144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10385	23307	36785	0.68	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
10419	23341	36827	1.59	8.2E-01	AF052659.1	NT	Homo sapiens thiodioxin-related protein mRNA, complete cds
10583	23505	36998	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10583	23505	36999	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10751	23673	37169	3.84	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10751	23673	37170	3.84	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11957	24836	38432	2.97	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
12038	24913	38507	4.82	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12043	24918	38514	6.1	8.2E-01	H87398.1	EST_HUMAN	yy14d02.1 Scars_placenta_8tc9weeks_2NbrHP809W Homo sapiens cDNA clone IMAGE:262195 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
12586	25290	31781	2.98	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2769	15761		1.48	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3472	16518	29439	3.67	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3472	16518	29440	3.87	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
5792	18884	32068	0.51	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6448	19513	32763	0.84	8.1E-01	U16790.1	NT	(MELANOCORTIN-1 RECEPTOR) (MC1-R)
6777	19832	33114	2.47	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6777	19832	33115	2.47	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7755	20708	34077	0.55	8.1E-01	O47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
							CYTCHROME B
8243	21212	34618	1.12	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylose-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8243	21212	34619	1.12	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylose-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8956	21922	35349	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8956	21922	35350	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
							xx01h03.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE.2692469.3 similar to SW:LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN; contains MER22.b1 PTR5 repetitive element
9122	22088	35516	1.13	8.1E-01	AW242647.1	EST_HUMAN	PROBABLE E4 PROTEIN
10484	23406	35902	0.84	8.1E-01	P06425	SWISSPROT	KK9872F Human fetal heart; Lambda ZAP Express Homo sapiens cDNA clone KK9872.5 similar to
10776	23697	37195	0.42	8.1E-01	N84541.1	EST_HUMAN	EST(CLONE C-0PE11)
11812	24897	38277	4.05	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11812	24897	38278	4.05	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12298	25109	31839	1.73	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
178	13279		3.32	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 15
288	13383	26310	5.97	8.0E-01	AJ132772.1	NT	Bos taurus tub and rlf genes
2951	15070		1.72	8.0E-01	BF630962.1	EST_HUMAN	602072473F1 NCI CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4215091.5
3093	16151	29055	1.41	8.0E-01	AF127897.1	NT	Samitri bolivensis olfactory receptor (SBO27) gene, partial cds
3324	16375	29296	1.3	8.0E-01	AB008193.1	NT	Mus musculus gene for olfactory glycoprotein, complete cds
3717	16760		2.36	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 717
4563	17566	30478	6.45	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
8322	21291		2.31	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
8870	21837	35289	1.05	8.0E-01	Y11095.1	NT	Rice st/pe virus RNA 3
11303	24253	37779	1.58	8.0E-01	Q92793	SWISSPROT	CREB-BINDING PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
454	13527	26457	0.78	7.9E-01	D11478.1	NT	Lymantia dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
716	13778		0.78	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 69 of the complete genome
1609	14641		23.05	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1663	14895		1.28	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2272	15285	28311	7.38	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2273	15286	28312	2.36	7.9E-01	AF130459.1	NT	Danio rerio Ttp4-associated protein Ttp4 (tpp1A) mRNA, complete cds
3528	16574	29497	3	7.9E-01	AF228564.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4330	17358		0.88	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635785 5'
4842	17663	30551	1.15	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4842	17663	30552	1.15	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
							Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
5244	18252	31123	1.03	7.9E-01	AF228843.1	NT	Human mRNA for prostacyclin synthase, complete cds
6479	19344	32792	0.76	7.9E-01	D38145.1	NT	P. sativum GR gene
8446	21415	34828	3.37	7.9E-01	X60996.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9905	22857	36319	4.3	7.9E-01	U01912.1	NT	SMALL HYDROPHOBIC PROTEIN
10409	23331	36816	4.3	7.9E-01	P19719	SWISSPROT	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
10451	23373	36864	0.82	7.9E-01	AV700860.1	EST_HUMAN	
10877	23797	37298	0.82	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
11350	24300		2.81	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11546	24487	38041	2.22	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
877	13932		1.86	7.9E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2283	15296	28320	6.12	7.9E-01	AW995957.1	EST_HUMAN	EST371637 MAGF resequences, MAGF Homo sapiens cDNA
4730	17750	30842	1.33	7.9E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5076	18085		0.8	7.9E-01	AW753353.1	EST_HUMAN	RC3-C70254-130100-023-c02 CT0254 Homo sapiens cDNA
6187	19262	32498	2.5	7.9E-01	AF115858.1	NT	Shenodon punctatus alpha endolase mRNA, partial cds
6344	19413	32555	1.04	7.9E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6608	19664	32939	0.72	7.9E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8836	21803	35221	1.29	7.9E-01	BF108927.1	EST_HUMAN	7154d05.x1 Soares NSF F8 9W OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9588	22551	36002	1.34	7.9E-01	Y10159.1	NT	D.discoideum racGAP gene
9887	22840	36087	0.52	7.9E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10483	23405		1.01	7.9E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12559	25948		2.32	7.8E-01	L29280.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
145	13248	26177	6.69	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
727	13788		3.26	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aalpha) and major histocompatibility protein class II beta chain (Ebeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-1b
2724	15718	28736	2	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3368	16418		0.76	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA
3814	18558	29578	3.83	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4425	17452	30343	3.04	7.7E-01	AF189488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4426	17452	30344	3.04	7.7E-01	AF189488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5640	18738	31889	1.25	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5640	18736	31900	1.25	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6068	19147	32359	0.53	7.7E-01	R08600.1	EST_HUMAN	yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
10204	23129	36616	0.72	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12447	25207		5.53	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
6218	19292	32526	4.49	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6218	19292	32526	4.49	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6667	19724	32899	0.65	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
7029	18361	31248	0.98	7.6E-01	A1253399.1	EST_HUMAN	ac14b12x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7029	18361	31282	0.98	7.6E-01	A1253399.1	EST_HUMAN	ac14b12x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7252	19987	33285	0.89	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-tetrolxin receptor mRNA, complete cds
8400	21369	34778	1.33	7.6E-01	AF146783.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8464	21433	34849	1.92	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8464	21433	34850	1.92	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8668	21636	35058	0.43	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8668	21636	35059	0.43	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9318	22283	35714	1.01	7.6E-01	8753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9634	22578	36028	5.25	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9634	22578	36028	5.25	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11885	24651	38228	2.09	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11885	24651	38228	2.09	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12020	24897	38230	3.05	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25045		3.8	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
514	13585		1.87	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
586	13654	26568	1.01	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7764	20717	34080	0.78	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12516	25247		4.53	7.5E-01	AF163151.2	NT	Homo sapiens derlin sialophosphoprotein precursor (DSPP) gene, complete cds
13027	25575	31697	1.57	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1132	14175	27124	1.35	7.4E-01	AI598146.1	EST_HUMAN	tn14b09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
2350	15359	28381	0.93	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3739	16781	29683	18.81	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
3919	16959	29872	2.01	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4340	17367	30250	6.99	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8176	21146	34553	1.04	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8176	21146	34554	1.04	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8980	21946	35370	0.78	7.4E-01	BF346266.1	EST_HUMAN	802018459F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154340 5'
9063	22028		0.84	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9452	22416	35854	7.09	7.4E-01	BE747503.1	EST_HUMAN	601573025F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9511	22474	35918	1.14	7.4E-01	AA187988.1	EST_HUMAN	zp87h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW-TCPO_MOUSE P42932 T-COMPLEX PROTEIN 1, THE TA SUBUNIT ;
10767	23688	37185	0.74	7.4E-01	11424933	NT	Homo sapiens NY-RN-45 antigen (LOC51133), mRNA
12171	25021		4.46	7.4E-01	8753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12284	25101		1.54	7.4E-01	A1472641.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
3999	17038		0.64	7.3E-01	AP000062.1	NT	Aeropyrum pernix genome DNA, section 57
4647	17668	30555	0.97	7.3E-01	AE001168.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4728	17749	30641	4.57	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5135	18144	31024	1.18	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6761	19815	33084	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6761	19815	33095	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7301	25879	33608	0.92	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7692	20650	34014	0.53	7.3E-01	Z14133.1	NT	D melanogaster Cdc mRNA for clathrin heavy chain
7794	20746	34119	7.46	7.3E-01	M26511.1	NT	V. alginolyticus sucrose (scrB) gene, complete cds
7794	20746	34120	7.46	7.3E-01	M26511.1	NT	V. alginolyticus sucrose (scrB) gene, complete cds
8115	21052	34450	0.51	7.3E-01	U34631.1	NT	Mus musculus alpha-4 integrin gene, exon 7
11759	24887	38287	3.11	7.3E-01	AA678019.1	EST_HUMAN	2125008.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11759	24887	38288	3.11	7.3E-01	AA678018.1	EST_HUMAN	2125008.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
832	13889		2.03	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1974	14995	27997	3.23	7.2E-01	X79140.1	NT	N. tabacum Nelf-4A13 mRNA
2468	15472	28495	1.91	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3080	16137	29048	1.47	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3467	16513	29434	2.44	7.2E-01	AF065608.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
4803	17620	30714	2.89	7.2E-01	D90314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5159	18168	31046	1.57	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
5159	18168	31047	1.57	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
7421	20388	33739	0.78	7.2E-01	U69633.1	NT	Solenum tuberosum cold-stress inducible protein (C17) gene, complete cds
8797	21764	35196	1.24	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9314	22279		0.52	7.2E-01	AF743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10705	23627	37123	2.59	7.2E-01	BF070061.1	EST_HUMAN	802118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
11091	24051	37574	3.38	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12523	18343	31291	1.43	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (Dva) mRNA, complete cds
12700	25360		5.56	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
683	13755	26685	13.3	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RYA1), complete cds
3075	16132	29045	13.21	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4236	17265	30151	3.29	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4236	17265	30152	3.29	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6058	19139	32350	1.55	7.1E-01	BF681034.1	EST_HUMAN	602155439F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6058	19139	32351	1.55	7.1E-01	BF681034.1	EST_HUMAN	602155439F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7137	20113	33426	6.92	7.1E-01	U96232.1	NT	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pt) gene, complete cds
8533	21501	34918	0.48	7.1E-01	H54244.1	EST_HUMAN	yc99d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202961 3'
9088	22054	35477	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0867-301299-011-d09 BT0867 Homo sapiens cDNA
9088	22054	35478	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0867-301299-011-d09 BT0867 Homo sapiens cDNA
10214	23139	36628	1.28	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10774	23695	37193	1.13	7.1E-01	M12981.1	NT	Human T-cell receptor gamma-chain J2 gene
12499	25773		2.34	7.1E-01	AA421492.1	EST_HUMAN	zu08h11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1233	14270	27229	1.13	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
1233	14270	27230	1.13	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
2455	15460	28482	1.09	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2455	15460	28483	1.09	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5096	18106		2.11	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6082	19143		0.95	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8721	21889		8.51	7.0E-01	AE000263.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9871	22824	36077	0.52	7.0E-01	U53868.1	NT	Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
9871	22824	36078	0.52	7.0E-01	U53868.1	NT	Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
11454	24397	37943	1.71	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11454	24397	37944	1.71	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13035	25811	31528	1.35	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
971	14023	26976	12.59	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
971	14023	26977	12.59	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1313	14349	27315	2.22	6.9E-01	AA593530.1	EST_HUMAN	nc28a09.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3233	16288	29210	1.8	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5249	18257	31126	0.92	6.9E-01	AV714502.1	EST_HUMAN	AV714502 DCB Homo sapiens cDNA clone DOBATO12 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5878	18967	32158	0.8	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BNA3 mRNA for notochord actin, complete cds
6104	19183	32402	0.55	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6508	19570	32822	1.5	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
8312	21281	34692	3.39	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8312	21281	34693	3.39	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8526	22489		0.73	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (alphase) gene, partial cds
10053	22980	36447	0.55	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10053	22980	36448	0.55	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11587	24525	38081	2.03	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11587	24525	38082	2.03	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12145	25766		3.91	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL-14)
958	14011	26964	1.52	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2682	15678		1.26	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2840	14851	27627	1.5	6.8E-01	AA854475.1	EST_HUMAN	aj75a05.s1 Soares parathyroid tumor NbhHPA Homo sapiens cDNA clone IMAGE:14022568 3' similar to gb:X56411.mat ALCOHOL DEHYDROGENASE CLASS II PL CHAIN (HUMAN);
4802	17623	30516	1.75	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
9996	22923	36388	1.67	6.8E-01	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11424	24368	37903	1.77	6.8E-01	AJ276675.1	NT	Siagonospora avenae bg1 gene for beta-glucosidase, exons 1-4
11424	24368	37904	1.77	6.8E-01	AJ276675.1	NT	Siagonospora avenae bg1 gene for beta-glucosidase, exons 1-4
11450	24393	37939	1.82	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11450	24393	37939	1.82	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11931	24812	38407	1.49	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11931	24812	38408	1.49	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
298	13392	26320	25.45	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
339	13428	26350	28.03	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1927	14951		1.07	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2157	15173	28192	1.79	6.7E-01	AA451864.1	EST_HUMAN	z12g12.s1 Soares total_fetus_Nb2-Hf8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2176	15886	28213	2.65	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3009	18067	28987	3.96	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4481	17506	30395	0.78	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
5002	18016	30803	0.97	6.7E-01	AW079110.1	EST_HUMAN	xa59g12.x1 NCLCGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3'
5587	18683	31651	0.7	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5587	18683	31652	0.7	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6073	19154	32366	0.93	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6456	18521	32771	1.26	6.7E-01	9535035	NT	Gallid herpesvirus 2, complete genome
6456	18521	32772	1.28	6.7E-01	9535035	NT	Gallid herpesvirus 2, complete genome
7537	20500		4.57	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PAO1, section 167 of 528 of the complete genome
7563	20526	33884	0.98	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10503	23425		0.82	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11300	24250	37776	2.62	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010800-197-c03 HT0769 Homo sapiens cDNA
11787	23942	37484	3.23	6.7E-01	O14357	SWISSPROT	N-ACETYL-GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
11869	24847	38444	1.82	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' and
2509	15512	28538	1.92	6.8E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2711	15705	28721	1.4	6.8E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3501	16548	29474	1.41	6.8E-01	4508880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3670	18713	29628	4.37	6.8E-01	Y07669.1	NT	Calicans random DNA marker, 282bp
4136	17168						Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5258	18266	31134	1.13	6.8E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
5282	18288	31130	0.95	6.8E-01	Z82002.1	NT	S.pneumoniae pcpB and pcpC genes
5282	18288	31151	0.95	6.8E-01	Z82002.1	NT	S.pneumoniae pcpB and pcpC genes
6466	19531	32779	3.83	6.8E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7949	20890	34281	3.57	6.8E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
8912	21878	35304	0.58	6.8E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
10023	22950		1.56	6.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12748	25305	31758	1.76	6.6E-01	AE004382.1	NT	Vbfo chloerae chromosome II, section 39 of 93 of the complete chromosome
624	13689	28608	0.96	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
624	13689	28607	0.96	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3446	16493	29412	4.63	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4311	17340	30220	4.28	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5102	18112	30984	3.71	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5204	18213	31088	1.13	6.5E-01	Z70628.1	NT	H.sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71)
5518	25940	31551	2.13	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
5802	18894	32077	0.58	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6887	19339	33234	1.24	6.5E-01	D88348.1	NT	Chicken mRNA for 116-kDa melanosomal matrix protein, complete cds
7841	20788	34163	0.84	6.5E-01	X04769.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7930	20873	34262	0.89	6.5E-01	A1799882.1	EST_HUMAN	wc48a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321642 3'
10197	23122		1.03	6.5E-01	T76904.1	EST_HUMAN	yd21b04.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108847 3'
10699	23621	37117	2.2	6.5E-01	AF118876.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10997	23963	37487	2.19	6.5E-01	H87583.1	EST_HUMAN	yw17f06.r1 Soares placenta_8to8weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:252515 5'
11045	24009	37535	2.88	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
11143	24103		3.43	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11925	24806	38399	2.3	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit iii, cytochrome c oxidase subunit i, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
11970	24848	38445	1.47	6.5E-01	AF146987.1	NT	Fugu rubripes U2 small nuclear ribonucleoprotein auxiliary factor subunit-related protein (U2AF1-RS2), 19 kDa Golgi adaptor protein adaptin (AP19), and phosphorylase kinase alpha 2 subunit (PHKA2) genes, complete cds; kelch protein (KELCH1) and kelch p>
12130	24999	38604	1.61	6.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 76
12554	25276		2.55	6.5E-01	BE465050.1	EST_HUMAN	nv74e10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
252	13349	26275	10.51	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3470	16516	29437	3.26	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3875	16914	28823	1.34	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4518	17544	30430	0.89	6.4E-01	Y12488.1	NT	M.musculus whn gene
4519	17544	30431	0.89	6.4E-01	Y12488.1	NT	M.musculus whn gene
5192	18201	31073	1	6.4E-01	H85337.1	EST_HUMAN	ys90e03.r1 Soares retina N2b5f-R Homo sapiens cDNA clone IMAGE:222086 5'
8960	21926	35353	1.57	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10449	23371	36863	6.94	6.4E-01	U92828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10464	23386	36879	1.18	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
12666	25342		5.76	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGC09 5'
434	13508	26442	3.27	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
536	19607	26525	2.19	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2171	15187	28208	3.4	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2583	15584	28603	2.72	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2583	15584	28604	2.72	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3029	16087		0.8	6.3E-01	Y17275.1	NT	Lycopodium obscurum p89a gene, complete CDS
6182	19257	32490	0.87	6.3E-01	BE093906.1	EST_HUMAN	PMO-BT0757-010500-002-e05 BT0757 Homo sapiens cDNA
6753	19807	33088	1.07	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6753	19807	33089	1.07	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
8866	21833		3.17	6.3E-01	BE02044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
9238	22204	35636	0.8	6.3E-01	S62927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9376	22537	35999	0.74	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102598 5'
9775	22716	36171	2.86	6.3E-01	9627521	NT	Varicella Virus, complete genome
9775	22716	36172	2.86	6.3E-01	9627521	NT	Varicella Virus, complete genome
10298	23223		0.63	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10792	23713	37215	1.55	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10895	23815	37322	0.96	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
11400	24345	37878	1.52	6.3E-01	AA877715.1	EST_HUMAN	nt09h06.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 O02916 HLARK.
11663	24599	38173	6.95	6.3E-01	AI904160.1	EST_HUMAN	CM-BT043-090299-046 BT043 Homo sapiens cDNA
11754	24682	38281	1.79	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11915	24798	38387	2.09	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12258	25928	31306	5.44	6.3E-01	9910293	NT	Mus musculus teratin complex 2, gene 5g (K12-5g), mRNA
12359	25149		1.81	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12570	25845		3.19	6.3E-01	X83528.1	NT	C. limicola pscD gene
5970	19055	32255	2.37	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.6 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7737	20692		2.75	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7791	25690	34117	1.12	6.2E-01	AL021127.2	NT	Mus musculus chromosome X configa; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase
8644	21612	35034	5.41	6.2E-01	U72255.1	EST_HUMAN	and Zinc finger protein 185
							ys01e08.s1 Soares fetal liver spleen 1NFUS Homo sapiens cDNA clone IMAGE:213542 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9208	22174	36805	0.54	6.2E-01	AF034441.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds, and dehydroquinase dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9804	21127	34531	1.87	6.2E-01	BE562687.1	EST_HUMAN	601338146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9868	22804		2.17	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
10438	23360	36849	7.04	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10902	23822	37332	5.32	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10902	23822	37333	5.32	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2404	15411		5.9	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5614	18710	31868	1.3	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CcMyoD (h1h-1) alternatively spliced genes, complete cds
7053	20075	33382	3.54	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7053	20075	33383	3.54	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7216	20238	33572	0.7	8.1E-01	AW105653.1	EST_HUMAN	xc50h03.x1 NCLCGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12671_jmet HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7312	20283	33624	0.64	6.1E-01	Q63769	SWISSPROT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8676	21543	34963	3.66	6.1E-01	AF033535.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9147	22113	35537	1.17	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9147	22113	35538	1.17	6.1E-01	11431065	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9770	22711	36165	23.08	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9770	22711	36166	23.08	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10202	23127	36613	0.99	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
10406	23328	36812	1.53	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11306	24256		1.91	6.1E-01	X74507.1	NT	P. sativum mdh mRNA for chloroplast malate dehydrogenase (NADP+)
12041	24916	38510	1.63	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12041	24916	38511	1.63	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12355	25731	31615	2.77	6.1E-01	AB041350.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
495	13567	26490	1.41	6.0E-01	D87675.1	NT	Homo sapiens DNA for anyfold precursor protein, complete cds
563	13633		2.75	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1354	14398	27369	1.92	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3828	16868	28770	0.9	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71

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4217	17246		1.61	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
4279	17308	30187	0.89	6.0E-01	AB025319.1	NT	Yaba monkey tumor virus DNA, BamH1 restriction fragment E, M and partial C, partial and complete cds
5353	18468	31327	2.14	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5514	18614	31547	2.22	6.0E-01	AW139713.1	EST_HUMAN	U1-HB1-eeb-a-10-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6889	19746	33022	2.68	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6818	19872	33181	0.67	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
6988	20211	33539	0.78	6.0E-01	L10234.1	NT	(CDW136) (CD136 ANTIGEN)
6988	20211	33540	0.78	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7577	20539	33898	5.51	6.0E-01	AJ277661.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
8461	21430	34847	4.55	6.0E-01	P02835	SWISSPROT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8461	21430	34848	4.55	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10182	23107	36589	1.84	6.0E-01	AB008193.1	NT	SEGMENTATION PROTEIN FUSHI TARAZU
10638	23558		1.66	6.0E-01	Q01497	SWISSPROT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10749	23871		0.48	6.0E-01	BE837779.1	EST_HUMAN	PEROXISOMAL MEMBRANE PROTEIN PERO (PEROXIN-3)
11878	24760	38345	2.79	6.0E-01	AI420623.1	EST_HUMAN	RC2-FN0094-180700-017-d08 FN0094 Homo sapiens cDNA
12638	25322	31788	1.87	6.0E-01	11421863	NT	f08f07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095621 3'
12731	25384		2.78	6.0E-01	AA706087.1	EST_HUMAN	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12918	25777	31522	4.71	6.0E-01	9055303	NT	z196g05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:482776 3'
12947	25715		3.4	6.0E-01	BE157617.1	EST_HUMAN	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
1002	14053	27005	0.97	5.9E-01	U32701.1	NT	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
3283	16337	29256	4.95	5.9E-01	AL163287.2	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3283	16337	29257	4.95	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4260	17279		4.09	5.9E-01	AF162756.1	NT	Homo sapiens chromosome 21 segment HS21C067
6609	19667	32943	1.45	5.9E-01	AF065440.2	NT	Rattus norvegicus connexin 2 mRNA, partial cds
7481	20447	33803	2.44	5.9E-01	AB023486.1	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
8332	21301	34718	0.46	5.9E-01	D90911.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
8985	21951	35375	0.48	5.9E-01	D12622.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
9901	22853	36314	0.89	5.9E-01	AF063204.2	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
							Chlamydia trachomatis strain KUW31/Cx major outer membrane protein (omp1) gene, complete cds

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10273	23188		0.66	5.9E-01	P06493	SWISSPROT	E6 PROTEIN
10548	23470	36965	1.19	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
11031	23995	37523	2.46	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
11037	24001	37526	49.8	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11309	24259	37785	2.49	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
11528	24467	38021	1.53	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/El CD48 antigen (Cd48) gene, partial cds
12297	25108	31838	2.43	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-lysozyme (alpha 1 AT) gene, promoter region
12541	25264		2.88	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12740	25390		6.24	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1924	14948	27944	1.28	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
2571	15572	28592	1	5.8E-01	7305230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4009	17048	29954	1	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4542	17565	30452	4.23	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
5448	18550		0.84	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5609	18705	31862	0.75	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6308	19379	32618	1.82	5.8E-01	D78669.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-500E06 5'
8445	19510	32760	0.73	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6985	20208		2.56	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8219	21188		2.63	5.8E-01	H41571.1	EST_HUMAN	yn91b03.s1 Soares adult brain N2b5HB56Y Homo sapiens cDNA clone IMAGE:176757 3' similar to
8423	21392	34802	0.59	5.8E-01	A1280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8423	21392	34803	0.59	5.8E-01	A1280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8532	21500	34916	2.57	5.8E-01	P14328	SWISSPROT	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8532	21500	34917	2.57	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
9243	22209	35640	9.77	5.8E-01	AJ270774.1	SWISSPROT	SPORE COAT PROTEIN SP96
9323	22288	35718	1.02	5.8E-01	Q27368	SWISSPROT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9324	22289	35719	0.48	5.8E-01	Q20471	SWISSPROT	TRANSCRIPTION FACTOR E2F
9354	22851		0.81	5.8E-01	BF031606.1	EST_HUMAN	PUTATIVE CASEIN KINASE 1F46F2.2 IN CHROMOSOME X
11334	24284	37808	6.9	5.8E-01	AJ243213.1	NT	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11373	24320		2.69	5.8E-01	BF700092.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11476	24419		1.61	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
1492	14525	27456	1.11	5.7E-01	P08727	SWISSPROT	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
1492	14525	27497	1.11	5.7E-01	P08727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3056	16113		0.77	6.7E-01	6755253	NT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
							Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3237	18282	28214	1.38	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3515	18561		2.79	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3922	18682	29875	1.05	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S72.B1S1) mRNA, partial cds
5213	18222	31097	11.22	5.7E-01	4505050	NT	Homo sapiens lymphocyte antigen 6 complex, locus H (LY6H) mRNA
6490	19555	32805	4.36	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6889	19922	33218	0.82	5.7E-01	AA194201.1	EST_HUMAN	z38cd6.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7042	18374	31262	1.3	5.7E-01	AL111440.1	NT	Bovylis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8041	20878	34374	2.13	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8303	21272		0.51	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc8 genes, alternative transcripts
8723	21691		0.52	5.7E-01	AI065061.1	EST_HUMAN	HA0895 Human fetal liver cDNA library Homo sapiens cDNA
10159	23084	36560	1.22	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10169	23084	36561	1.22	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10940	23860	37376	0.75	5.7E-01	BF940982.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
12252	25078		1.49	5.7E-01	BE116051.1	EST_HUMAN	MR3-H70736-180700-003-a02 HT0736 Homo sapiens cDNA
1889	14914	27807	1.6	5.6E-01	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
1889	14914	27808	1.8	5.6E-01	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
3376	16426	29351	1.53	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3376	16426	29352	1.63	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4268	17297	30174	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
5205	18214	31089	0.93	5.6E-01	BF032377.1	EST_HUMAN	601452855F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856717 5'
9155	22121	36550	14.66	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9155	22121	35551	14.66	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9730	22758	36211	1.23	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25011		3.4	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
12270	25092	38178	1.73	5.6E-01	AA463535.1	EST_HUMAN	ng76g10.s1 NCI_CGAP_P6 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element
12636	18341	31280	1.51	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12662	25340		3.05	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13060	25596		4.95	5.6E-01	BF973829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
13110	25830		1.33	5.6E-01	AA863881.1	EST_HUMAN	ae74b04.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:989871 3'
1216	14254	27212	0.82	5.6E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2712	15708	28722	5.31	5.6E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2712	15706	28723	5.31	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2929	15987	28908	0.78	5.6E-01	E902085	NT	Homo sapiens superkiller viral activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3079	16136		1.48	5.6E-01	H48219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N255HB5Y Homo sapiens cDNA clone IMAGE:178266 3'
3248	16303	29227	4.75	5.5E-01	AF227240.1	EST	Rabbit oral papillomavirus, complete genome
3704	16747	29661	2.24	5.6E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
5209	18218	31094	1.08	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain BclA-DIB1 gene, partial cds
7467	20433	33789	0.58	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7467	20433	33780	0.58	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7504	20469		0.67	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8762	21759	35181	0.66	5.5E-01	A1791768.1	EST_HUMAN	cr2a201.y3 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
10125	23051		0.69	5.5E-01	U88416.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10743	23865	37180	0.87	5.5E-01	T05047.1	EST_HUMAN	EST02835 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCQ35
146	13249	26178	9.02	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
146	13249	26179	9.02	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
587	13655	26589	1.34	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsIA (gsIA) genes, complete cds; and unknown genes
587	13655	26570	1.34	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsIA (gsIA) genes, complete cds; and unknown genes
1278	14311	27272	2.99	5.4E-01	AW86087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2116	15133		2.81	5.4E-01	AE002247.2	NT	Chlamydomonas reinhardtii AR39, section 74 of 94 of the complete genome
2265	15279	28304	2.28	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15.15' beta carotene dioxygenase (beta-diox gene)
5740	18834	32014	0.91	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6315	19366	32628	0.8	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7226	20248	33592	0.77	5.4E-01	BE968592.2	EST_HUMAN	60160276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7558	20521	33877	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7558	20521	33878	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7560	20523	33981	1.78	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10349	23273		1.93	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11414	24358	37893	2.19	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11652	24859	38159	1.82	5.4E-01	AW373694.1	EST_HUMAN	QV4-BT0636-271299-059-r04 BT0636 Homo sapiens cDNA
11941	24821	38416	3.29	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11941	24821	38417	3.29	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
12215	25054		3.88	5.4E-01	A1856398.1	EST_HUMAN	w87g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
517	13588	26508	1.86	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2150	15166	28182	0.97	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2160	15166	28183	0.97	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2794	15786	28803	8.62	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2794	15786	28804	8.62	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3257	16311	29232	3.25	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (SLCCL) gene, complete cds
4239	17268		1.33	5.3E-01	U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5533	18631	31569	2.06	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5533	18631	31570	2.06	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5533	18729	31890	0.76	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.r1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5533	18729	31891	0.76	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.r1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5729	18923	32003	2	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5729	18923	32004	2	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9255	22221		1.94	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
9307	22272	35703	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
9307	22272	35704	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;

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10572	23494	36986	0.74	5.3E-01	A1954210.1	EST_HUMAN	w94b02.x1 NCL_OGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
10977	23997	37410	0.7	5.3E-01	11428833	NT	Homo sapiens nucleoprotein 214kd (CAIN) (NUP214), mRNA
11886	24787	38354	5.19	5.3E-01	BE568291.1	EST_HUMAN	601339667F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
12144	25776		4.97	5.3E-01	AA916053.1	EST_HUMAN	og30e05.s1 NCL_OGAP_B7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
817	13875	26823	16.24	5.2E-01	L20770.1	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN); Drosophila melanogaster helix-loop-helix mRNA, complete cds
1168	14209	27163	7.88	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1195	14235	27190	3.01	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1903	14927		3.19	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2156	15172	28191	2.36	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3136	16193	29102	1.57	5.2E-01	U65942.1	NT	Chlamydomonas abortus strain S20/3 POMP91A and POMP90A precursor, genes, complete cds
3251	16306		1.14	5.2E-01	D73443.1	NT	Azobacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
3416	16464		1.39	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3458	16504	29424	2.72	5.2E-01	AA984165.1	EST_HUMAN	am77g05.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3648	16691		1	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5180	18189		1.04	5.2E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5736	18930	32008	1.02	5.2E-01	AA284261.1	EST_HUMAN	zc44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
10088	25700	36489	0.84	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10088	25700	36480	0.84	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10292	23217	36701	0.52	5.2E-01	AA194518.1	EST_HUMAN	zq05b09.r1 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5'
10387	23309	36787	1.76	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13031	25578		6.62	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
619	13694	26602	2.34	5.1E-01	M58609.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
649	13715	26636	3.53	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
649	13716	26637	3.53	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
1660	14692		1.28	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
4103	17137	30032	4.81	5.1E-01	AI859495.1	EST_HUMAN	w39b12.x1 NCL_OGAP_UH Homo sapiens cDNA clone IMAGE:2427263 3'
4216	17245	30130	2.99	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6348	19417	32658	0.57	5.1E-01	BE541068.1	EST_HUMAN	601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6407	19475		0.83	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAU07 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7102	20036	33339	1.52	5.1E-01	R80873.1	EST_HUMAN	y94409.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148872 3'
8918	21884	35309	0.82	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8918	21884	35310	0.82	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
10043	22970	36437	4.3	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
10048	22973	36440	3.2	5.1E-01	W22302.1	EST_HUMAN	55B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
10521	23443	36941	0.89	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12264	25088	38174	2.09	5.1E-01	BF40777.1	EST_HUMAN	602087471F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068744 5'
12368	25709		2.47	5.1E-01	BF030207.1	EST_HUMAN	60156663F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828767 5'
12811	25310		3.82	5.1E-01	BF439882.1	EST_HUMAN	nae5110.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element;
2144	15161	28176	0.97	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2144	15161	28177	0.97	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2154	15170	28187	2.39	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2154	15170	28188	2.39	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2172	15188		0.91	5.0E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3761	16802	29714	0.8	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3842	16882	29786	1	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3887	16927	29835	2.74	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6801	19855		0.84	5.0E-01	BF576189.1	EST_HUMAN	602132842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7928	20869	34256	0.66	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7928	20869	34257	0.66	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8876	21842		1.87	5.0E-01	M82304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8918	21884	35404	0.59	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9813	21136	34638	3.18	5.0E-01	BF917212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136832 5'
9883	22910	36375	1.31	5.0E-01	P35573	SWISSPROT	GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9883	22910	36376	1.31	5.0E-01	P35573	SWISSPROT	GLYCOTEN DEBRANCHING ENZYME (GLYCOTEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10756	23678		1.38	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
12302	25113		6.28	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13004	26658		2.21	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13011	25593		5.8	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
790	13849	26798	2.03	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1668	14700	27676	2.37	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1921	14945	27941	0.99	4.9E-01	U40869.1	NT	Caixa porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5480	18580	31491	1.43	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6153	19228	32457	2.67	4.9E-01	AF020631.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6153	19228	32458	2.67	4.9E-01	AF020631.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7685	20843	34007	1.69	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7672	20911	34301	0.7	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYL-GLUCOSAMINYLTRANSFERASE
7972	20911	34302	0.7	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYL-GLUCOSAMINYLTRANSFERASE
9341	22306		1.77	4.9E-01	BF209781.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102850 5'
9542	22505	35954	0.89	4.9E-01	AW333905.1	EST_HUMAN	hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:O95714
9551	26009		2.64	4.9E-01	10948663	NT	O95714 HERC2.1
10881	23603	37097	0.86	4.9E-01	AF053980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10888	23608	37314	0.57	4.9E-01	X90000.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12186	25041		1.41	4.9E-01	AF176912.1	NT	H. sapiens DNA for BCL7A gene and BCL7A/IGH locus fusion
12997	25063		6.43	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
5585	18881	31849	8.83	4.8E-01	J02987.1	NT	ng22e11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
6336	19889	33184	0.69	4.8E-01	U92882.1	NT	Saccharomyces cerevisiae sporulation protein (SP011) gene required for meiotic recombination, complete cds
6946	19899		3.82	4.8E-01	AA656878.1	EST_HUMAN	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
7338	20501		1.98	4.8E-01	5031650	NT	nu85f09.s1 NCL_CGAP_AW1 Homo sapiens cDNA clone IMAGE:1217513
7928	20872	34261	0.78	4.8E-01	AL163209.2	NT	Homo sapiens reproduction 8 (D8S2288E) mRNA
8037	20974	34369	3.56	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21C009
8037	20974	34370	3.56	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8237	21206	34611	0.98	4.8E-01	A1820744.1	EST_HUMAN	yf77f10.y5 Soares breast 2Nbl-Hst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element
9500	22504		0.97	4.8E-01	BE155148.1	EST_HUMAN	MER6 repetitive element ;
10368	23291		0.56	4.8E-01	BF568633.1	EST_HUMAN	PM1-HT0350-201299-004-b04 HT0350 Homo sapiens cDNA
11081	24043		1.75	4.8E-01	X83502.1	NT	602184287F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
						NT	S. cerevisiae ORFs from chromosome X

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12277	25098		1.65	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12503	25737		3.32	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
13088	25788		1.49	4.8E-01	AJ132984.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8
6864	18721	32996	8.88	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7241	19876	33273	0.92	4.7E-01	A1204374.1	EST_HUMAN	q172a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
8187	21167	34577	0.59	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8187	21167	34578	0.59	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9430	22394	35834	0.57	4.7E-01	6981501	NT	Rattus norvegicus Spermlne binding protein (Sbp), mRNA
11193	24148		4.78	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
11422	24366	37801	1.78	4.7E-01	U41069.1	NT	Human collagen alpha2(X) (COL11A2) gene, exons 6 through 16, and partial cds
11613	24551	38111	1.74	4.7E-01	BF529658.1	EST_HUMAN	602043389F1 NCL_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4181303 5'
11704	24669	38246	1.49	4.7E-01	AW899448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12999	25173		1.53	4.7E-01	BE887763.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912483 5'
12929	25513		1.38	4.7E-01	BF679515.1	EST_HUMAN	602153926F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294974 5'
3756	18798	29709	1.53	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3156	16798	29710	1.53	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5180	18198		0.93	4.6E-01	M11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5493	18593	31503	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5493	18593	31504	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5548	18645	31586	3.33	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5548	18645	31587	3.33	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5825	18721	31880	1.85	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5839	18735	31887	3.12	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5839	18735	31898	3.12	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5847	18743	31909	1.46	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5730	18824		0.85	4.6E-01	AF212124.1	NT	Anolis schwartzi cytochrome b gene, partial cds, mitochondrial gene for mitochondrial product
5821	18911		0.78	4.6E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6002	18085	32285	0.51	4.6E-01	D28215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6386	19454	32689	0.92	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6881	19933	33231	0.52	4.6E-01	AF115340.1	NT	Bacillus subtilis Bbma (bbma) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6932	20156	33474	1.43	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6932	20156	33475	1.43	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7441	25881	33759	0.53	4.6E-01	L07320.1	NT	Murine cytomegalovirus e1 protein gene, complete cds
8001	20840	34333	0.78	4.6E-01	AA493577.1	EST_HUMAN	nt04h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8093	21029		0.53	4.6E-01	AE004031.1	NT	Xyella fastidiosa, section 177 of 229 of the complete genome
8663	21631	35052	13.26	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
8099	22065	35490	0.47	4.6E-01	AA932237.1	EST_HUMAN	6076608.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9099	22065	35491	0.47	4.6E-01	AA932237.1	EST_HUMAN	6076608.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9856	22599	36048	0.99	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9856	22599	36049	0.99	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10024	22951	36418	0.89	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10024	22951	36419	0.89	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10335	23259	36736	1.62	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10335	23259	36737	1.62	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11335	24285		2.28	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
11343	24293	37818	4.94	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11343	24293	37819	4.94	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11445	24368	37930	3.88	4.6E-01	BE272325.1	EST_HUMAN	601126068F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5'
11799	23954	37476	4.41	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11799	23954	37477	4.41	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12449	25208		1.69	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03 5'
1718	14748		0.92	4.5E-01	BE311420.1	EST_HUMAN	601142105F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505993 5'
1928	14950	27846	1.34	4.5E-01	AE001931.1	NT	Dainococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1926	14950	27947	1.34	4.5E-01	AE001931.1	NT	Dainococcus radiodurans R1 section 68 of 229 of the complete chromosome 1

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2881	15940	28857	5.36	4.5E-01	AA677088.1	EST_HUMAN	255d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3328	16379	29300	3.85	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3389	16438	29384	1.62	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4060	17096		1.23	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4101	17135	30030	1.12	4.5E-01	A1708908.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4205	18325		4.08	4.5E-01	AW873495.1	EST_HUMAN	as96609.x1 Barstead actin HPLR88 Homo sapiens cDNA clone IMAGE:2353480 3'
4990	17995	30894	1.09	4.5E-01	BE963445.2	EST_HUMAN	h60g02.x1 Soares_NFL_I_QBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5628	18724	31885	1.3	4.5E-01	AW608814.1	EST_HUMAN	601957225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
6760	19814		1.74	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7844	20804	33989	0.93	4.5E-01	M37036.1	NT	COAT PROTEIN
7867	20811	34188	2.64	4.5E-01	A1858849.1	EST_HUMAN	Rat nucleolar proteins B23.1 and B23.2
7991	20930	34325	0.51	4.5E-01	P60070	SWISSPROT	w82e02.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8650	21818		0.87	4.5E-01	M32661.1	NT	SWISNF COMPLEX 170 KDA SUBUNIT. ;
8746	21714	35137	3.86	4.5E-01	A1848596.1	EST_HUMAN	D melanogaster Shaw2 protein mRNA, complete cds
							tz56g11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
							POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE)
8905	21871	35297	0.74	4.5E-01	Q52728	SWISSPROT	(PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
9133	22099		1.72	4.5E-01	11444786	NT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
9351	22316	36742	0.78	4.5E-01	AE000218.1	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
10300	23225		0.89	4.5E-01	8630818	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10961	23781	37281	26.2	4.5E-01	M86006.1	EST_HUMAN	Bombay mori nuclear polyhedrosis virus, complete genome
10961	23781	37282	26.2	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
11212	24165	37695	2.3	4.5E-01	AW591271.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
12165	25955		5.3	4.5E-01	BE671461.1	EST_HUMAN	xo14h01.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
12349	25144		1.48	4.5E-01	O18638	SWISSPROT	Q84262 VIRAL INTEGRATION SITE PROTEIN INT-6. [1];
12452	25211		1.64	4.5E-01	AJ132045.1	NT	OUT AT FIRST PROTEIN
12991	25478		8.22	4.5E-01	11422099	NT	Thelazia annulata shAT2 gene
2052	15071		2.23	4.5E-01	6680503	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
							Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2398	15405	28430	7.02	4.5E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3326	16377	28298	1.36	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3326	16377	28299	1.36	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3330	16381	28302	1.9	4.4E-01	BF086726.1	EST_HUMAN	7191d02.y1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4262	17281		1.75	4.4E-01	BE378707.1	EST_HUMAN	601237139Ft NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603993 5'
5494	18594	31505	1.63	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5494	18594	31506	1.63	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5772	18884	32045	1.77	4.4E-01	S65019.1	NT	musin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5790	18882	32064	1.82	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
6064	19145	32356	1.42	4.4E-01	AI198413.1	EST_HUMAN	q162h11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;
6064	19145	32357	1.42	4.4E-01	AI198413.1	EST_HUMAN	q162h11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;
6368	19436	32680	1.9	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154 AFLATOXIN B1-ALDEHYDE REDUCTASE. ;
6462	19527		1.17	4.4E-01	AA776132.1	EST_HUMAN	aa55d11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN);
7627	20587	33950	0.95	4.4E-01	AE000571.1	NT	Helicobacter pylori 26895 ec93349 of 134 of the complete genome
8173	21143		12.58	4.4E-01	Z11879.1	NT	S tuberosum mRNA for induced stolon tip protein (partial)
9116	22081	35609	0.74	4.4E-01	AA056427.1	EST_HUMAN	z169a03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509836 3'
9506	22469	35913	0.72	4.4E-01	AF112540.1	NT	HIV-1 isolata 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9538	22501	35949	0.56	4.4E-01	AW612578.1	EST_HUMAN	h105c08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9845	22589	36038	1.21	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10321	23245	36725	2.1	4.4E-01	AI268650.1	EST_HUMAN	q639f09.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
10322	23246		3.91	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10457	23379	36872	5.07	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10740	23662	37155	1.27	4.4E-01	S78404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10740	23662	37157	1.27	4.4E-01	S78404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12432	25198	31824	5.76	4.4E-01		NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12861	25465	31727	2.83	4.4E-01	6677874	NT	Autographa californica nucleopolyhedrovirus, complete genome
12867	25535		1.45	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (H-IR23A)
411	13484	26418	2.49	4.3E-01	AF156218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
411	13484	26420	2.49	4.3E-01	AF156218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1607	14639	27616	0.96	4.3E-01	AW86550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2883	15942		1.83	4.3E-01	AW935269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3073	16130	28042	0.94	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4178	17209	30095	1.32	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4435	13484	28419	1.63	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4435	13484	28420	1.63	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5154	18164		1.17	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
5291	18296	31157	1.16	4.3E-01	BE780182.1	EST_HUMAN	601468030F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871255 5'
5438	18540	31449	0.89	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5438	18540	31450	0.89	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5990	19075	32273	1.5	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-408 HT0638 Homo sapiens cDNA
6010	19093	32293	1.93	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC186) gene, partial cds
6866	19919	33214	4	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica ifnG gene
7049	20071		0.88	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7682	20622		1.83	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'
8116	21053		0.62	4.3E-01	M58843.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
8770	21737		2.56	4.3E-01	U97040.1	NT	Melanococcus voliae flagella-related protein C-1 (flaC-flaI) genes, complete cds
9810	22614	36068	1.04	4.3E-01	Y14804.1	NT	Erwinia amylovora rcsV gene
10084	23011	36483	1.88	4.3E-01	AW630048.1	EST_HUMAN	hn74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
10084	23011	36484	1.68	4.3E-01	AW630048.1	EST_HUMAN	hn74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
10589	23511	37005	0.85	4.3E-01	AW170559.1	EST_HUMAN	xn63s05.x1 Soares_NHCEc cervical tumor Homo sapiens cDNA clone IMAGE:2688400 3' similar to
10879	23799	37301	0.48	4.3E-01	H65292.1	EST_HUMAN	TR-O00189 O00189 MU-ADAP TIN-RELATED PROTEIN 2 ;
11277	20178	33503	1.55	4.3E-01	AF075828.1	NT	yr45b05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208209 3'
11539	24480	38031	1.77	4.3E-01	AW993658.1	EST_HUMAN	Equus caballus microsatellite LEX027
11539	24480	38032	1.77	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
13055	25592		2.24	4.3E-01	AJ003022.1	NT	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
1360	15865	27365	1.77	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor whiH gene
3623	18666	29580	4.43	4.2E-01	AE003947.1	NT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3651	18694	29809	1.04	4.2E-01	AI280338.1	EST_HUMAN	Xyella fastidiosa, section 93 of 229 of the complete genome
3724	18324		1.22	4.2E-01	N81203.1	EST_HUMAN	q194b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3893	18933	29843	0.69	4.2E-01	AW935527.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
4007	17048	29953	1.72	4.2E-01	Q04886	SWISSPROT	QV0-LT0015-180200-127-r01 LT0015 Homo sapiens cDNA
4726	17746	30837	4.9	4.2E-01	AA534093.1	EST_HUMAN	SOX-8 PROTEIN
							ri69h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4820	17837	30735	3.62	4.2E-01	R13487.1	EST_HUMAN	y77e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5801	18993	32076	1.38	4.2E-01	BF242055.1	EST_HUMAN	601878721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5876	18965	32166	1.23	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6329	19399	32841	0.91	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7139	20115	33428	9.39	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7139	20115	33429	9.39	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7207	25877	33563	5.51	4.2E-01	S82504.1	NT	Breast-invasive cancer gene (rata, WF, spleen, Genomic, 419 nt, segment 2 of 2)
7300	20272	33607	5.9	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7822	20770	34146	0.52	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8325	21294	34708	2.58	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
8325	21294	34709	2.58	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
8548	21516	34934	0.49	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit Vc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
10329	23253		0.72	4.2E-01	AA705007.1	EST_HUMAN	z895f01.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462649 3'
10541	23463	36958	0.43	4.2E-01	AF181864.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10862	23782	37283	1.53	4.2E-01	AW863666.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
11382	24329	37858	2.39	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11723	24609	38185	1.77	4.2E-01	BE968485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
13090	25618		1.4	4.2E-01	AJ392837.1	EST_HUMAN	tg10c05.x1 NCI OGAP CLL1 Homo sapiens cDNA clone IMAGE:2108360 3'
1096	14140	27090	1.96	4.1E-01	AJ905481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1105	14149	27099	1.33	4.1E-01	AV705243.1	EST_HUMAN	AV705243 AD5 Homo sapiens cDNA clone ADBAHF08 5'
1105	14149	27100	1.33	4.1E-01	AV705243.1	EST_HUMAN	AV705243 AD5 Homo sapiens cDNA clone ADBAHF08 5'
2722	15716	28734	1.43	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2951	16008	28932	2.07	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2951	16008	28933	2.07	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3314	16367	29287	0.69	4.1E-01	AA906344.1	EST_HUMAN	q94b08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4303	17332	30212	2.54	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 IsoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF, genes
4334	17362		0.94	4.1E-01	AA909287.1	EST_HUMAN	om33d02.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4694	17715	30610	1.71	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6103	19182	32401	4.57	4.1E-01	BF681393.1	EST_HUMAN	602196590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6877	19930	33227	0.58	4.1E-01	U02298.1	NT	Mus musculus NIH 3T3 chemokine rantes (Scyb5) gene, complete cds
7666	20525	33989	2.96	4.1E-01	U07535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
8370	21339	34760	1.16	4.1E-01	BF574604.1	EST_HUMAN	602133281F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'

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Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9445	22409	35848	1.45	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA
9923	22807		0.58	4.1E-01	AF160597.1	NT	Voalavo gymnocauidus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10628	23548		1.18	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
10775	23696	37194	1.1	4.1E-01	AV649578.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCBVD12.3
10873	23793	37294	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10873	23793	37295	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10943	23893		2.1	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200999-010-408 HT0137 Homo sapiens cDNA
11188	24144	37677	39.55	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
12751	25931		3	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
142	15833		0.65	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-290999-012-d10 CT0201 Homo sapiens cDNA
1040	14085	27036	0.71	4.0E-01	8404856	NT	Lequeus rubellus mitochondrion, complete genome
1342	14377	27346	1.17	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1481	14514		5.11	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2022	15893	28054	1.12	4.0E-01	Z95933.1	NT	Ascaris lumbricoides masc2 gene
2022	15893	28055	1.12	4.0E-01	Z95933.1	NT	Ascaris lumbricoides masc2 gene
2187	15183	28203	1.09	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2187	15183	28204	1.09	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2816	13246	28178	1.27	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recognin (Ubr1), mRNA
2979	16037	28959	1.34	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2979	16037	28960	1.34	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl- phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3709	18752	29668	2.32	4.0E-01	AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3840	18880	29783	3.28	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3840	18880	29784	3.28	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4855	17872		9.36	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6015	19098	32299	1.14	4.0E-01	AW970610.1	EST_HUMAN	EST382691 MAGE resequences, MAGK Homo sapiens cDNA
6226	19300	32533	0.51	4.0E-01	BF243741.1	EST_HUMAN	601877853F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106221 5'
							STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 8 KD PEPTIDE]
6578	19638	32904	0.92	4.0E-01	P27285	SWISSPROT	Homo sapiens OCTN2 gene, complete cds
8345	21314	34729	0.8	4.0E-01	AB016625.1	NT	EST126066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
9360	22325	35753	0.96	4.0E-01	AA323289.1	EST_HUMAN	EST126066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11895	24776		2	4.0E-01	BF030282.1	EST_HUMAN	601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
12030	24906		1.75	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12448	25783		3.03	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12668	25536		1.6	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-ST-E3 INTERGENIC REGION
1378	14412	27383	1.65	3.9E-01	AF205618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2650	15647	28670	3.62	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2716	15710	28726	4.26	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2716	15710	28727	4.26	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3113	16170	29080	4.56	3.9E-01	AJ225896.1	NT	Shorhizobium meliloti egl, syrB2, cys3 genes and orf3
4106	17140	30035	1.25	3.9E-01	BF592811.1	EST_HUMAN	761d01.x1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339189 3'
5027	18041	30924	1.74	3.9E-01	BE728687.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6042	19124	32329	5.95	3.9E-01	BF206036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6411	19479	32726	0.66	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8286	21255	34684	0.8	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9213	22179	35610	0.73	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
9222	22188	*	0.88	3.9E-01	BF348634.1	EST_HUMAN	602019944F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155322 5'
9590	22552	36003	1.41	3.9E-01	AW195888.1	EST_HUMAN	xn66404.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821
9903	22855	36316	1.83	3.9E-01	AI937337.1	EST_HUMAN	094821 KIAA0713 PROTEIN ;
10237	23162	36550	2.99	3.9E-01	M19879.1	NT	wp76a02.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to
10305	23230		0.46	3.9E-01	11456620	NT	SW:RFX5 HUMAN P48982 BINDING REGULATORY FACTOR. ;
10527	23449	36947	0.62	3.9E-01	D86722.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
10665	23885	37397	0.48	3.9E-01	M18440.1	NT	Porphyra purpurea mitochondrion, complete genome
12219	25868		4.08	3.9E-01	AF304354.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
12344	26142		2.01	3.9E-01	Q61670	SWISSPROT	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
12840	25452		1.49	3.9E-01	11433335	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
161	13264		9.02	3.8E-01	7019498	NT	HOMEOBOX PROTEIN HLX1
506	13577		0.9	3.8E-01	AB028291.1	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
1886	14911		1.19	3.8E-01	AE003870.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
2465	15469	28493	1.24	3.8E-01	U41846.1	NT	Homo sapiens pom-1 mRNA for pericentriolar material-1, complete cds
2577	16578	28597	2.28	3.8E-01	AF214117.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
							Ceanothus divaricatus bruggae acetylcholinesterase (ace-1) gene, complete cds
							Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2640	15900	28662	4.89	3.8E-01	6978002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3015	16073		0.88	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3061	16118	29033	2.11	3.8E-01	AF043363.1	NT	Pleuroctes americanus aminopeptidase N (ampN) gene, partial cds
3495	16542	29466	9.24	3.8E-01	AL161818.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3549	16595		0.75	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3566	16595		0.97	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3769	16811	29720	0.99	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
5691	18786	31957	1.08	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6473	19538		0.6	3.8E-01	S46825.1	NT	prion protein (Prn), Genomic, 2448 nt
6779	19834	33117	5.49	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
6924	20148	33468	4.76	3.8E-01	AI374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
7126	20059	33385	1.24	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7743	20697	34063	0.51	3.8E-01	AA626274.1	EST_HUMAN	zu88c05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745064 3'
7759	20712		4.27	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
7988	20937	34331	0.49	3.8E-01	V00683.1	NT	Yeast mitochondrial gene for ATPase (genes oli-2 and oli-4)
8840	21608	35031	0.45	3.8E-01	M81395.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8903	21889	35294	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8972	21938	35363	0.79	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9169	22135	35561	1.47	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9819	22740		6.02	3.8E-01	T85413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;
11882	23744		3.41	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
12000	24877	38473	2.81	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12000	24877	38474	2.61	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12433	25199		4.23	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12557	25889		2.63	3.8E-01	U94788.1	NT	Human p63 (TP53) gene, complete cds
12667	25343		2.84	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0083-190700-271-e05 ET0083 Homo sapiens cDNA
13056	25864		2.03	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
13063	25905	31422	1.4	3.8E-01	T54787.1	EST_HUMAN	yb42b11.s1 Stragene fetal spleen (4937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN)
13080	25611	31590	1.57	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2490	15493	28518	12.56	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3474	16520	29442	11.71	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3884	16924	29833	0.7	3.7E-01	AA319482.1	EST_HUMAN	EST121715 Adrenal gland tumor Homo sapiens cDNA 5' end
4257	17288	30168	6.92	3.7E-01	AI218707.1	EST_HUMAN	ak39c07.x1 Soares_NSF_F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4348	17375	30255	1.84	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4416	17443	30334	3	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 205 of the complete genome
5857	18947	32132	1.16	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6060	19141	32353	1.35	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6659	19716	32993	0.66	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6680	19737		0.77	3.7E-01	L10953.1	NT	Mus saxicola haptoglobin mRNA, complete cds
7350	20320	33667	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7658	20618	33983	0.65	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
7658	20618	33984	0.65	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
8069	21006	34404	0.71	3.7E-01	T66802.1	EST_HUMAN	ya50a07.13 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66324 5'
8672	21640	35084	1.93	3.7E-01		NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8672	21640	35066	1.93	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8708	21676	35101	0.69	3.7E-01	AA902912.1	EST_HUMAN	ak43b11.s1 NCI CGAP_La2 Homo sapiens cDNA clone IMAGE:1516701 3'
9558	22518		3.78	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bcdo gene)
10530	23452		0.92	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exons region
10570	23492	36984	3.65	3.7E-01	AI33641.1	EST_HUMAN	q146p07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
11205	24159	37889	1.9	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11369	24316	37842	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11369	24316	37843	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11794	23949	37470	2.34	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12014	24891		1.53	3.7E-01	AA973540.1	EST_HUMAN	0046d03.s1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698
12060	24933		3.22	3.7E-01	6677678	NT	TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12136	25501		2.6	3.7E-01	J04982.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12309	25117		4.23	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12764	25406		1.86	3.7E-01	AL121154.1	EST_HUMAN	Chlamydomonas reinhardtii omp1 gene for outer membrane protein 1
12829	25447	31722	2.71	3.7E-01	Y18000.1	NT	DKFZp762K075.t1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
997	14048		11.36	3.6E-01	U88241.1	NT	Homo sapiens NF2 gene
1317	14352	27320	2.66	3.6E-01	T80255.1	EST_HUMAN	Human mlbp gene, partial cds
1317	14352	27321	2.66	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1931	14955	27951	6.09	3.6E-01	AW590184.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1931	14955	27952	6.09	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'
1931	14955	27952	6.09	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1968	14989	27892	6.4	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2399	15406		3.58	3.6E-01	X78725.1	NT	P. irregularis (P3804) gene for actin
2483	15487	28510	1.29	3.6E-01	LD5435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2483	15487	28511	1.29	3.6E-01	LD5435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2496	15498	28524	1.63	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181089-011-g07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2638	16637	28660	1.23	3.6E-01	P24206	SWISSPROT	ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE
2910	18322		5.89	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sutr3) mRNA, complete cds
3483	18529	29453	2.01	3.6E-01	X78758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3483	18529	29454	2.01	3.6E-01	X78758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4436	17462	30351	1.14	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4787	17805	30697	0.72	3.6E-01	Y11528.1	NT	Z. mays mRNA for casein kinase II alpha subunit
5045	18058	30937	2.81	3.6E-01	AW339593.1	EST_HUMAN	hac2g04.x1 NCI CGAP LU24 Homo sapiens cDNA clone IMAGE:2872566 3'
5139	18145	31025	0.85	3.6E-01	BE067699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5274	18280	31143	0.81	3.6E-01	AF087959.1	NT	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds
5274	18280	31144	0.91	3.6E-01	AF087959.1	NT	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds
5456	18558	31469	0.71	3.6E-01	AJ065655.1	NT	Homo sapiens lipo gene intron 5
							FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6205	19279	32512	1.1	3.6E-01	P16431	SWISSPROT	COMPONENT E
6623	19881	32958	1.8	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
7355	20325		3.63	3.6E-01	R94090.1	EST_HUMAN	Y74a06.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:275987 5'
							w72c10.x1 Soares_thymus_NHFTth Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
7500	20465	33828	1.86	3.6E-01	AW027174.1	EST_HUMAN	O15117 FYN BINDING PROTEIN. [1];
8566	21534	34954	0.84	3.6E-01	P98167	SWISSPROT	SCO-SPONDIN
8622	21590	35008	14.05	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 79
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9330	22295	35724	0.53	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9330	22295	35725	0.53	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9355	22320	35746	2.84	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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Single Exon Probes Expressed in Bone Marrow

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9355	22320	35747	2.84	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9547	22510	35969	1.12	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9754	22895	38151	0.93	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9754	22895	38152	0.93	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9824	22673		0.54	3.6E-01	X62825.1	NT	C. perfingens plc gene for phospholipase C upstream region containing bent DNA fragment
10222	23147	36636	16.66	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
10352	23278	36750	0.48	3.6E-01	AW75290.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10352	23278	36751	0.48	3.6E-01	AW75290.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
11292	24242	37769	3.04	3.6E-01	BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11442	24385	37925	3.26	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11772	23927	37448	5.63	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12174	25989		2.05	3.6E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
12247	25076		1.42	3.6E-01	D90901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
12257	25083		6.35	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12417	25187		6.26	3.6E-01	U69888.1	NT	Mus musculus Enr1 mRNA, complete cds
12770	25410		1.97	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) (Drosophila) homolog), translocated to, 10 (AF10), mRNA
13033	25934		3.33	3.6E-01	AW190229.1	EST_HUMAN	x60611.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
115	13226	26160	1.42	3.6E-01	AL161636.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
210	13311	26236	3.29	3.5E-01	6878933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
726	13787	26722	1.48	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51309), mRNA
726	13787	26723	1.48	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51309), mRNA
780	13840	26785	4.95	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1623	14656	27634	0.96	3.5E-01	BF310698.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1646	14678	27651	2.67	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2291	15303	28328	1.28	3.5E-01	P06768	SWISSPROT	HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (H-3)
2613	15899	28636	1.13	3.5E-01	AA223252.1	EST_HUMAN	z08a09.s1 Striatogene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
3818	16858		7.27	3.5E-01	AA642138.1	EST_HUMAN	m604003.s1 NCL CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4291	17320	30189	2.18	3.5E-01	AF071233.1	NT	Danio rerio homeobox protein (hox5b) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4922	17939	30831	0.7	3.5E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
4989	17984	30874	6.46	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5407	18510	31387	0.84	3.5E-01	Q86687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5407	18510	31388	0.84	3.5E-01	Q86687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5629	18725	31886	1.36	3.5E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6365	19434		0.77	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA
6548	19609	32871	0.82	3.5E-01	AA431833.1	EST_HUMAN	zw79703.r1 Soares_Jestis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935
6593	19653	32925	0.88	3.5E-01	U37150.1	NT	G1066935 F10F2.1 ;
6821	19875	33184	0.92	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
7257	19992		3.65	3.5E-01	X98505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7789	20742	34115	0.81	3.5E-01	P47281	SWISSPROT	S. scrofa mRNA for CD31 protein (PECAM-1)
7789	20742	34116	0.81	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8023	20960	34358	0.7	3.5E-01	X06091.1	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8406	21375		2.17	3.5E-01	11448042	NT	E. coli L-arabinose transport operon with genes araF, araG and araH
8409	21378	34784	0.87	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8810	21777		0.58	3.5E-01	AF051581.1	NT	RC4-ET0024-280600-014-d07 ET0024 Homo sapiens cDNA
9279	22245	35874	1.14	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
10093	23019	36494	6.94	3.5E-01	Q02294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10246	23171	36660	5.51	3.5E-01	Z26825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L
10326	23250	36728	1.01	3.5E-01	BE174794.1	EST_HUMAN	TYPE, ALPHA-1 POLYPEPTIDE (ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
11086	24047	37569	2.48	3.5E-01	X61084.1	NT	X.laavis gene for albumin including HP1 enhancer
11362	24311	37838	1.68	3.5E-01	AJ243178.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11362	24311	37839	1.68	3.5E-01	AJ243178.1	NT	C. griseus rhodopsin gene for opsin protein
11919	24800	38391	1.67	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11940	24820		1.77	3.5E-01	M82885.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11991	24868	38463	1.6	3.5E-01	U05145.1	NT	y290h12.1 Soares_multiple_sclerosis_2NpHMSHP Homo sapiens cDNA clone IMAGE:290375 5'
12269	25991		1.8	3.5E-01	AF297468.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
12341	26139		1.31	3.5E-01	X64695.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12501	26240		2.58	3.5E-01	AE001774.1	NT	Schistosoma mansoni strain NMR1 chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
13085	25842	31430	3.37	3.5E-01	H80814.1	EST_HUMAN	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
13085	25842	31431	3.37	3.5E-01	H80814.1	EST_HUMAN	Thermotoga maritima section 86 of 136 of the complete genome
							ys64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
							ys64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13106	25627		1.57	3.5E-01	4758297	NT	Homo sapiens v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neurofiblastoma derived oncogene homolog) (ERBB2), mRNA
708	13770		1.87	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
977	14028	26982	9.08	3.4E-01	Y09788.2	NT	Pseudomonas fluorescens colR, cds genes, orf222 and partial inaA gene
1329	14364	27332	2.78	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2410	15417	28441	2.01	3.4E-01	D90509.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3014	16072	28992	0.86	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3014	16072	28993	0.86	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3175	16230	29146	6.62	3.4E-01	U83905.1	NT	Carls familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3354	16405	29328	0.94	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3542	16588	29512	3.42	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3804	16844		1.78	3.4E-01	BF449010.1	EST_HUMAN	794601.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8JU15
4082	17116		1.48	3.4E-01	AA584186.1	EST_HUMAN	Q9JU15 DJ18C8.1
4674	17695	30582	1.72	3.4E-01	BE069912.1	EST_HUMAN	nc1b10.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
							MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4989	18004		4.71	3.4E-01	AI240973.1	EST_HUMAN	q95c05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
5768	18860	32040	2.74	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90.
5909	18895		5.14	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
6122	19200		1.74	3.4E-01	LO2971.1	NT	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6146	19221	32451	0.8	3.4E-01	BE748912.1	EST_HUMAN	601571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838828 3'
6229	19303	32535	1.91	3.4E-01	AW204606.1	EST_HUMAN	UI-H-B11-aal-e-12-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6362	19431	32674	1.78	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6807	19859		1.19	3.4E-01	N95225.1	EST_HUMAN	zb53e12.s1 Soares_faial_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
							hm3g05.x1 NCL_CGAP_Brr25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
7135	20111	33424	1.14	3.4E-01	AI468082.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7281	19998	33293	0.61	3.4E-01	BF676702.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8238	21207		0.54	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8579	21547	34966	0.55	3.4E-01	Y14930.1	NT	Homo sapiens TCRAV28 gene, allele A4, partial
8832	21789		1.8	3.4E-01	AA337063.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8909	21875	35301	0.64	3.4E-01	L04860.1	NT	Citric acid 7- α -hydroxylase gene, complete cds
9204	22170	35600	1.89	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
9567	22529	35978	4.43	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9567	22529	35978	4.43	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9776	22717	34527	0.49	3.4E-01	AB017510.1	NT	Ephydra fluvialis mRNA for PLC-gammaS, complete cds
9801	21124	34527	6.03	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9801	21124	34528	6.03	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9855	22761	36243	0.43	3.4E-01	AF183857.1	NT	Dictyostelium discoideum putative CMF receptor CMFR1 mRNA, complete cds
10054	22981	36449	1.09	3.4E-01	U98763.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
10249	23174	36664	2.14	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10843	23763		0.68	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11357	24307		3.51	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11393	24339	37869	4.96	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11427	24371	37909	1.67	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11828	24711	38295	1.58	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerol/MUC18, complete cds
11856	24738	38323	3.3	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12099	24970	38557	1.9	3.4E-01	AJ559986.1	EST_HUMAN	ig77g06.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2214874 3' similar to contains L1.b1 L1 repetitive element ;
12149	25008		2.08	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12261	25085		1.59	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
12485	25231		13.04	3.4E-01	L26339.1	NT	Human autocaligen mRNA, complete cds
12512	25761		3.88	3.4E-01	BE218652.1	EST_HUMAN	hy42h08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.i3 PTR5 repetitive element ;
12567	25865		2.19	3.4E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12673	25345	31763	3.46	3.4E-01	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
12972	25538		1.94	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
15	13135	26033	10.37	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1i nodX gene
106	13135	26033	4.34	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1i nodX gene
448	13521	26454	1.3	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
534	13700	26621	2.26	3.3E-01	7662465	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1205	14244	27203	3.29	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1310	14346	27312	2.44	3.3E-01	BF668880.1	EST_HUMAN	602164016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1610	14642	27618	1.55	3.3E-01	6753885	NT	Mus musculus disintegrin 5 (Dtgnt5), mRNA
1752	14781		1.13	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2043	15062		1.01	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2414	15421		4.45	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (rotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2960	16018	28945	1.76	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3028	16088		0.8	3.3E-01	I002743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3068	16125	29038	0.91	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3506	16553	28479	1.27	3.3E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3822	16862	29768	2.18	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3832	16872	29773	0.8	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3989	17029	29939	1.54	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4026	17064	29965	2.02	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4395	17423		1.51	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4715	17736		1.41	3.3E-01	AI539114.1	EST_HUMAN	tp78b12.x1 NCI CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORT 1 (HUMAN);
4875	17892	30781	1.33	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2869766
5397	18500	31377	2.48	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5397	18500	31378	2.48	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5664	18759	31928	0.55	3.3E-01	P39055	SWISSPROT	DYNAMIN
5664	18759	31929	0.55	3.3E-01	P39055	SWISSPROT	DYNAMIN
5884	18973	32186	0.61	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6056	19137	32347	1.75	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6056	19137	32348	1.75	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6154	19229	32459	0.82	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6960	20185	33508	0.63	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6980	20185	33509	0.63	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7073	20095	33404	4.16	3.3E-01	AI928131.1	EST_HUMAN	h64h01.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7073	20095	33405	4.16	3.3E-01	AI628131.1	EST_HUMAN	h564h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285609 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
8052	20969	34395	1.81	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8908	21874	35300	22.63	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
9080	22046	35469	0.66	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9469	22493	35871	0.85	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9733	22791	36215	0.98	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9733	22761	36216	0.98	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9869	22805	36258	2.8	3.3E-01	N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9910	22731	36186	2.61	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10350	23274		2.12	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
11076	24038	37561	2.85	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11076	24038	37562	2.85	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11365	24313		2.16	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
11565	24505	38062	8.16	3.3E-01	BE219351.1	EST_HUMAN	h51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11673	24639	38218	3.19	3.3E-01	P47953	SWISSPROT	
12027	24903		3.43	3.3E-01	AA806621.1	EST_HUMAN	6571g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12044	13135	26033	1.97	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
12246	25075	38170	1.84	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12958	25630		4.92	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (277)
13113	25832	31621	1.59	3.3E-01	BE312920.1	EST_HUMAN	601146730F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162006 5'
467	13530		2.08	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
719	13781		0.76	3.2E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1166	14207	27161	10.6	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1267	14322	27285	1.77	3.2E-01	Z50202.1	NT	P.vulgaris arcs-1 gene
1391	14425	27394	5.96	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1639	14671		0.9	3.2E-01	AF209730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1769	14818	27803	1.5	3.2E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1799	14828	27815	5.47	3.2E-01	AW957194.1	EST_HUMAN	EST369284 IMAGE resequences, MAGD Homo sapiens cDNA
1799	14828	27816	5.47	3.2E-01	AW957194.1	EST_HUMAN	EST369284 IMAGE resequences, MAGD Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1860	14886	27882	1.03	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2168	15184	28205	2.33	3.2E-01	BF203817.1	EST_HUMAN	601868604F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:411512 5'
2548	15549		2.3	3.2E-01	7710079	NT	Mus musculus Pbx1-knotted 1 homeobox (Pbx1), mRNA
2720	15714	28732	1.56	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3622	16665		0.79	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4367	17394	30273	0.93	3.2E-01	4759195	NT	Homo sapiens symplekin (SYM) mRNA
4422	17449	30340	1.62	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4526	17551	30439	1.3	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4767	17787		8.32	3.2E-01	BF693817.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4915	17932	30823	0.69	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5250	18258	31127	0.86	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5280	18286		4.18	3.2E-01	A1989472.1	EST_HUMAN	vs25506.x1 NCI_CGAP_G8 Homo sapiens cDNA clone IMAGE:2498195 3' similar to contains Alu repetitive element; contains element PTR7 repetitive element;
5344	18449	31320	2.71	3.2E-01	BE173964.1	EST_HUMAN	CM0-HT0569-060300-269-f10 HT0569 Homo sapiens cDNA
6068	19149	32361	1.36	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6436	19602	32753	0.68	3.2E-01	AF018494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6749	19803	33084	0.91	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FHTA Homo sapiens cDNA clone FHTAABH01 5'
6897	19949		1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8189	21159	34588	0.44	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8512	21480	34894	1.43	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8608	21577	34993	0.45	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12Wox1
8710	21678	35103	18.12	3.2E-01	X02508.1	NT	H.sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8713	21681	35108	17.12	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8805	21772		1.54	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8845	21812	35231	1.13	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8845	21812	35232	1.13	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8919	21885	35311	2.13	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
9019	21985	35405	0.63	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
9019	21985	35406	0.63	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9422	22387	35826	0.49	3.2E-01	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9432	22386		2.28	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9505	22468	35911	0.45	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9505	22468	35912	0.45	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10353	23277	36752	3.37	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
10559	23481	36976	0.5	3.2E-01	BE326230.1	EST_HUMAN	h69f05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10674	23596		3.71	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11028	23992	37519	3.03	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Stragelene (cat#936206) Homo sapiens cDNA clone HFBD221
12286	25990		3.67	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12674	25943		1.39	3.2E-01	BE886946.1	EST_HUMAN	601507820F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3909532 5'
12804	25431		4.84	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12890	25719		1.48	3.2E-01	AF157625.1	NT	Bos taurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
12936	25516		1.57	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
13001	25925	31306	1.33	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3616746 5'
13108	25628	31646	1.38	3.2E-01	A1745111.1	EST_HUMAN	tr21c06.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218954 3' similar to contains MER10.11 MER10 repetitive element ;
2679	15675	28696	3.02	3.1E-01	R18051.1	EST_HUMAN	yes0h05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2708	15828	28717	4.64	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2708	15828	28718	4.64	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2869	15929		1.63	3.1E-01	AW629036.1	EST_HUMAN	h46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:29755391 3'
3188	16243		4.03	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
3927	16967	28880	0.93	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4999	18014	30801	1.25	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5239	18247	31119	0.79	3.1E-01	AF130370.1	NT	Rattus norvegicus MEN1 tumor suppressor (Men1) mRNA; alternative splice product, complete cds
5297	18320	31162	2.59	3.1E-01	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5555	18652	31596	9.78	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5681	18776	31948	0.65	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN HI1236
5682	18777	31949	0.87	3.1E-01	Z74883.1	NT	S cerevisiae chromosome XV reading frame ORF YOL141w
5653	18788		1.01	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5866	18955	32142	2.3	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6416	25680	32732	0.61	3.1E-01	R94322.1	EST_HUMAN	yc41f04.f1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:198367 5'
6610	19688	32944	2.69	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6683	19740	33015	0.85	3.1E-01	A1284458.1	EST_HUMAN	q139d01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'
6840	19893	33188	0.88	3.1E-01	X71887.1	NT	H.sapiens gene for Immunoglobulin kappa light chain variable region A8 and A9
6930	20154		0.7	3.1E-01	AW377394.1	EST_HUMAN	MR2-CT0222-281099-005-H05 CT0222 Homo sapiens cDNA
7162	25834	31238	2.55	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7942	20884	34275	0.56	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8038	20875	34371					Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
8166	21104	34502	0.49	3.1E-01	AF242431.1	NT	
8166	21104	34503	0.54	3.1E-01	AW850188.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8995	21851	35386	0.83	3.1E-01	R45318.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
10262	23187	36571	0.52	3.1E-01	6678322	NT	yg46f01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
10427	23349	36833	1	3.1E-01	BF696639.1	EST_HUMAN	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10427	23349	36834	1	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10488	23410	36907	1.73	3.1E-01	A1244001.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10656	23588		0.58	3.1E-01	T55325.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
11186	24142	37676	2.35	3.1E-01	BF216117.1	EST_HUMAN	q161e11.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:U91038_ma2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11864	24746	38328	2.3	3.1E-01	7662281	NT	601883592F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4095814 5'
12133	25002	38608	1.68	3.1E-01	AF048693.1	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
12133	25002	38609	1.68	3.1E-01	AF048693.1	NT	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
12415	25186		1.57	3.1E-01	AF294308.1	NT	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
12451	25210		4.64	3.1E-01	AF304162.1	NT	Andis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12592	25296		4.19	3.1E-01	AF195953.1	NT	Slitostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12944	25523		3.39	3.1E-01	AF196776.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
73	15808	26112	1.78	3.0E-01	6755093	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
254	13351	26277	8.98	3.0E-01	AJ271735.1	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
127	14265	27222	2.16	3.0E-01	AW300400.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
1508	14541	27512	5.96	3.0E-01	AJ006755.1	NT	x563f08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
							Balaenoptera physalus gene encoding atrial natriuretic peptide

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2146	16162	28178	1.13	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3225	16280		1.26	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyP gene for polyglutamate lyase, complete cds
3879	16918	29827	1.46	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
3898	17037	29944	1.02	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4541	17564	30451	2.17	3.0E-01	AJ006756.1	NT	Balanoptera physalus gene encoding atrial natriuretic peptide
5425	18528	31407	5.19	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5506	18606	31536	0.66	3.0E-01	AF224969.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5510	18610	31541	0.76	3.0E-01	AF229247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
5582	18678	31641	3.81	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-g03 BT0333 Homo sapiens cDNA
5582	18678	31642	3.81	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-g03 BT0333 Homo sapiens cDNA
5619	18715	31874	4.05	3.0E-01	U01247.1	NT	Mus musculus 129/ev Clara cell 10 kd protein (mCC10) gene, complete cds
7005	20131	33446	2.86	3.0E-01	D16313.1	NT	Mouse cytokerin 15 gene, complete cds
7041	18373	31281	0.71	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7111	20045	33347	0.96	3.0E-01	AF229247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
7195	20219	33551	0.59	3.0E-01	X63941.1	NT	S Cerevisiae GAC1
7328	20289	33643	0.82	3.0E-01	AL183206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7549	20512	33870	4.68	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7744	20698	34054	1.33	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8259	21228	34638	1.28	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8716	21684		4.13	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec5f9), mRNA
8819	21786	35210	1.34	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
9181	22147	35574	0.74	3.0E-01	AF141676.1	NT	Streptomyces sulfonofaciens isopenicillin N synthase (pcbC) gene, partial cds
9223	22189		0.71	3.0E-01	7661885	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9573	22535	35986	0.95	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (cmmB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9932	22859	36320	0.51	3.0E-01	IP76389	SWISSPROT	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
10327	23251	36730	0.73	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81-Homo sapiens cDNA clone IMAGE:4288338 5'
10501	23423	36922	0.47	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans TadaA (tadaA), TadaB (tadB), TadaC (tadC), TadaD (tadD), TadeE (tadE), TadeF (tadF), and TadeG (tadG) genes, complete cds
10501	23423	36923	0.47	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans TadaA (tadaA), TadaB (tadB), TadaC (tadC), TadaD (tadD), TadeE (tadE), TadeF (tadF), and TadeG (tadG) genes, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10760	23681	37177	0.85	3.0E-01	AW118111.1	EST_HUMAN	xc03410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10762	23683	37179	2.14	3.0E-01	AB030231.1	NT	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds
10782	23703	37201	0.82	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301087 5'
10782	23703	37202	0.82	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301087 5'
12061	24934	38529	2.5	3.0E-01	HS1029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:194107 5'
12061	24934	38530	2.5	3.0E-01	HS1029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:194107 5'
12696	25875		1.57	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12978	25917		2.52	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rplp), mRNA
1747	14776		0.92	2.9E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and lgf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
2039	15088	28077	1.19	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2280	15274	28298	1.2	2.9E-01	AF222718.1	NT	Chrysodidymus synuroides mitochondrion, complete genome
3265	16319	29240	1.92	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-112 CT0326 Homo sapiens cDNA
3265	16319	29241	1.92	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-112 CT0326 Homo sapiens cDNA
3912	16952	29863	1.03	2.9E-01	AI610836.1	EST_HUMAN	lp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb.D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
3955	16995	29911	0.81	2.9E-01	AI769472.1	EST_HUMAN	wt14d10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP.C34F6.7 CE15676;
4112	17146		0.7	2.9E-01	AW002902.1	EST_HUMAN	wt02f10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2480396 3'
4511	17538	30420	1.24	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4710	17731		1.5	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5156	18168		1.25	2.9E-01	AI670899.1	EST_HUMAN	wa06103.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element;
5275	18281	31145	3.3	2.9E-01	AJ131017.1	NT	Mus musculus SCL gene locus
5277	18283	31146	1.12	2.9E-01	BE741380.1	EST_HUMAN	601594241F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948178 5'
5330	18436		1.49	2.9E-01	R37485.1	EST_HUMAN	yf77e12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28291 3'
5459	20055	33372	0.75	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5858	18948	32133	5.1	2.9E-01	X56098.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5858	18948	32134	5.1	2.9E-01	X56098.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5871	18950	32149	6.12	2.9E-01	6879862	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6174	19249	32482	1.35	2.9E-01	AA418145.1	EST_HUMAN	z07b12.r1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6412	19480	32727	1.05	2.9E-01	AI797428.1	EST_HUMAN	we27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1 repetitive element;
6459	19524	32775	2.3	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6599	19659	32931	0.6	2.9E-01	R09194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6599	19659	32932	0.6	2.9E-01	R09194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6883	19935		0.84	2.9E-01	Z50156.1	NT	D.discoideum gene for 34 kD actin binding protein
7043	20065	33372	0.58	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salisa S-adenosylmethionine synthetase 2 mRNA, complete cds
7179	18410	31211	1.57	2.9E-01	AF142329.1	NT	Mus musculus Filin protein (Filin) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7303	20274	33610	2.99	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7367	20337	33887	1.68	2.9E-01	AF100866.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1, 3-galactosyl tr>
8252	21221	34830	1.87	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8262	21221	34831	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8489	21457	34874	0.49	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8489	21457	34875	0.49	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8502	21470		1.16	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8682	21650		0.45	2.9E-01	AF197459.1	NT	Buchnera aphidicola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3- isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds
8942	21908	35333	0.77	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9277	22243	35672	1.01	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
9388	22363	35784	0.8	2.9E-01	M22462.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9601	22805	36053	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
9601	22805	36054	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
11240	24193	37711	1.7	2.9E-01	V01394.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11497	24440	37689	1.86	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11497	24440	37690	1.86	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11913	24794	38385	2.95	2.9E-01	AL130078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
12109	24979	38579	2.1	2.9E-01	AW294742.1	EST_HUMAN	U1-H-BW0-aim-F-10-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729994 3'
12551	25334	31760	1.47	2.9E-01	AW005671.1	EST_HUMAN	wz88f05.x1 NCI_CGAP_Brr25 Homo sapiens cDNA clone IMAGE:2555921 3' similar to contains element MER29 repetitive element;
12728	25381	31747	4	2.9E-01	AF082453.1	NT	Homo sapiens TNF-a-inducible RNA binding protein (TRIP) gene, complete cds
13025	25573	31694	1.35	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13025	25573	31695	1.35	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
570	13640		2.2	2.8E-01	U87136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
576	13644		1.41	2.8E-01	L28145.1	NT	Prupe dwarf virus movement protein, complete cds; coat protein, complete cds
1085	14129	27083	3.9	2.8E-01	AF168050.1	NT	Guira guira oocyte maturation factor Mos (c-mos) gene, partial cds
1282	14317	27279	1.06	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1282	14317	27280	1.06	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1295	14330	27291	2.65	2.8E-01	D86560.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1740	14770	27756	2.22	2.8E-01	AW880020.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
2028	15048	28062	2.08	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586i2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586i2321
2141	15158	28174	1.51	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2479	15483	28507	2.18	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2479	15483	28508	2.18	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2554	15556		3.07	2.8E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2874	15671	28689	1.35	2.8E-01	AB020375.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2982	16040		1.48	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2983	16041	28983	2.57	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
2983	16041	28984	2.57	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3390	16439	29365	1.16	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
4021	17058	28860	1.72	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4150	17181		0.67	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 929 of the complete genome
4228	17255		2.41	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4488	17513	30401	2.62	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L. PROTEIN)
4822	17839	30737	0.92	2.8E-01	D16050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4822	17839	30738	0.92	2.8E-01	D16050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4896	17883	30771	2.71	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4897	17914	30804	1.37	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180129 5'
4920	17937	30829	1.69	2.8E-01	A1272669.1	EST_HUMAN	qf59c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876828 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
5384	25637	31362	23.73	2.8E-01	AA349997.1	EST_HUMAN	EST167072 Infant brain Homo sapiens cDNA 5' end
5687	18782	31954	2.52	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5915	18001		1.04	2.8E-01	AW992583.1	EST_HUMAN	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6028	19111	32313	0.57	2.8E-01	AA765296.1	EST_HUMAN	oa01008.st NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK500-BINDING PROTEIN (HUMAN);

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6048	10120		0.49	2.8E-01	AA0404576.1	EST_HUMAN	z141f01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element
6300	25994		0.78	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6343	19412	32653	2.02	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6343	19412	32654	2.02	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6895	19947	33244	8.31	2.8E-01	BF511215.1	EST_HUMAN	U1-H.B14-act-4-04-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085162 3'
7201	20226	33557	0.52	2.8E-01	U65300.1	NT	Orthogeomys heterodus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7579	20541	33900	0.51	2.8E-01	BE881455.1	EST_HUMAN	601460157F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3892142 5'
7675	20833		1.03	2.8E-01	U05833.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7724	20680	34044	0.77	2.8E-01	X69880.1	NT	L. esculentum ypt2 mRNA for GTP-binding protein
8429	21398	34808	1.12	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8429	21398	34809	1.12	2.8E-01	A1346128.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8551	21519	34938	2.25	2.8E-01	U51088.1	NT	Homo sapiens lenssterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8859	21826	35249	0.46	2.8E-01	AA911629.1	EST_HUMAN	0702h05.s1 NCL_CGAP_C012 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8936	21902		7.34	2.8E-01	BF347847.1	EST_HUMAN	602022987F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158525 5'
9821	22670	36127	0.91	2.8E-01	U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
10066	22906		0.85	2.8E-01	L13654.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
10248	23173	36662	0.93	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10248	23173	36663	0.93	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10310	23234	36716	0.6	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10420	23342	36828	4.98	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10676	23598		0.94	2.8E-01	9826154	NT	Fujinami sarcoma virus, complete genome
10718	23640	37133	0.44	2.8E-01	BE869727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839785 3'
11065	24055	37578	1.9	2.8E-01	BF241032.1	EST_HUMAN	60180794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11065	24055	37579	1.9	2.8E-01	BF241032.1	EST_HUMAN	60180794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11125	24085	37612	2.96	2.8E-01	BF696970.1	EST_HUMAN	60185214F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
11508	24548		4.02	2.8E-01	BF674023.1	EST_HUMAN	60213741F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
12312	25120	31843	1.39	2.8E-01	AF268477.1	NT	Ovis aries tissue inhibitor of metalloproteinase 1 (TIMP1) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12684	25351		23.64	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12788	25420	31736	3.09	2.8E-01	BE176999.1	EST_HUMAN	PM4-HT0808-030400-001-a07 HT0808 Homo sapiens cDNA
12817	25439	31742	1.37	2.8E-01	BE9000116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
12969	25879		3.15	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
13097	25973		1.76	2.8E-01	AW025400.1	EST_HUMAN	wu98905.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2527928 3'
477	13549	26477	2.95	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
615	13680	26598	9.43	2.7E-01	AA450061.1	EST_HUMAN	z039b10.s1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788927 3' similar to contains Alu repetitive element;
1268	14301	27282	2.18	2.7E-01	AB004908.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1626	14658		2.21	2.7E-01	X79815.1	NT	G.lambila SR2 gene
1742	14772	27757	2.88	2.7E-01	W58067.1	EST_HUMAN	zf22h10.r1 Soares fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1791	14820	27805	2.49	2.7E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2145	15885		2.29	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monocamine transporter type 2, promoter region and exon 1
2375	15383	28405	9.36	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial
2461	15465	28488	3.97	2.7E-01	A1310658.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
2909	15968	28691	1	2.7E-01	AF251276.1	NT	Mus musculus serine protease inhibitor 14 (Spi14) mRNA, complete cds
2997	16055		0.91	2.7E-01	BF089284.1	EST_HUMAN	CM1-HT0875-060900-385-a05 HT0875 Homo sapiens cDNA
4038	17076	29876	1.74	2.7E-01	A1928015.1	EST_HUMAN	wu92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4053	17090	29885	0.76	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4053	17090	29886	0.76	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4061	17097	29991	2.33	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4928	17945	30837	0.76	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs86) gene, complete cds
5079	18089		4.11	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5339	18444	31197	2.13	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
5587	18684		1.11	2.7E-01	AB033171.1	NT	Astreopora myriophthalma mitochondrial cytb gene for cytochrome b, partial cds
6476	19541	32787	0.51	2.7E-01	Q00818	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6476	19541	32788	0.51	2.7E-01	Q00919	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6765	19819	33100	1.06	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6765	19819	33101	1.06	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6946	20170	33494	2.1	2.7E-01	Q61954	SWISSPROT	FIBRILLIN 1 PRECURSOR
7263	19988		0.64	2.7E-01	AI540070.1	EST_HUMAN	h08h08.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7580	20542	33901	0.8	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7811	20760	34135	0.86	2.7E-01	Q01198	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7811	20760	34136	0.86	2.7E-01	Q01198	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7952	20893	34286	1.9	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7952	20893	34286	1.9	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8012	20950	34343	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST89740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
8012	20950	34344	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST89740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
8084	21021	34421	0.63	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8198	21166	34576	0.86	2.7E-01	AA013147.1	EST_HUMAN	z835b11.s1 Soares retina N2b4-IR Homo sapiens cDNA clone IMAGE:360567 3' similar to contains Alu repetitive element;
8360	21329		0.52	2.7E-01	AF048820.1	NT	Carrassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8475	21444	34861	0.43	2.7E-01	AW868503.1	EST_HUMAN	MRI-SN0082-100500-002-409 SN0082 Homo sapiens cDNA
8527	21495	34909	0.52	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8634	21602	35025	0.74	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
9112	22078	35505	0.52	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9382	22347	35779	0.51	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn564
9688	22641	36098	11.09	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9688	22641	36099	11.09	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9691	22844		2.17	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10160	23085	36562	0.64	2.7E-01	D89680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10441	23363	36853	0.85	2.7E-01	AF091846.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10477	23399	36896	2.83	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc1 isoform a (NF-ATc1) mRNA, complete cds
10611	23533	37029	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10611	23533	37030	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
11163	24121	37648	4.87	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11163	24121	37648	4.87	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11171	24128	37658	2.31	2.7E-01	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12066	24939		2.08	2.7E-01	BE141036.1	EST_HUMAN	MR0-HT0067-201069-002-c10 HT0067 Homo sapiens cDNA
12090	24981		1.52	2.7E-01	O14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C
12509	25244	31802	1.39	2.7E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
12757	25758		1.46	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12851	25460		1.63	2.7E-01	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
12948	25526		3.16	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
470	15841	26470	1.97	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
481	13564		1.5	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1394	14428	27397	1.66	2.6E-01	BE85087.1	EST_HUMAN	607510839F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1431	14465	27441	1.36	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1912	14936	27631	6.4	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1912	14936	27632	6.4	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M38072 80S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2104	15121		7.48	2.6E-01	AW733152.1	EST_HUMAN	B. malitimus rbcL gene
2480	15484		0.99	2.6E-01	Y12996.1	NT	
2553	15555		8.24	2.6E-01	BE272440.1	EST_HUMAN	601128016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
3108	16165		1.02	2.6E-01	AW974631.1	EST_HUMAN	EST386635 MAGe resequences, MAGM Homo sapiens cDNA
3594	16639	29559	1.02	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3657	16700	29616	2.11	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3982	17022	29932	0.77	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial rnpB gene for RNase P RNA subunit
3982	17022	29933	0.77	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial rnpB gene for RNase P RNA subunit
4181	17212	30100	17.99	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4384	17412	30296	1.39	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4522	17547	30434	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4522	17547	30435	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4679	17601	30497	1.47	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4677	17698	30585	2.31	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4745	17765	30659	1.46	2.6E-01	AF142703.1	NT	Ophiostoma radiocosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product

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Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5007	18021	30909	4.38	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288.5
5081	18091		0.76	2.6E-01	AA884625.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468905.3
5414	18517		1.06	2.6E-01	AB035972.1	NT	Paramedium caudatum gene for PAP, complete cds
5524	18623	31598	0.69	2.6E-01	M96050.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAx genes, complete cds
5651	18747		0.71	2.6E-01	A1862398.1	EST_HUMAN	td16a03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2075788.3 similar to contains element MER35 repetitive element;
5869	18958	32146	0.68	2.6E-01	AF207650.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JIM2 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g+
6189	28993		2.61	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6325	19395	32637	1.81	2.6E-01	A1582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227498.3 similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR1 repetitive element;
6325	19395	32638	1.81	2.6E-01	A1582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227498.3 similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR1 repetitive element;
6562	19622	32887	1.01	2.6E-01	AL162767.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
6825	19879	33169	0.6	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156.5
6825	19879	33170	0.6	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156.5
7238	20259	33593	0.75	2.6E-01	A1914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366.3 similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7620	20590	33944	0.72	2.6E-01	BE148981.1	EST_HUMAN	GM0-H70245-031169-086-104 HT0245 Homo sapiens cDNA
7663	25686		0.73	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
7700	20658		0.61	2.6E-01	AA196149.1	EST_HUMAN	zp92e01.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672.5
8013	20951	34345	1.53	2.6E-01	R10365.1	EST_HUMAN	y37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004.3 similar to gb:X12817 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8071	21008	34406	0.65	2.6E-01	Q09855	SWISSPROT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E6.07 IN CHROMOSOME 1
8182	21152	34559	1.13	2.6E-01	R02411.1	EST_HUMAN	y82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212.5
8236	21205	34610	1.17	2.6E-01	BE144331.1	EST_HUMAN	MR0-H70166-181196-003-d12 HT0168 Homo sapiens cDNA
8480	21449	34866	0.62	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1.2 mannosidase (Berlin)
8480	21449	34867	0.62	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1.2 mannosidase (Berlin)
8677	21645	35069	2.87	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150396.5
8753	21721	35143	1.92	2.6E-01	Q10189	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9042	22008	35428	4.09	2.6E-01	BE830339.1	EST_HUMAN	RC9-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9042	22008	35429	4.09	2.6E-01	BE830339.1	EST_HUMAN	RC9-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9922	22671	36128	0.99	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
10096	23022		0.63	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10227	23152	36841	1.08	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
10227	23152	36842	1.08	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFH-G)
10550	23472		0.61	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10875	23795		0.91	2.6E-01	Y10198.1	NT	Homo sapiens PHEX gene
10978	23998		0.48	2.6E-01	Y16874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11854	24736		32.27	2.6E-01	X51765.1	NT	Homo sapiens myoglobin constant region complex (germline)
12268	25091		2.77	2.6E-01	10190655	NT	Mus musculus jerky (Jrk), mRNA
12464	25883		3.3	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12528	25297	31806	4.42	2.6E-01	AF318896.1	NT	Homo sapiens NaK-ATPase gamma subunit (FXD2) gene, complete cds, alternatively spliced
12846	25456		2.01	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12974	25539		1.74	2.6E-01	AF141326.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
13010	25862		3.07	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
241	13340	26265	2.33	2.6E-01	4502238	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	13340	26265	1.97	2.5E-01	4502238	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
265	13352		4.63	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
833	13890	26844	1.87	2.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1123	14167	27119	9.8	2.5E-01	T89837.1	EST_HUMAN	ye11g07.11 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1522	14554	27525	1.55	2.5E-01	AL115924.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1741	14771		5.06	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1900	16880	27920	0.94	2.5E-01	BE696804.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
1900	15880	27921	0.94	2.5E-01	BE696804.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
2417	15424		13.96	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2503	15508		1.09	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:684862 5'
2844	15841	28685	0.94	2.5E-01	X95310.1	NT	B. laurus mRNA for D-aspartate oxidase
3423	16471		2.83	2.5E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3545	16591	29516	0.87	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3560	16608	29526	7.94	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3861	16900	29803	1.15	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3861	16900	29804	1.15	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4096	17130		1.76	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4346	17373		0.86	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4780	17800		1.34	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4788	17808	30608	4.71	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4821	17838	30736	2.32	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4840	17857		3.69	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4870	17867	30775	0.64	2.5E-01	BE96785.1	EST_HUMAN	h02f11.x1 Soares NFL_T_GBC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
5086	18096	30972	0.84	2.5E-01	AW873598.1	EST_HUMAN	WP:Y71F9A_294.D CE22898 ;
5243	18251		0.96	2.5E-01	AA768389.1	EST_HUMAN	ca83a08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316920 3' similar to contains Alu repetitive element
5399	18502	31390	13.58	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6070	19151	32363	0.84	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6071	19152		0.87	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6525	19568	32847	0.49	2.5E-01	P22219	SWISSPROT	PROTEIN KINASE VPS15
6760	19835	33118	0.86	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
7245	19880	33277	0.8	2.5E-01	8394138	NT	Rattus norvegicus rabin 3 (RABIN3), mRNA
7575	20637	33896	0.79	2.5E-01	U13992.1	NT	Feline calicivirus CF/168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds, and unknown gene
7604	20665		1.13	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7852	20798	34174	0.88	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7898	20841	34223	3.88	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8177	21147	34555	2.72	2.5E-01	BF108040.1	EST_HUMAN	7167a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8188	21158	34567	0.62	2.5E-01	BE96712.1	EST_HUMAN	601663391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8568	21536	34956	2.02	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662809 5'
8740	21708	35131	0.67	2.5E-01	P04492	SWISSPROT	ETB PROTEIN, SMALL T-ANTIGEN (ETB 19K)
8983	21948	35373	3.37	2.5E-01	H53236.1	EST_HUMAN	xq84f07.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202501 5'
9227	22193	35623	0.81	2.5E-01	M8626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9874	22827	36280	16.45	2.5E-01	U89851.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9874	22827	36281	16.45	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9831	22814	36268	2.03	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9931	22814	36269	2.03	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10468	23380	36873	1.7	2.5E-01	AW581967.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10707	23629	37124	0.44	2.5E-01	11469652	NT	Porphyrin purpurea chloroplast, complete genome
10909	23829	37342	1.58	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element ;
10912	23832	37346	1.38	2.5E-01	X98491.1	NT	Mouse L1M LINE DNA
10992	23912	37427	0.45	2.5E-01	AI934721.1	EST_HUMAN	wp88e11.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2468876 3' similar to SW:CEBD_HUMAN P49716 CCAAT/ENHANCER BINDING PROTEIN DELTA ;
10992	23912	37428	0.45	2.5E-01	AI934721.1	EST_HUMAN	wp88e11.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2468876 3' similar to SW:CEBD_HUMAN P49716 CCAAT/ENHANCER BINDING PROTEIN DELTA ;
11413	24357	37892	4.47	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
12120	24980	38591	2.34	2.5E-01	AE000711.1	NT	Aquifex aeolicus section 43 of 109 of the complete genome
12204	25046	38925	4.55	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
12230	25959		5.87	2.5E-01	AL181641.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12691	25805	31827	1.64	2.5E-01	AF170072.1	NT	Spodoptera frugiperda GAL4UC mRNA, complete cds
555	13625	26543	0.86	2.4E-01	AA936316.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_OBC_ST Homo sapiens cDNA clone IMAGE:1562023 3'
849	13905	26864	2.67	2.4E-01	BF576124.1	EST_HUMAN	502132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1307	14343	27307	15.11	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1307	14343	27308	15.11	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1384	14418	27387	1.01	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1868	14893		27.14	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1916	14940	27936	1.21	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2148	15164	28180	0.87	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
2178	15193		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAT PROTEASE)
2271	15284	28310	2.23	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2391	15399	28424	1.65	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2544	15546	28569	2.37	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A ;
2772	15764	28785	2.11	2.4E-01	X71783.1	NT	D discoideum (Ax3-K) pora gene
2797	15789	28807	3.03	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
						NT	Bovine adenovirus 3 complete genome
3149	16206		3.16	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3163	16219	29134	1.71	2.4E-01	X74209.1	NT	H.sapiens AGT gene, PstI fragment of intron 4
3675	16718	29632	1	2.4E-01	AF169793.1	NT	Podospira anserina HET-C protein (Het-c) gene, complete cds
3773	16815	29724	0.95	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4082	17098		0.87	2.4E-01	D29960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4974	17989		0.98	2.4E-01	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5089	18099	30975	0.95	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5537	18634	31574	0.77	2.4E-01	A1925707.1	EST_HUMAN	wo33405.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5537	18634	31575	0.77	2.4E-01	A1925707.1	EST_HUMAN	wo33405.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5592	18659	31605	0.69	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5738	18832	32011	9.32	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5738	18832	32012	9.32	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5766	18858		0.65	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5991	25649		1.03	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2) gene
5998	19082	32279	2.06	2.4E-01	BF592336.1	EST_HUMAN	754d04.x1 NCI CGAP Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SPR4_HUMAN
6098	19177	32395	2.07	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6209	19283	32515	2.02	2.4E-01	7661801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6264	19337	32570	0.94	2.4E-01	AV733787.1	EST_HUMAN	Homo sapiens HSPG142 protein (HSPG142), mRNA
6523	19586	32844	0.69	2.4E-01	AA398672.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cdaADE11 5'
6685	19742	33018	1.72	2.4E-01	A1698989.1	EST_HUMAN	z70d02.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727683 3'
7247	19982	33279	0.54	2.4E-01	AF163863.1	NT	wc82c71.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
7598	20529	33888	7.93	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7748	20701	34068	0.55	2.4E-01	N48732.1	EST_HUMAN	Mustela vison tyrosine aminotransferase gene, complete cds
7994	20933		0.51	2.4E-01	U05013.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7998	20935	34329	0.97	2.4E-01	AF229644.1	NT	y55c11.1 Soares_multiple_sclerosis_2NblHMSF Homo sapiens cDNA clone IMAGE:277460 5'
8416	21385	34782	0.51	2.4E-01	X97252.1	NT	Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds
8416	21385	34783	0.51	2.4E-01	X97252.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8682	21600	35083	1.5	2.4E-01	AJ012585.1	NT	M.musculus pch gene and promoter
8946	21912	35337	0.98	2.4E-01	BF242794.1	EST_HUMAN	M.musculus pch gene and promoter
9001	21967		0.57	2.4E-01	BF878275.1	EST_HUMAN	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
9487	22451	35891	0.51	2.4E-01	AL139077.2	NT	601877678F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
							602086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
							Campylobacter jejuni NCTC11168 complete genome, segment 4/6

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9487	22451	35892	0.51	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9921	22742	36193	7.63	2.4E-01	AI693515.1	EST_HUMAN	wd43602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
10062	22889	36457	0.57	2.4E-01	AF220067.1	NT	MER22 b1 TAR1 repetitive element :
10062	22989	36458	0.57	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10806	23728	37227	1.69	2.4E-01	Q03692	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
11119	24079	37603	2.68	2.4E-01	AI161494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11185	24141	37675	1.77	2.4E-01	AF030199.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11534	24475		1.52	2.4E-01	Z21647.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
12096	24967	38564	4.88	2.4E-01	P06800	SWISSPROT	P. asiatica mosaic virus genomic RNA
12160	25015	38617	2.5	2.4E-01	AF217491.1	NT	PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR
12294	25749		1.93	2.4E-01	AF004213.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12361	26150		2.1	2.4E-01	AJ278191.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EL1) mRNA, complete cds
12576	28734		2.27	2.4E-01	V01507.1	NT	Mus musculus mRNA for putative mcf7 protein (mcf7 gene)
12782	28945		1.31	2.4E-01	BF229975.1	EST_HUMAN	Gallus gallus gene coding for a-actin
13008	28559		8.49	2.4E-01	AL163281.2	NT	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
389	13464	26394	0.98	2.3E-01	S75898.1	NT	Homo sapiens chromosome 21 segment HS21C081
638	13704		5.85	2.3E-01	U99713.1	NT	aromatase [Poephila guttata-zebra finches, ovary, mRNA, 3188 nt]
668	13733	26658	21.34	2.3E-01	U67596.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
934	13987	26937	4.19	2.3E-01	BE311893.1	EST_HUMAN	Methanococcus jannaschii section 138 of 150 of the complete genome
1511	14543	27514	1.33	2.3E-01	6677980	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3605818 5'
1588	14601		1.02	2.3E-01	U22837.2	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
1608	14640	27617	1.21	2.3E-01	AJ245480.1	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1636	14668	27644	2.52	2.3E-01	Y10987.2	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
2081	15079		1.33	2.3E-01	AJ235333.1	NT	Mus musculus cdf5 gene, exon 1, partial
2452	15457	28478	2.76	2.3E-01	BE297718.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF-4/FEEL gene
2550	15657	28676	1.27	2.3E-01	MI1319.1	NT	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2835	14422	27381	2.34	2.3E-01	AB015033.1	NT	Human erythropoietin gene, complete cds
2874	15032	28955	1.25	2.3E-01	AA601379.1	EST_HUMAN	Martiniabilla agarosyrans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
3100	16157		7.16	2.3E-01	R21732.1	EST_HUMAN	no16d08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu
3383	16432	29360	1.26	2.3E-01	U69836.1	EST_HUMAN	repetitive element:contains element THR repetitive element :
							YF21D07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
							YF97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3854	16894	29798	1.06	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, Intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3956	16998		5.02	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4212	17241		0.92	2.3E-01	J03267.1	NT	Rat atrial natriuretic factor (ANF) gene, 5' end
4377	17405	30285	0.84	2.3E-01	R82252.1	EST_HUMAN	y17f01.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4428	17455		2.24	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4479	17504	30392	1.07	2.3E-01	D90899.1	NT	Synchoyellus sp. PCC6903 complete genome, 1/27, 1-133859
4515	17540	30426	1.9	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4584	17608	30502	7.42	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5087	18097	30973	0.65	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5200	18209	31083	0.91	2.3E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5377	18481	31356	2.19	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5503	18603	31832	2.51	2.3E-01	BF058381.1	EST_HUMAN	7430b05.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]; ;
5608	18704	31861	4.56	2.3E-01	X96587.1	NT	C. familiaris rom1 gene
5733	18827		1.01	2.3E-01	L39112.1	NT	Vitellogenin small subunit ribosomal RNA gene
5845	18935	32119	0.81	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2666 nt]
6051	19132	32340	2.02	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318448 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6051	19132	32341	2.02	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318448 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6812	19866	33164	0.76	2.3E-01	AF198089.1	NT	Oryzobolus cuniculus cytochrome oxidase subunit 1 (cox1a2) mRNA, complete cds; nuclear gene for mitochondrial product
7061	20083	33391	5.28	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Aliu repetitive element;
7318	20289	33632	0.69	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7505	20470	33830	0.79	2.3E-01	AF000227.1	NT	Secale cereale omega ocobin gene, complete cds
7646	20606	33972	2.65	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7649	20609	33974	10.72	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7649	20609	33975	10.72	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7866	20810		3.39	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7871	20815	34183	1.36	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
8028	20965		2.69	2.3E-01	N80983.1	EST_HUMAN	za12c08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:2923558 5'
8073	21010	34408	0.63	2.3E-01	11418821	NT	Homo sapiens protocadherin alpha cluster (LOC633960), mRNA
8073	21010	34409	0.63	2.3E-01	11418821	NT	Homo sapiens protocadherin alpha cluster (LOC633960), mRNA
8184	21154	34582	0.6	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
8326	21295	34710	2.02	2.3E-01	M68931.1	NT	Oxyficha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8838	21805	35222	0.54	2.3E-01	U57999.1	NT	Mus musculus prosapoin (psap/SGP-1) gene, complete cds
9125	22091	35519	0.48	2.3E-01	AW090541.1	EST_HUMAN	xc90e06.x1 NCJ_CGAP_Br35 Homo sapiens cDNA clone IMAGE:2591554 3'
9240	22206	35639	0.45	2.3E-01	AW964480.1	EST_HUMAN	EST376533 IMAGE resequences, MAGH Homo sapiens cDNA
9496	22460	35900	0.59	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X633368)
9498	22460	35901	0.59	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X633368)
9940	22867	36329	0.63	2.3E-01	6879318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
10088	23013	36486	0.78	2.3E-01	BE277860.1	EST_HUMAN	Mus musculus NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'
10141	23067	36543	0.69	2.3E-01	AW964460.1	EST_HUMAN	EST376533 IMAGE resequences, MAGH Homo sapiens cDNA
10191	23116	36600	1.36	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
10226	23151	36640	0.57	2.3E-01	AW364633.1	EST_HUMAN	PM2.DT0036-281259-001-104 DT0036 Homo sapiens cDNA
10284	23219	36702	2.8	2.3E-01	BE173060.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10351	23275	36749	2.33	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10809	23730	37232	0.8	2.3E-01	AF201828.1	NT	Murine hepatitis virus strain 2, complete genome
10820	23741		6.12	2.3E-01	BF133977.1	EST_HUMAN	601946155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102082 3'
11355	24305	37832	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11355	24305	37833	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11622	24463	38015	1.69	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11622	24463	38016	1.69	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11679	24645	38222	2.81	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
12068	24669	38566	1.47	2.3E-01	AE004868.1	NT	Pseudomonas aeruginosa PA01, section 229 of 529 of the complete genome
12279	25098		5.42	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9.6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25168		6.49	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT28M6 Homo sapiens cDNA clone HCOE44 5'
12403	25176		2.24	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b08 SN0012 Homo sapiens cDNA
12460	25892	31417	2.82	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2 :contains PTRS.b2 TAR1 repetitive element :

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12494	25937	31312	11.07	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12544	25267		2.36	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12591	25295		3.71	2.3E-01	AJ005519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12680	25348		2.12	2.3E-01	U49645.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12928	25511		1.49	2.3E-01	BF475611.1	EST_HUMAN	mac30h12.x1 Lupski_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element:
90	13208	26130	0.99	2.2E-01	AI052190.1	EST_HUMAN	oz14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
1587	14800	27576	2.33	2.2E-01	AF187850.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2100	16117	28139	2.2	2.2E-01	M34640.1	NT	Homo sapiens PPAR delta gene, promoter region
2412	15419	28443	8.18	2.2E-01	BF677538.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2593	15594	28611	2.54	2.2E-01	BE618258.1	EST_HUMAN	602085078F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2593	15594	28612	2.54	2.2E-01	BE618258.1	EST_HUMAN	601462829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866190 5'
2893	15952	28888	4.89	2.2E-01	BE156625.1	EST_HUMAN	601462829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866190 5'
2893	15952	28889	4.89	2.2E-01	BE156625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2893	15952	28889	4.89	2.2E-01	BE156625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2932	15990		1.29	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3403	16452		2.28	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3927	16987		0.66	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4240	17269		1.2	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4247	17276	30158	5.86	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4292	17321	30200	2.33	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4292	17321	30201	2.33	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4383	17411	30294	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4383	17411	30295	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4436	17482	30370	23.17	2.2E-01	AW361098.1	EST_HUMAN	RC1-C10249-141199-021-g04 G10249 Homo sapiens cDNA
4663	17880		1.38	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP6) pseudogene
4663	17880		1.38	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP6) pseudogene
4968	17895	30773	1.67	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stralagene INT neuron (#837233) Homo sapiens cDNA clone IMAGE:648968 5'
5082	18092		1.34	2.2E-01	L13289.1	NT	Mus musculus vinculin gene, exon 3
5160	18169	31048	1.22	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA
5181	18190	31066	1.51	2.2E-01	H60548.1	EST_HUMAN	y42h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208001 5' similar to
5263	18271		1.06	2.2E-01	AL163206.2	NT	gb:Z14116_jna1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21C006

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5838	18928	32112	2.18	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5849	18939		3.59	2.2E-01	D64000.1	NT	Synechocystis sp. PCC8803 complete genome, 19/27, 2392729-2538999
6114	19192	32415	0.61	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6114	19192	32416	0.61	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6864	19917	33211	0.7	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
6864	20189	33514	0.58	2.2E-01	AA490706.1	EST_HUMAN	ab02e09.s1 Stratiogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:839656 3'
6864	20189	33515	0.68	2.2E-01	AA490706.1	EST_HUMAN	ab02e09.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839656 3'
7222	20244	33578	7.78	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7336	20307	33650					Streptococcus pyogenes phosphoglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spA) genes, complete cds; and unknown genes
7336	20307	33651	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spA) genes, complete cds; and unknown genes
7609	20474	33834	2.11	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7609	20474	33835	2.11	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7728	20684	34048	0.59	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7886	20905	34297	0.6	2.2E-01	AF287967.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
8000	20909	34332	0.5	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8354	21323		2.51	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8425	21394	34805	1	2.2E-01	Z49933.1	NT	E. coli sepA and sepB genes
8896	21862	35284	0.49	2.2E-01	AJ132818.1	NT	Pan troglodytes MeCP2 gene 3'UTR
9234	22200	35629	0.51	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9234	22200	35630	0.51	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9247	22213	35643	4.12	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 138 of the complete genome
9257	22233	35663	0.47	2.2E-01	U09964.1	NT	Mus musculus ICR/Swiss glycerinaldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
9378	22341		3.89	2.2E-01	AW856039.1	EST_HUMAN	PM3-C10263-241298-009-b07 C10263 Homo sapiens cDNA
9470	22434	35872	1.4	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9553	22515	35966	1.4	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9644	22588	36037	1.3	2.2E-01	W02988.1	EST_HUMAN	za04f08.11 Soares melanocyte 2kb-HM Homo sapiens cDNA clone IMAGE:291591 5'
9662	22819	36274	15.89	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9707	22660	36116	0.86	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9718	22746	36197	0.78	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9731	22759	36212	4.38	2.2E-01	IM89643.1	NT	Brachydanio rerio epandym beta and gamma chains (Epd) gene, complete cds

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9979	22908	36371	0.5	2.2E-01	Q90980	SWISSPROT	CYCLOC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10174	23099	36579	3.74	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
10313	23237	36719	1.78	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10337	23459	36956	1	2.2E-01	9825671	NT	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10997	23619	37113	0.52	2.2E-01	T59472.1	EST_HUMAN	Human herpesvirus 6, complete genome
10997	23619	37114	0.52	2.2E-01	T59472.1	EST_HUMAN	y663d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'
							y663d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'
							Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c660 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinone synthase A (pqqA) genes, complete cds; and pyrroloquinone
10795	23857	37150	0.51	2.2E-01	AF068284.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10810	23731		0.68	2.2E-01	AF071001.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10856	23776	37274	0.67	2.2E-01	AE001882.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10856	23776	37275	0.67	2.2E-01	AE001882.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11751	24836	38215	3.77	2.2E-01	X01818.1	NT	Drosophila 88C glue gene cluster
11789	23944	37486	3.41	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12317	25950		2.32	2.2E-01	U82671.2	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12406	25179		3.88	2.2E-01	AF188943.1	NT	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12513	17482	30370	6.62	2.2E-01	AW361088.1	EST_HUMAN	h17b02.x1 NCI_CGAP_G01 Homo sapiens cDNA clone IMAGE:2972523 3'
12514	25246		1.7	2.2E-01	AF661922.1	EST_HUMAN	Phodopus sungorus uncoupling protein 3 mRNA, partial cds
13111	25946		1.36	2.2E-01	AF271265.1	NT	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
972	14024	26978	1.58	2.1E-01	AA569289.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
975	14026	26980	1.06	2.1E-01	AL161504.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1126	14169		2.38	2.1E-01	AE002314.2	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1203	14242	27189	0.88	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1203	14242	27200	0.88	2.1E-01	6754289	NT	Mus musculus mas proto-oncogene and Igf2 gene for insulin-like growth factor type 2 and L41 ps and Au76 pseudogenes
1512	14544	27515	1.05	2.1E-01	AJ249995.1	NT	6k73e02.e1 NCI_CGAP_G04 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
1929	14953	27949	1.94	2.1E-01	AA906824.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2185	15181	28201	3.26	2.1E-01	BF695073.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2499	15895	28516	2.19	2.1E-01	HT3968.1	EST_HUMAN	yy04f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	15895	28517	2.19	2.1E-01	H73968.1	EST_HUMAN	yu0407.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:232837 3'
2936	15994	28914	2	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3481	16507	29428	0.92	2.1E-01	AA639482.1	EST_HUMAN	nc90b10.s1 NC1 CGAP_Co8 Homo sapiens cDNA clone IMAGE:1159579 3'
3819	16869		6.5	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4045	17083		1.16	2.1E-01	AE001793.1	NT	Thermotoga maritima section 105 of 135 of the complete genome
4084	17118	30013	1.48	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4084	17118	30014	1.48	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4403	17431		1.62	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4607	17628	30520	1.75	2.1E-01	AB010273.1	NT	Homo sapiens pshp47 gene, complete cds
5063	18073	30953	5.08	2.1E-01	D13587.1	NT	Lampetra leptonica mRNA for alpha-2-macroglobulin, complete cds
5110	18120	30994	1.13	2.1E-01	Q01338	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)
5216	18225	31099	0.92	2.1E-01	AE001528.1	NT	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5374	18479	31352	5.48	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
7071	20093	33403	1.16	2.1E-01	AJ223392.1	NT	Drosophila melanogaster 16S rRNA gene, partial cds
7083	20017	33320	1.92	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7636	20596	33959	0.78	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7636	20596	33960	0.78	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7648	20608		2.34	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7973	20912	34303	1.77	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
8027	20964	34359	1.08	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8027	20964	34360	1.08	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8066	21022		0.61	2.1E-01	T87354.1	EST_HUMAN	yd83501.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:114783 5'
8407	21376		1.04	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8847	21814	35234	5.05	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcB, putative haemochrom processing protein (hmcC), putative ABC transporter (hmcB), putative haemochrom structural protein (hmcA), and haemochrom immunity protein (hmcI) genes, complete cds
9149	22115	35540	0.84	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
9149	22115	35541	0.84	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
9392	22357	35787	6.08	2.1E-01	N34786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
9862	22798	36251	0.59	2.1E-01	N42536.1	EST_HUMAN	Y11e10.r1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:270954 5'
9862	22798	36252	0.59	2.1E-01	N42536.1	EST_HUMAN	Y11e10.r1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:270954 5'

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9871	22824	36277	2.77	2.1E-01	X97378.1	NT	A.thaliana mRNA for AIRanBP1b protein
9876	22803	36367	1.28	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10892	23614	37109	1.13	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10725	23847	37140	2.89	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE)(DGK-DELTA)(DGK KINASE DELTA)
10731	23853	37146	0.93	2.1E-01	BF574254.1	EST_HUMAN	(80 KD DIACYLGLYCEROL KINASE)
11009	23974	37488	3.69	2.1E-01	AF294298.1	NT	Anolis lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11890	24771		2.15	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11905	24786	38376	1.61	2.1E-01	BE180422.1	EST_HUMAN	RC3-HY0822-040500-013-b11 HT0822 Homo sapiens cDNA
12137	25502		1.38	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12660	25339		1.94	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12860	25860		1.8	2.1E-01	L32388.1	NT	Human granulosa gene
12914	26493		2	2.1E-01	BE62149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915676 5'
13045	25586	31682	1.62	2.1E-01	BE672330.1	EST_HUMAN	7A59602x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3223034 3'
201	13302	26231	1.32	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
535	13606		1.82	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
700	13762	26594	1.25	2.0E-01	M77085.1	NT	O. cuniculus gemline lgh heavy chain V-H pseudogene, allotype VH2
811	13569	26818	1.96	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1013	14061	27012	0.72	2.0E-01	D90605.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1127	14170	27121	2.83	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1259	14294	27258	1.42	2.0E-01	AJ132595.5	NT	Homo sapiens rac1 gene
1311	14347	27313	2.04	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1454	14487		1.39	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1483	14516	27490	15.27	2.0E-01	4503408	NT	Homo sapiens dystrobrein, alpha (DTNA), mRNA
1555	14587	27559	2.13	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1560	14592	27585	1.52	2.0E-01	AF260700.1	NT	Homo sapiens sodiumiodide symporter mRNA, partial cds
1706	14736	27718	1.38	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1730	14760		2.09	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1772	14801		3.8	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1907	14931	27826	0.84	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1907	14931	27827	0.94	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2355	15364		1.88	2.0E-01	X82877.1	NT	H. sapiens Nat-D-glucose cotransport regulator gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3499	16546	29472	0.74	2.0E-01	P46807	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3582	16627		0.82	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI_CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3720	16763	28674	0.79	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ;
3855	16895	28789	1.14	2.0E-01	AL163204.2	NT	CED-11 PROTEIN
3977	17017	28831	0.7	2.0E-01	Z46808.1	NT	Homo sapiens chromosome 21 segment HS21C004
4597	17618		10.26	2.0E-01	BE826165.1	EST_HUMAN	<i>Sus scrofa</i>
5079	18088	30868	7.06	2.0E-01	8922080	NT	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5144	18163	31033	0.97	2.0E-01	Y19216.1	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5298	18302	31163	0.93	2.0E-01	BE439491.1	EST_HUMAN	Homo sapiens putative pailHbD pseudogene for hair keratin, exons 1 to 9
5520	18619	31553	2.31	2.0E-01	X66800.1	NT	HTM1-122F1 HTM1 Homo sapiens cDNA
5831	18921	32104	1.89	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5940	19026	32220	0.89	2.0E-01	X97856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6178	19253	32486	5.47	2.0E-01	U15300.1	NT	F.rubripes DNA encoding for valyl-tRNA synthetase
6298	19370		0.79	2.0E-01	M75967.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6417	19484	32733	0.56	2.0E-01	P02467	SWISSPROT	Human hepatocyte growth factor gene, exon 1
6569	19829	32895	3.05	2.0E-01	X61033.1	NT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6879	19736	33012	4.25	2.0E-01	AW360865.1	EST_HUMAN	M. auratus mu class glutathione transferase gene
7512	20477	33838	1.27	2.0E-01	AF250371.1	NT	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
7679	20637	33999	0.72	2.0E-01	P54422	SWISSPROT	Mus musculus phosphofructokinase-1 C isozyme (Pfk) gene, exons 3 through 7
8064	20991	34389	0.61	2.0E-01	V00726.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8285	21254		6.17	2.0E-01	AF028020.1	NT	Mouse germ line gene coding for beta-globin (Y2)
8542	21510	34927	3.1	2.0E-01	X91151.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
9074	22040		0.43	2.0E-01	BE562247.1	EST_HUMAN	M. musculus scp2 gene exon 14
9706	22659	36115	1.08	2.0E-01	U82511.1	NT	601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9745	22686	36141	0.76	2.0E-01	U71122.1	NT	Dichostellium discoideum random elug cDNA19 protein (rcs19) mRNA, partial cds
9914	22735		8.23	2.0E-01	AE001278.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
10103	23029	36506	0.62	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
10103	23029	36507	0.62	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10251	23176		1.94	2.0E-01	AF146692.1	NT	DAUGHTERLESS PROTEIN
10401	23323	36807	1.94	2.0E-01	AF086507.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
10401	23323	36808	1.94	2.0E-01	AF086507.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10528	23450	36948	0.84	2.0E-01	AF157814.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
							Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10528	23450	38949	0.94	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10575	23497		0.78	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppe)
10770	23691	37188	0.97	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
11189	24145	37678	2.24	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11189	24145	37679	2.24	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
12841	25325		1.42	2.0E-01	AF206637.2	NT	Plumbeola promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12828	25779		1.66	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12837	25711	31609	1.34	2.0E-01	AW975287.1	EST_HUMAN	EST387405 MAGE resequencas, MAGN Homo sapiens cDNA
12875	25508	31707	4.12	2.0E-01	AI023592.1	EST_HUMAN	ov80a10.61 Soares testis NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12898	25483		2.98	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
110	13221		9.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlnt1), mRNA
352	13441	28366	6.09	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
657	13723	28647	2.66	1.9E-01	U32581.2	NT	Homo sapiens lamtadialota protein kinase C-interacting protein mRNA, complete cds
657	13723	28648	2.66	1.9E-01	U32581.2	NT	Homo sapiens lamtadialota protein kinase C-interacting protein mRNA, complete cds
684	13730	28655	8.69	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
685	13730	28655	8.69	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
988	14039		1.19	1.9E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (il2rg), mRNA
1106	14150	27101	9.83	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1372	14406	27376	2.9	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1430	14484		3.22	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (tbp-2) gene, complete cds
2390	15398	28423	3.89	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2934	16992	28912	3.47	1.9E-01	U66066.1	NT	Sigmoidon hispidus p53 gene, partial cds
2949	16008		4.89	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3406	16455	28378	4	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3492	16539	29464	5.36	1.9E-01	R16467.1	EST_HUMAN	y42f10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3817	16857	29763	0.87	1.9E-01	AF284017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3848	16888	29781	2.26	1.9E-01	P39768	SWISSPROT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4018	17057	28859	3.91	1.9E-01	AB006784.1	NT	PAIR-RULE PROTEIN ODD-PAIRED
4110	17144	30038	1.42	1.9E-01	AW754106.1	EST_HUMAN	OM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4259	17288	30169	1.24	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA
4498	17521	30408	0.83	1.9E-01	JAL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
5047	18080		1.15	1.9E-01	AF223042.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5231	18239		1.01	1.9E-01	AI631199.1	EST_HUMAN	ts93g12x1 NCJ CGAP_G06 Homo sapiens cDNA clone IMAGE:2238886 3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5685	18780		5.2	1.9E-01	AW130149.1	EST_HUMAN	x129a07.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC
5728	18822	32002	8.11	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
5939	19025	32219	0.71	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5987	19072		2.15	1.9E-01	AU133116.1	EST_HUMAN	Mus musculus Wm protein (Wm) gene, complete cds
6461	19526	32776	0.95	1.9E-01	AI762391.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6527	19590	32850	0.88	1.9E-01	AW148452.1	EST_HUMAN	w154f02.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394099 3'
7164	18395	31240	1.46	1.9E-01	R43212.1	EST_HUMAN	x14c08.x1 NCL CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP
7193	20217	33547	0.95	1.9E-01	AF034920.1	NT	SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7193	20217	33548	0.95	1.9E-01	AF034920.1	NT	y009a12.61 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13
7474	20440	33798	0.65	1.9E-01	U73846.1	NT	repetitive element ;
7709	20666	34033	0.76	1.9E-01	U93688.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7734	20689	34053	1.35	1.9E-01	U80922.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7784	20737	34109	2.64	1.9E-01	AF072724.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
8318	21287	34701	1.41	1.9E-01	AL161567.2	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds
8034	22000	35421	12.68	1.9E-01	AB033024.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9297	22263	35692	1.32	1.9E-01	M14568.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
9297	22263	35693	1.32	1.9E-01	M14568.1	NT	Marasupial cat beta-globin gene mRNA, partial cds
10234	23159	36847	0.67	1.9E-01	AA912486.1	EST_HUMAN	Marasupial cat beta-globin gene mRNA, partial cds
10602	23524	37019	0.72	1.9E-01	BE830353.1	EST_HUMAN	o96g10.s1 NCL CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu
10602	23524	37020	0.72	1.9E-01	BE830353.1	EST_HUMAN	repetitive element;
11106	24068	37588	1.87	1.9E-01	AF223391.1	NT	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
11631	24714	38298	1.47	1.9E-01	M22253.1	NT	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
12033	24909	38504	3.54	1.9E-01	AJ243213.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12049	24922	38519	1.63	1.9E-01	L07344.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
12975	25540		1.62	1.9E-01	AF036959.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
34	13154	26055	2.78	1.8E-01	U73200.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 8) gene, 5' end
260	15937	26281	1.39	1.8E-01	AB022090.1	NT	Rattus norvegicus nuclear serine/threonine protein kinase mRNA, complete cds
							Mus musculus p116Rip mRNA, complete cds
							Mus musculus Ccig gene for chaperonin containing TCP-1 gamma subunit, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
370	13456	26386	1.91	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
983	14034	26986	0.89	1.8E-01	AI912212.1	EST_HUMAN	w47102.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337061 3'
1093	14136	27087	1.05	1.8E-01	AF000580.1	NT	Dicystostellum discoideum plasmid Ddp5, complete genome
1293	14328	27280	9.43	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1503	14536	27507	1.17	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1503	14538	27508	1.17	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1664	14889		1.37	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1882	14907		1.47	1.8E-01	AI733708.1	EST_HUMAN	qg22410.x5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE
1930	14954	27850	1.66	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2702	15698		3.94	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081298-038-g04 DT0018 Homo sapiens cDNA
2908	15987		1.95	1.8E-01	AF184589.1	NT	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds
2914	15972	28896	0.85	1.8E-01	AW182300.1	EST_HUMAN	X41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3141	16198	29108	1.35	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3379	16428	29354	0.82	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3637	16680	29594	1.69	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3637	16680	29595	1.69	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4360	17387		0.75	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BdA-DQB), complete cds
4596	17608	30503	6.42	1.8E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4806	17823	30718	2.5	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5051	18083	30941	2.11	1.8E-01	X79794.1	NT	N.tubacum mRNA pNLA-35
5084	18094	30970	1.96	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA
5099	18109	30982	0.93	1.8E-01	AI792382.1	EST_HUMAN	en28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5131	18140	31018	2.66	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5214	18223		0.73	1.8E-01	U66150.1	NT	Loligo forbesi TTA repeat microsatellite region Lfor4
5371	18478	31349	0.84	1.8E-01	BE082626.1	EST_HUMAN	RC8-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA
5806	18992	32183	1.91	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90

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12301	25112	31840	1.88	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCL_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4156318 5'
12752	25398		2.05	1.8E-01	Q86982	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12886	26469		1.85	1.8E-01	R24494.1	EST_HUMAN	Yn48h10.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:133027 5'
12907	25489		1.96	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hxt1)
579	13648	26561	1.77	1.7E-01	BE385184.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
806	13864	26814	2.22	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
962	14015		1.93	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1998	15019		3.18	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2871	15931	28848	2.3	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2871	15931	28849	2.3	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2938	15996	28917	1.69	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3010	16068	28988	1.22	1.7E-01	AJ238736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3010	16068	28989	1.22	1.7E-01	AJ238736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3122	16179	29089	1.68	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3378	16427	29353	0.82	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3482	16508	29429	1.48	1.7E-01	AJ269603.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3959	16999	29914	5.69	1.7E-01	AJ236377.1	NT	Homo sapiens derivative 11 breakpoint fragment partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4591	17612		1.9	1.7E-01	X62936.1	NT	Schistosoma gregaria alpha repetitive DNA
4876	17893	30782	1.21	1.7E-01	A1247635.1	EST_HUMAN	qh57e09.x1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 OFR repetitive element;
5165	18174		0.82	1.7E-01	AF072726.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5210	18219	31095	0.74	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5482	18582	31493	1.88	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5482	18582	31494	1.88	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5674	18769	31941	0.74	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6463	19528	32777	12.89	1.7E-01	H72118.1	EST_HUMAN	ys02g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213668 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6528	19589	32848	0.9	1.7E-01	A1370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6528	19589	32849	0.9	1.7E-01	A1370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
7031	18363	31250	0.78	1.7E-01	BE300288.1	EST_HUMAN	600944087T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860248 3'
7083	20085		1.76	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7196	20220		0.79	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7430	20397	33749	1.58	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7515	20480	33841	6.55	1.7E-01	BE734178.1	EST_HUMAN	601589022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
7721	20678	34043	1.42	1.7E-01	P18724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7739	26688	34057	0.71	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
8194	21164	34573	1.24	1.7E-01	AF000573.1	NT	Homo sapiens homogenitase 1, 2-dioxygenase gene, complete cds
8295	21285	34676	0.92	1.7E-01	AF150689.1	NT	Pseudomonas putida long-chain-fatty-actid-CoA ligase (fadD) gene, complete cds
8620	21588	35004	7.37	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8620	21588	35005	7.37	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9043	22011	35433	0.6	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
9079	22045	35468	3.22	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9196	22162	35590	0.81	1.7E-01	AF217413.1	NT	Homo sapiens neurologilin 3 isoform gene, complete cds, alternatively spliced
9196	22162	35591	0.81	1.7E-01	AF217413.1	NT	Homo sapiens neurologilin 3 isoform gene, complete cds, alternatively spliced
9349	22314	35739	0.44	1.7E-01	R77002.1	EST_HUMAN	y66902.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144242 5'
9523	22486	35933	0.43	1.7E-01	BE283142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3337184 5'
9523	22486	35934	0.43	1.7E-01	BE283142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3337184 5'
9848	22875	36337	8.16	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
10056	22983	36451	0.47	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGe sequences, MAGO Homo sapiens cDNA
10056	22983	36452	0.47	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGe sequences, MAGO Homo sapiens cDNA
10073	23000	36470	1.93	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
10148	23074	36548	0.59	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10148	23074	36549	0.59	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10167	23092	36570	0.7	1.7E-01	AJ281749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10593	23515		2.43	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21G084
10789	23680	37176	1.24	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10761	23682	37178	1.81	1.7E-01	AA627872.1	EST_HUMAN	nc60e07.s1 NCJ_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1146292 3' similar to gb.L25081
10866	23886		0.42	1.7E-01	AL161542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN);
11040	24004	37530	8.17	1.7E-01	BE390835.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42
							601288547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11157	24115	37841	2.61	1.7E-01	AA814617.1	EST_HUMAN	af43a03.s1 NCI_CGAP_CKIS1 Homo sapiens cDNA clone IMAGE:1426924 3'
11447	24390	37833	8.03	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11447	24390	37834	8.03	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11703	24668	38245	1.6	1.7E-01	AA883375.1	EST_HUMAN	af45f09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
12021	24898		1.68	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12141	25005	38615	1.74	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12273	25993		1.54	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12437	25738	31618	1.55	1.7E-01	AA847421.1	EST_HUMAN	ce18h02.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1386291
12555	25739		1.69	1.7E-01	AI824404.1	EST_HUMAN	b69g05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12833	25450	31723	14.15	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
126	13233	26162	2.02	1.6E-01	AF217332.1	NT	Homo sapiens mevalonate kinase gene, exon 8 and 7
680	15814	26870	1.58	1.6E-01	R31497.1	EST_HUMAN	yt78f12.f1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1504	14537	27509	1.4	1.6E-01	AA648863.1	EST_HUMAN	nk28a12.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014839 3'
1525	14557	27528	4.54	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1941	14955	27982	1.79	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2001	15022		1	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2393	15992	28427	0.99	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2501	15504	28531	1.19	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2902	15961	28881	10.42	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2902	15961	28882	10.42	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3649	16692	29607	1.2	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3649	16692	29608	1.2	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3788	16827	29734	0.78	1.6E-01	AE000982.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4025	17063		2.81	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4358	17383	30265	10.43	1.6E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4494	17509		3.1	1.6E-01	AW068601.1	EST_HUMAN	EST380677 IMAGE:1386291
4491	17516		4.57	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4916	17893	30824	1.43	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4916	17893	30825	1.43	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4982	17897	30885	4.36	1.6E-01	AA088343.1	EST_HUMAN	zB4h09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5004	18018	30905	1.94	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV ;
5004	18018	30906	1.94	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5004	18018	30906	1.94	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5069	18079	30960	1.16	1.6E-01	BE018707.1	EST_HUMAN	bb83h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715
5461	18563	31475	0.87	1.6E-01	L40608.1	NT	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE); Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5600	18696	31666	2.82	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5600	18696	31667	2.82	1.6E-01	AW197496.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN ;
5612	18708	31865	2.31	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
6144	19219	32449	0.9	1.6E-01	BE925803.1	EST_HUMAN	Rattus norvegicus CCAATenhancer binding protein epsilon (cebpe) gene, complete cds
6385	19463	32697	0.57	1.6E-01	BF183594.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6385	19453	32698	0.57	1.6E-01	BF183594.1	EST_HUMAN	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6568	19628	32993	1.99	1.6E-01	AL161588.2	NT	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6568	19628	32994	1.99	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6950	20174	33498	0.55	1.6E-01	AA388047.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
9869	20192	33519	0.66	1.6E-01	AB046786.1	NT	z89c04.r1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:729511 5'
7156	19388	31232	4.63	1.6E-01	AW291215.1	EST_HUMAN	Homo sapiens mRNA for KIAA1566 protein, partial cds
7518	20483	33944	0.61	1.6E-01	Z49632.1	NT	U1-H-B12-agi-b-08-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
8056	20993	34390	1.59	1.6E-01	AW246359.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR132w
8090	21026	34425	0.57	1.6E-01	AW246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8102	21038	34582	1.15	1.6E-01	AU136525.1	EST_HUMAN	Mus musculus Cdc2x>dependent activator protein for secretion (Cdcps), mRNA
8201	21171	34582	1.26	1.6E-01	L49349.1	NT	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004466 5'
8359	21328		0.51	1.6E-01	BE244087.1	EST_HUMAN	Gorilla gorilla androgen receptor gene, partial exon
8456	21425	34841	0.66	1.6E-01	U38243.1	NT	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8979	21945	35359	0.85	1.6E-01	Z99119.1	NT	Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
9178	22144	35671	0.71	1.6E-01	R13673.1	EST_HUMAN	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
9285	22251		0.63	1.6E-01	L36691.1	NT	Y60h08.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:26873 5'
9322	22287	35717	1.9	1.6E-01	Z49501.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9466	22430		0.63	1.6E-01	AF111167.2	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
10009	22836		2.05	1.6E-01	BF376171.1	EST_HUMAN	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10012	22839	36404	2	1.6E-01	Z49501.1	NT	RC3-SJ0200-041199-011-h01 S10200 Homo sapiens cDNA
10048	22975		0.96	1.6E-01	BE155684.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR001w

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11017	23982	37509	2.59	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11122	24082	37607	1.82	1.6E-01	Z28073.1	NT	S.cerevisiae chromosome XI reading frame ORF YKL073w
11122	24082	37608	1.82	1.6E-01	Z28073.1	NT	S.cerevisiae chromosome XI reading frame ORF YKL073w
11344	24294	37820	1.5	1.6E-01	BE259649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11431	24394		3.84	1.6E-01	AF106064.1	NT	Plasmidium falcatum calcium-dependent protein kinase-3 (cdp3) gene, complete cds
11740	24835	38204	6.59	1.6E-01	8871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12155	25906		1.75	1.6E-01	6679468	NT	Mus musculus protein kinase, cGMP-dependent, type II (Pkg2), mRNA
12275	25095	38179	6.76	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GIG Homo sapiens cDNA clone GLCEMF07 5'
12608	25307		1.62	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-H01_1 LT0074 Homo sapiens cDNA
12697	25721		22.15	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12856	25453		2.73	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12945	25524		2.58	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12971	25537	31716	2.24	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12978	25543		1.93	1.6E-01	BE267894.1	EST_HUMAN	801125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'
248	13345	26270	1.73	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	13345	26271	1.73	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
589	15813		2.4	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
783	13843	26788	1.51	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1094	14138	27089	1.01	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1099	14143	27093	2.55	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1115	14159		1.57	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1280	14315	27276	3.58	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1280	14315	27277	3.58	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1478	14511	27487	2.54	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
1923	14947	27943	1.65	1.5E-01	AW444451.1	EST_HUMAN	UI-H-B13-alk-b-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2723	15717	28735	1.47	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2924	15982		1.1	1.5E-01	AW572516.1	EST_HUMAN	xw56a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_ma1
3048	16105	29019	0.78	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3363	16413	29338	5.55	1.5E-01	AA835049.1	EST_HUMAN	cc68406.at NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3381	16430	29357	0.74	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN); L.stagnalis mRNA for G protein-coupled receptor
3381	16430	29358	0.74	1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3440	16487	29405	0.97	1.5E-01	AW612237.1	EST_HUMAN	h129f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element;
3768	16810	29719	2.22	1.5E-01	U09884.1	NT	Mus musculus ICR/Swiss glyceralddehyde 3-phosphate dehydrogenase (Gapdh-S) gene, complete cds Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3782	16823	29731	0.8	1.5E-01	7108358	NT	XYNA; Thermoanaerobacterium; xynA; 4182 base-pairs
3785	16835	29740	0.86	1.5E-01	M97882.1	NT	h10f06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3881	16920	29829	2.26	1.5E-01	AW665983.1	EST_HUMAN	Populus trichocarpa cv. Trichobel ABI3 gene
3886	16936	29846	0.71	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3896	16936	29847	0.71	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4080	17115	30011	2.63	1.5E-01	AW366559.1	EST_HUMAN	RC2-HT0149-181098-012-c09 HT0149 Homo sapiens cDNA
4213	17242	30127	8.83	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4513	17538	30422	0.91	1.5E-01	BE791253.1	EST_HUMAN	601583988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4513	17538	30423	0.91	1.5E-01	BE791253.1	EST_HUMAN	601583988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4756	17776	30872	1.88	1.5E-01	BF687685.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4783	17717	28735	2.86	1.5E-01	BF686381.1	EST_HUMAN	602067192F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247637 5'
4830	17847	30747	1	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4830	17847	30748	1	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5034	18048	30828	1.2	1.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5134	18143	31023	1.07	1.5E-01	5579451	NT	Homo sapiens calbindin 1, (28kD) (CALB1), mRNA
5328	18434	31186	2.46	1.5E-01	P07998	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5357	18482	31331	1.03	1.5E-01	AF256652.1	NT	Calman crocodilus MHC class II beta chain (hcIIbeta) gene, complete cds
5401	18504		5.5	1.5E-01	P15198	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5516	18712	31870	4.35	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-084-F10 CT0219 Homo sapiens cDNA
5559	18755	31922	7.17	1.5E-01	U85016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
5559	18755	31923	7.17	1.5E-01	U85016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
6012	19095	32295	0.79	1.5E-01	4508810	NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA
6120	19188	32422	1.74	1.5E-01	6763659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6120	19188	32423	1.74	1.5E-01	6763659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6181	19236	32467	1.96	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6319	19390	32630	3.25	1.5E-01	BE1727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6375	19443		1.86	1.5E-01	4506398	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6478	19543	32781	1.7	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6651	25664	32985	1.8	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6681	19738	33013	4.63	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6692	19749	33026	1.8	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6740	19795	33075	2.35	1.5E-01	Q28482	SWISSPROT	AMELOGENIN
6842	19895	33189	0.85	1.5E-01	AA714760.1	EST_HUMAN	rw30d10.s1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:1241971 3'
6871	19924	33220	1.8	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 517 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7171	18402	31247	5.15	1.5E-01	AW970285.1	EST_HUMAN	EST382376 IMAGE resequences, MAGK Homo sapiens cDNA
7214	25678		0.71	1.5E-01	AA811545.1	EST_HUMAN	cb7302.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element
7424	20391		1.91	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7621	20581	33945	1.68	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.s1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7846	20793	34169	0.96	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7846	20793	34170	0.96	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7857	20802	34177	1.84	1.5E-01	AW500811.1	EST_HUMAN	UI-HF-BND-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7857	20802	34178	1.84	1.5E-01	AW500811.1	EST_HUMAN	UI-HF-BND-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
8014	20952	34346	0.71	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of Ies1-1 (SOL3) gene, complete cds
8393	21362	34769	1.21	1.5E-01	P21303	SWISSPROT	MEROZITE RECEPTOR PK68 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8562	21530	34950	0.97	1.5E-01	AA970317.1	EST_HUMAN	0085g12.s1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8655	21623		1.01	1.5E-01	BE884769.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8743	21711		13.33	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8776	21743	35165	1.69	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'
8840	21808	35330	1.79	1.5E-01	D84476.1	NT	Pangasinanodon glgase growth hormone (GH) mRNA, complete cds
8962	21928		0.74	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9190	22156	35565	1.31	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9460	22424	35862	3.06	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9548	22511	35960	1.03	1.5E-01	BF585465.1	EST_HUMAN	za59e06.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:266866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9555	22517		2.73	1.5E-01	AV754819.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9760	22701		0.87	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9808	21131	34634	6.92	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
							Acipenser transmontano vitellogenin mRNA, partial cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10176	23101	36581	0.58	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10281	23208	36680	6.22	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10281	23206	36691	6.22	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10563	23483	36878	2.67	1.5E-01	X98852.1	NT	P. lentusculus mRNA for integrin beta subunit
10651	23573		0.52	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10671	23593	37089	2.49	1.5E-01	AJ814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10671	23593	37090	2.49	1.5E-01	AJ814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10793	23675	37172	2.19	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds
10906	23826	37338	2.14	1.5E-01	AJ011964.1	NT	Claycoptes purpurea ps1 gene
10906	23826	37339	2.14	1.5E-01	AJ011964.1	NT	Claycoptes purpurea ps1 gene
11173	24130	37689	4.35	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11173	24130	37690	4.35	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11412	24366	37891	1.71	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-026-D04 CN0024 Homo sapiens cDNA
11449	24392	37837	3.86	1.5E-01	AA426488.1	EST_HUMAN	zw46d02.r1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:773091 5' similar to contains element MER22 repetitive element;
11501	20581	33945	1.69	1.5E-01	AJ973167.1	EST_HUMAN	wr62c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
12229	25769		11.17	1.5E-01	BF700592.1	EST_HUMAN	602128753F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285549 5'
12607	25306		1.62	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12610	25309		1.81	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-obliterant-1 (Dio-1)
12668	25791		12.47	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
12748	25814		2.45	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA GD04 5'
12855	25722	31613	7.87	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
13073	25606	31689	1.53	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
289	13393		2.07	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S9P to TCRBV21S2A2 region
911	13966		3.95	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1264	14299		2.77	1.4E-01	T91864.1	EST_HUMAN	y454c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1763	14792		1.61	1.4E-01	6679080	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1766	14795	27780	1.82	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
2002	15023		12.82	1.4E-01	AF420615.1	EST_HUMAN	h072d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2482	15486	28509	1.15	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2804	15798	28815	7.57	1.4E-01	AJ833496.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3914	16954	29865	0.93	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3914	16954	29866	0.93	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4202	17233	30120	11.04	1.4E-01	A1899094.1	EST_HUMAN	b56c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4202	17233	30121	11.04	1.4E-01	A1899094.1	EST_HUMAN	b56c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4265	17294	30173	3.96	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							z480101.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057.mai1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN)/contains Alu repetitive element;
4440	17466		0.71	1.4E-01	AA776287.1	EST_HUMAN	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
4703	17724	30618	0.69	1.4E-01	5453861	NT	
4907	17924	30817	0.92	1.4E-01	AV689659.1	EST_HUMAN	AV689659 GKGC Homo sapiens cDNA clone GKCDUG09 5'
5379	18483	31358	4.72	1.4E-01	T90677.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5402	18506	31381	4.06	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5402	18505	31382	4.06	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6430	19496	32749	2.9	1.4E-01	BE326991.1	EST_HUMAN	hr87c02.x1 NCL_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:3133538 3'
6629	19687	32965	5.1	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6629	19687	32966	5.1	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6723	19779	33058	3.48	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6737	19793		1.28	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6759	19813	33093	2.02	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7333	20304		0.74	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7615	20575		1.67	1.4E-01	AW015375.1	EST_HUMAN	U1H-B10-aak-c-09-c-UJ.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7841	20601	33965	0.51	1.4E-01	F08746.1	EST_HUMAN	HSCGTDB011 normalized Infant brain cDNA Homo sapiens cDNA clone c-1db01
							w04f12.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW1CE4_HUMAN
7694	20652		0.61	1.4E-01	A1762827.1	EST_HUMAN	P49662 CASPASE-4 PRECURSOR ;
7883	20827	34203	0.82	1.4E-01	U85645.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
8029	20996	34361	1.24	1.4E-01	A305192.1	EST_HUMAN	q80b12.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8818	21765		1.24	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
							th92b12.x1 Soares_NSF_F8_9W_OT_P_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:002710 002710 GAG POLYPROTEIN ;
9136	22102		0.67	1.4E-01	AK360893.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9264	22230	35661	4.68	1.4E-01	AA307073.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9345	22310	35735	0.56	1.4E-01	AW023636.1	EST_HUMAN	y10h08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138973 5'
9478	22442	35883	0.94	1.4E-01	R62746.1	EST_HUMAN	y10h08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138973 5'
9478	22442	35884	0.94	1.4E-01	R62746.1	EST_HUMAN	y10h08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138973 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9541	22504	35953	9.19	1.4E-01	BF310959.1	EST_HUMAN	601885465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9630	22574	36024	1.19	1.4E-01	W63411.1	EST_HUMAN	z09404.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
9702	22655	36109	0.43	1.4E-01	X73293.1	NT	M.vannelli genes rpoH, rpoB and rpoA
9702	22655	36110	0.43	1.4E-01	X73293.1	NT	M.vannelli genes rpoH, rpoB and rpoA
9713	22666	36123	1.44	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9713	22666	36124	1.44	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9805	21128	34532	2.06	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
10164	23089	36567	0.55	1.4E-01	X68092.1	NT	C.perfringens ORF for putative membrane transport protein
10346	23270	36747	1.12	1.4E-01	AF023813.1	NT	Macromitrium leuatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10448	23370	36861	0.57	1.4E-01	AW021008.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10448	23370	36862	0.57	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10619	23541	37039	0.67	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10619	23541	37040	0.67	1.4E-01	BF375286.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10829	23760		0.68	1.4E-01	T84293.1	EST_HUMAN	y47d03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:111365 5'
10962	23882	37395	0.71	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
11191	24147	37680	2.69	1.4E-01	R63400.1	EST_HUMAN	y70c05.r1 Soares breast 2NBHBst Homo sapiens cDNA clone IMAGE:154088 5'
11432	24376	37916	2.53	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11762	24637		1.59	1.4E-01	AL161496.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8
11797	23952		2.38	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11855	24737	37474	1.55	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
12549	25272	31776	2.33	1.4E-01	X74773.1	NT	P.sailina plastid gene secY
12562	25280		2.24	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA
12605	25904		2.35	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12702	25382		2.29	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
12776	25981		4.86	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12995	25792		3.72	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
13067	25601		2.63	1.4E-01	AW377698.1	EST_HUMAN	MR0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
322	13414	26338	2.48	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
322	13414	26339	2.48	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA

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Single Exon Probes Expressed in Bone Marrow.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
530	13601	26519	2.91	1.3E-01	AB013138.1	NT	Homo sapiens gene for NBS1, complete cds
637	13703	26624	0.78	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
637	13703	26625	0.78	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
845	13901	26859	1.04	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
895	13950	26908	1.76	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1028	14074	27024	1.8	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1129	14172		2.88	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1220	14258	27215	1.51	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1438	14471		0.93	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein GMS mRNA, complete cds
1976	14987	27999	2.07	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2180	15195		1.69	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidiphila pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2298	15310		0.96	1.3E-01	AW842104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2389	15397		3.94	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 81 of 172 of the complete genome
2592	15593	28610	2.23	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3485	16511	29432	0.98	1.3E-01	M21672.1	NT	Bovine branched chain alpha-keto acid dihydrolyl transacylase mRNA, complete cds
3735	16777	29689	0.91	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3735	16777	29690	0.91	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3741	16783	28695	0.89	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodipicol dehydrogenase 4 [AKR1C4], exon 2
3794	16777	29689	0.67	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3794	16777	29690	0.67	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3816	16858	29762	0.74	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4014	17053		1.48	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4081	13703	26624	7.11	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4081	13703	26625	7.11	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4153	17194		1.12	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4185	17216		4.1	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4194	17225	30114	2.47	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4215	17244	30129	20.19	1.3E-01	AW273741.1	EST_HUMAN	x22310.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4343	17370		1.49	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	17530	30414	0.8	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolypolyl transacylase mRNA, complete cds
4564	17587	30478	2.72	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
5014	18028		0.91	1.3E-01	AU136619.1	EST_HUMAN	AU136619 PLACE1 Homo sapiens cDNA clone PLACE1004693 5'
5060	18070		0.63	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-180900-012-c05 TN0077 Homo sapiens cDNA
5398	18501	31379	0.76	1.3E-01	AW465988.1	EST_HUMAN	ha07b06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1 L1 repetitive element:
5436	18538	31446	1.98	1.3E-01	AW804417.1	EST_HUMAN	QVO-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5578	18673		0.91	1.3E-01	AF107793.1	NT	Emaricella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5665	18760		0.68	1.3E-01	AF056880.1	NT	Hepatitis C virus 58_CL10 genome polyprotein gene, partial cds
5813	18903	32086	0.85	1.3E-01	BF210920.1	EST_HUMAN	601874391F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6099	19178	32396	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6099	19178	32397	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6630	19688	32987	17.29	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6720	19778	33055	2.08	1.3E-01	X88891.1	NT	C.jacchus Intron 4 of visual pigment gene (red allele)
6940	20164	33487	0.64	1.3E-01	H73425.1	EST_HUMAN	yu02d01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232609 5'
6955	20180		0.82	1.3E-01	W26367.1	EST_HUMAN	263 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7009	20135	33450	1.04	1.3E-01	BE782928.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7009	20135	33451	1.04	1.3E-01	BE782928.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7211	20234		0.72	1.3E-01	BF529560.1	EST_HUMAN	602044345F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7477	20443		2.15	1.3E-01	H48664.1	EST_HUMAN	602044345F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181866 5'
8292	21261		0.97	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8306	21275	34686	1.59	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
8336	21305	34720	1.18	1.3E-01	BF690622.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8680	21548		0.56	1.3E-01	BE592528.1	EST_HUMAN	601335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8617	21585	35001	0.8	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8688	21656		4.68	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8728	21697		4.2	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8873	21840	35263	1.05	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
9300	22265	35694	0.55	1.3E-01	R11172.1	EST_HUMAN	y339g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9300	22265	35695	0.55	1.3E-01	R11172.1	EST_HUMAN	y339g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9574	22536	35987	0.65	1.3E-01	11088003	NT	Plutella xylostella granulovirus, complete genome
9574	22536	35988	0.65	1.3E-01	11088003	NT	Plutella xylostella granulovirus, complete genome

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9827	22876	36132	3.9	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
10129	23055		0.74	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL
10411	23333		0.89	1.3E-01	8393940	NT	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10489	23411	36908	0.86	1.3E-01	AW851599.1	EST_HUMAN	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
10757	25702	37173	1.06	1.3E-01	AL163246.2	NT	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10891	23811	37318	0.66	1.3E-01	AU121237.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
10936	23856	37372	0.45	1.3E-01	AW247836.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10998	23982		2.57	1.3E-01	BF330996.1	EST_HUMAN	2820637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
11591	24519		3.66	1.3E-01	6871745	NT	MR4-BT0358-130700-010-108 BT0358 Homo sapiens cDNA
11670	24606	38182	1.77	1.3E-01	AW082636.1	EST_HUMAN	Mus musculus cofilin 2, muscle (Cif2), mRNA
11670	24606	38183	1.77	1.3E-01	AW082636.1	EST_HUMAN	xc20709.x1 NCI CGAP_Co19 Homo sapiens cDNA clone IMAGE:2584841 3'
11922	24803	38395	2.33	1.3E-01	BE279449.1	EST_HUMAN	xc20709.x1 NCI CGAP_Co19 Homo sapiens cDNA clone IMAGE:2584841 3'
12397	25171	31817	1.83	1.3E-01	BE618346.1	EST_HUMAN	601158032F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12535	25260		3.3	1.3E-01	AJ242780.1	NT	601462741F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3866003 5'
12692	25357	31756	1.37	1.3E-01	BF572303.1	EST_HUMAN	Gallus gallus scyl1 gene for lymphoblastin, exons 1-3
12885	25475		1.48	1.3E-01	AB026826.1	NT	60207752F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4252082 5'
12915	25494		2.52	1.3E-01	AW001114.1	EST_HUMAN	Ephydella fluviatilis mRNA for sALK-8, complete cds
383	13496	26428	14.66	1.2E-01	AJ421744.1	EST_HUMAN	wu24d09.x1 Soares_Dieckgraebe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to
424	13119		1.38	1.2E-01	U66912.1	NT	TR:O60287 O60287 KIAA0539 PROTEIN. ;
549	13619		2.78	1.2E-01	AF039442.1	NT	tf39b02.x1 NCI CGAP_Brm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1
1377	14411	27381	2.19	1.2E-01	AU149146.1	EST_HUMAN	ANNEXIN V (HUMAN);
1377	14411	27382	2.19	1.2E-01	AU149146.1	EST_HUMAN	Dictyostelium discoideum ORF DG1016 gene, partial cds
1383	14417		4.89	1.2E-01	AV735249.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1388	14421		0.92	1.2E-01	AL445086.1	NT	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1507	14540		1.23	1.2E-01	AA897474.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1635	14667	27643	1.62	1.2E-01	Q14934	SWISSPROT	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1658	14690	27666	2.99	1.2E-01	AJ285402.1	EST_HUMAN	Thermoplasma acidophilum complete genome, segment 4/5
1783	14812		18.69	1.2E-01	X89211.1	NT	ai48a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:O16671
1824	14958		1.76	1.2E-01	AW449368.1	EST_HUMAN	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
							NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR
							NFAT3) (NF-ATC4) (NF-AT3)
							q169f09.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960563 3'
							H.sapiens DNA for endogenous retroviral like element
							UI-H-B13-aki-e-10-0-UJ.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2734554 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2193	15208	28227	1.95	1.2E-01	BF248490.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4048224 5'
2294	15306	28329	1.21	1.2E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2595	15596	28614	2.05	1.2E-01	AW995556.1	EST_HUMAN	QV3-BN0046-220300-129-110 BN0048 Homo sapiens cDNA
2602	15602	28624	1.81	1.2E-01	BE218989.1	EST_HUMAN	h65f04.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178303 3'
							ts18g07.x1 NCJ_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
							COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN [1] contains element PTR5 repetitive element;
2738	15732	28748	37.59	1.2E-01	AI623388.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2855	15915	28838	1.4	1.2E-01	U18018.1	NT	aa80c09.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb.L05095
2913	15971	28885	2.03	1.2E-01	AI720470.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L30 (HUMAN);
2946	16004	28929	2.82	1.2E-01	MI16394.1	NT	Human creatine kinase-B mRNA, complete cds
3017	16075	28996	0.73	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3244	16209	29224	1.34	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT0259-261099-321-d05 BT0259 Homo sapiens cDNA
3271	16325		0.82	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3533	16579	29502	0.86	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3533	16579	29503	0.86	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3620	16538		1.06	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3780	16821		0.7	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053688 3'
4211	17240	30125	2.16	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR77)
4211	17240	30126	2.16	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR77)
4751	17771	30567	0.98	1.2E-01	Z48183.1	NT	Lescaultium mRNA for glyoxalase-I
5116	18126		1	1.2E-01	PT6466	SWISSPROT	HEMOLYSIN PRECURSOR
5150	18159	31038	0.91	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5150	18159	31039	0.91	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5164	18173	31052	1	1.2E-01	AL161618.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
5234	18242	31114	0.81	1.2E-01	BE974502.1	EST_HUMAN	601680438R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:39950711 3'
5322	18428	31178	0.75	1.2E-01	AA744369.1	EST_HUMAN	h63c04.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282850 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5373	18478	31351	0.91	1.2E-01	AF223391.1	NT	zco8d02.r1 Soares parathyroid tumor Nbl-IPA Homo sapiens cDNA clone IMAGE:321699 5'
5383	18487	31361	2.27	1.2E-01	W33035.1	EST_HUMAN	Homo sapiens gene encoding plakophilin (exons 1-13)
5442	18544	31458	2.15	1.2E-01	Z98268.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
5583	18679	31643	0.95	1.2E-01	Z48234.1	NT	
6324	19394	32536	2.66	1.2E-01	BE620948.1	EST_HUMAN	601495518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6376	19444	32586	1.1	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6431	19497	32750	2.19	1.2E-01	AW945276.1	EST_HUMAN	IL0-CT0031-221089-113-e04 CT0031 Homo sapiens cDNA
6499	19563	32815	1.38	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6804	19858	33145	0.98	1.2E-01	BF347895.1	EST_HUMAN	602023112F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158386 5'
6966	20180	33517	0.55	1.2E-01	AF295739.1	NT	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7210	20233	33567	0.67	1.2E-01	H47789.1	EST_HUMAN	yp80f04.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7210	20233	33568	0.67	1.2E-01	H47789.1	EST_HUMAN	yp80f04.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7854	20769	34175	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76, drbp76 gamma, drbp76 alpha and ILF3)
8063	21000	34396	0.9	1.2E-01	BF680613.1	EST_HUMAN	602155195F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296382 5'
8098	21034	34433	0.57	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8098	21034	34434	0.57	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8224	21193		1.24	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA
8295	21264	34875	3.1	1.2E-01	AI913753.1	EST_HUMAN	wes9g03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326604 3' similar to S/W.GST2_HUMAN
8341	21310	34724	0.76	1.2E-01	Q02369	SWISSPROT	Q89735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II
8652	21620	35040	0.61	1.2E-01	AI832581.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
8739	21707		10.85	1.2E-01	AW083652.1	EST_HUMAN	af71b10.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc49d07.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587567 3' similar to gp.M13452 LAMIN A (HUMAN);
8759	21726						Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8798	21765	35187	3.98	1.2E-01	AF053772.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8798	21765	35188	0.99	1.2E-01	J03958.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8948	21914		0.81	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
9037	22003		2.01	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
9073	22039		0.64	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9930	22813	36267	1.69	1.2E-01	X17961.1	NT	S.cerevisiae HXT5 gene
10365	23288	36765	1.64	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
11232	24185		2.36	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11404	24348		2.55	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11482	24425		1.57	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11584	24522	38077	2.45	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAIL1 (DNAIL1) gene, exon 17
11738	24623	38201	1.6	1.2E-01	9994174	NT	Homo sapiens UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4GALT4), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11836	24719		1.54	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12162	25016		3.86	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFB12 3'
12517	25246		2.78	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12593	25922	31304	6.17	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
12805	25432		2.86	1.2E-01	X53981.1	NT	R.norvegicus NF88 gene for 68kDa neurofilament
12867	25935	31310	1.58	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
12889	25477	31731	9.62	1.2E-01	AI299903.1	EST_HUMAN	qn20g05.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12911	25490		2.91	1.2E-01	L10187.1	NT	Xenopus laevis Integrin alpha 3 subunit mRNA, partial cds
12917	25862		9.28	1.2E-01	O86433	SWISSPROT	OYCLIN T
12846	25525	31712	1.76	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13092	16538		2.08	1.2E-01	Z997118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
13098	25623		1.5	1.2E-01	BF374481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
566	13636	26552	1.01	1.1E-01	AI551003.1	EST_HUMAN	tn18c08.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
617	13682	26599	1.84	1.1E-01	AA569006.1	EST_HUMAN	hm08g11.s1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06995_ma1
1057	14103	27054	1.55	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1087	14131		1.48	1.1E-01	AL161560.2	NT	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1163	15860	27158	4.6	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1254	14280	27255	2.03	1.1E-01	D64004.1	NT	EST384142 IMAGE resequences; MAGL Homo sapiens cDNA
1524	14566	27527	2.46	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
2322	15333		2.72	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2545	15926		0.93	1.1E-01	6978876	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
2574	15575		0.93	1.1E-01	AW821909.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
3046	16103	29017	0.95	1.1E-01	F03265.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3352	18403		1.66	1.1E-01	6753231	NT	HSC-TRF022 normalized Infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3432	16480	28389	2.18	1.1E-01	BE393186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caen1g), mRNA
3466	16512	29433	1.3	1.1E-01	X62135.1	NT	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3598	16641	29560	0.8	1.1E-01	Y07095.1	NT	C.reichardtli nuclear gene on linkage group XIX
3715	16758		0.86	1.1E-01	P97384	SWISSPROT	A.limmerus gene for transposase
3722	16765	29678	1.23	1.1E-01	X52708.1	NT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4137	17169	30054	1.14	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4137	17169	30055	1.14	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-026-g07 ST0290 Homo sapiens cDNA
4281	17310		9.36	1.1E-01	AF157065.1	NT	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
							Drosophila melanogaster Karsicht protein (klar) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4316	17345	30229	0.69	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-088-a08 UM0070 Homo sapiens cDNA
4670	17691	30577	1.02	1.1E-01	S44957.1	NT	Tapa-1=Integral membrane protein TAPA-1 [mouse, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4869	17886	30774	0.98	1.1E-01	Y07695.1	NT	A. Immsus gene for transposase
5056	17174		0.76	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
5753	18847		1.36	1.1E-01	AA747216.1	EST_HUMAN	nc78a03.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5829	18919	32102	1.16	1.1E-01	AF020927.1	NT	g Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5868	18957	32145	0.95	1.1E-01	AL110985.1	NT	Boltyis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5904	18990	32180	0.73	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5904	18990	32181	0.73	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5935	19021	32215	1.67	1.1E-01	X68851.1	NT	S. pombe ste8 gene encoding protein kinase
5971	19056	32256	4.98	1.1E-01	MB9533.1	NT	Providencia reitgeri penicillin G amidase gene
6142	19217	32446	1.63	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6164	19239	32470	1.54	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-112 FT0024 Homo sapiens cDNA
6184	19259	32493	8	1.1E-01	AW853599.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
6564	19624	32689	0.5	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6571	19631	32698	1.26	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Homo sapiens cDNA clone RL43
6617	19675	32953	0.84	1.1E-01	A1216307.1	EST_HUMAN	qg76d06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6762	19816	33096	6.18	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6862	19915		2.81	1.1E-01	AF032622.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6962	20187	33512	2.23	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7249	19984	33251	0.65	1.1E-01	AE002155.1	NT	Homo sapiens urea lyticum section 56 of 59 of the complete genome
7249	19984	33282	0.65	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7393	25969		0.94	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050663 5'
7523	25983	33850	1.59	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (677)
7781	20734	34105	7.69	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7781	20734	34106	7.69	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7839	20786	34161	0.54	1.1E-01	AA985908.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7917	20860	34249	1.77	1.1E-01	P41067	SWISSPROT	6044903.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1629172 3'
7959	20900		0.79	1.1E-01	Z14098.1	NT	TRAB PROTEIN
						NT	B. subtilis gene encoding hypothetical polyketide synthase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7961	20902	34294	2.99	1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
8111	21048	34448	0.65	1.1E-01	BE782280.1	EST_HUMAN	CHROMOGHRANIN A PRECURSOR (HUMAN);
8301	21270	34882	0.48	1.1E-01	U67492.1	NT	601470055F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873229 5'
8550	21518	34936	1.61	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8550	21518	34937	1.61	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8598	21568	34982	1.1	1.1E-01	X91233.1	NT	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8637	21605		1.06	1.1E-01	AW817918.1	EST_HUMAN	H.sapiens L15 gene
8694	21662	35086	1.59	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
9170	22136	35562	1.82	1.1E-01	U02482.1	NT	DKFZp547P194_r1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547P194 5'
9263	22228	35660	0.96	1.1E-01	AI807474.1	EST_HUMAN	Pedococcus acidilactici H plasmid pSMB74 pediocin Ach production (pap) gene cluster papA, papB, papC and papD genes, complete cds
9362	22327	35758	0.56	1.1E-01	AF050081.1	NT	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element
9398	22363	35794	2.27	1.1E-01	AA192163.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
9398	22363	35795	2.27	1.1E-01	AA192163.1	EST_HUMAN	zp93b12.r1 Stralagena muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9480	22454	35894	0.77	1.1E-01	Y12727.1	NT	zp93b12.r1 Stralagena muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9520	22483	35929	2.1	1.1E-01	T72675.1	EST_HUMAN	P.furiosus partial dph5 gene and argF gene
9546	22509		0.62	1.1E-01	BE893260.1	EST_HUMAN	yt18h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
9777	22718		0.89	1.1E-01	BE142305.1	EST_HUMAN	gb-M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9853	22789		2.05	1.1E-01	BF065149.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
10270	23195		0.88	1.1E-01	AL161543.2	NT	CM3-HT0142-271099-026-g11 HT0142 Homo sapiens cDNA
10476	23398		0.45	1.1E-01	BE315509.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10666	23488		1.01	1.1E-01	R80590.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10701	23623	37119	1.05	1.1E-01	U60528.1	NT	601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5'
11156	16103	29017	1.7	1.1E-01	F03265.1	EST_HUMAN	y98a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
11267	24219		3.13	1.1E-01	AF169032.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
11384	24331	37860	3.51	1.1E-01	R23708.1	EST_HUMAN	HSCIRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
11392	24338	37868	1.54	1.1E-01	6981351	NT	Carassius auratus actinin beta A precursor. mRNA, complete cds
11542	24483	38035	2.18	1.1E-01	Z11910.1	NT	yt35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11542	24483	38036	2.18	1.1E-01	Z11910.1	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkfb), mRNA
11636	24573	38137	3.66	1.1E-01	P17437	SWISSPROT	Z.mobilis tgt and lig genes encoding RNA guanine transglycosylase and DNA ligase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12360	25084		2.03	1.1E-01	AA192153.1	EST_HUMAN	z953b12.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12379	25161		3.66	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12826	25732		2.18	1.1E-01	BE974656.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950804 3'
13038	25580	31699	1.89	1.1E-01	BF239753.1	EST_HUMAN	601906360F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
13099	25912		1.32	1.1E-01	P14400	SWISSPROT	ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1
1206	14245		2.05	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1277	14312	27273	1.95	1.0E-01	A1985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1393	14427	27396	2.25	1.0E-01	AL161504.2	NT	MER7 repetitive element;
2497	15500	28528	1.16	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3524	16570	29493	1.32	1.0E-01	BF033991.1	EST_HUMAN	UIH-B13-abc-d-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3732	16774	29886	0.68	1.0E-01	BF239878.1	EST_HUMAN	601456301F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3859849 5'
3849	16889	29792	2.49	1.0E-01	AF287061.1	NT	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3849	16889	29793	2.49	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3978	17018	29930	2.66	1.0E-01	BF368703.1	EST_HUMAN	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4585	17607		0.86	1.0E-01	AF792349.1	EST_HUMAN	QV2-NT0048-160800-318-a05 NT0048 Homo sapiens cDNA
4741	17761	30555	1.32	1.0E-01	U50450.1	NT	an32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4957	17972	30863	2.34	1.0E-01	AW652344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 Isoform (fer) mRNA, complete cds
5267	18274	31138	0.97	1.0E-01	AV721471.1	EST_HUMAN	EST3364414 MAGE resequences, MAGB Homo sapiens cDNA
5273	18279		1.04	1.0E-01	AV763960.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBBQET0 5'
5394	18487		8.1	1.0E-01	W88490.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSBQB11 5'
5492	18562		0.59	1.0E-01	X84015.1	NT	zn62h04.s1 Soares_fetal_liver_spleen_1NF15_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5980	19055		0.87	1.0E-01	AK024472.1	NT	X.campestris genes for sensor and regulator protein
6140	19216	32445	12.15	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6469	19534	32782	0.9	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6483	19548	32787	0.65	1.0E-01	AA406039.1	EST_HUMAN	z941g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains
7220	20242		1.62	1.0E-01	R23821.1	EST_HUMAN	L1.13 L1 repetitive element;
8009	20947		2.16	1.0E-01	Y12488.1	NT	z941g10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Aliu
8108	21045	34444	0.65	1.0E-01	AJ011400.1	NT	repetitive element;
8108	21045	34445	0.65	1.0E-01	AJ011400.1	NT	M.musculus wtn gene
8265	21234	34645	0.63	1.0E-01	AA881091.1	EST_HUMAN	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
							Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
							ak32g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb.M34182 CAMP-
							DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8287	21256	34666	0.45	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8287	21256	34666	0.45	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8505	21474		0.68	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8837	21804		0.94	1.0E-01	AW169797.1	EST_HUMAN	xi06b01.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2675680 3' similar to gb.X17208 40S
9540	22503	35952	1.19	1.0E-01	AF102855.2	NT	RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element ;
9852	22788	36241	0.54	1.0E-01	R44993.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9865	22801		2.05	1.0E-01	M76729.1	NT	yp33h04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9908	22729		2.65	1.0E-01	AE001501.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9922	22808	36259	0.61	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
10180	23105	36596	1.63	1.0E-01	BF240154.1	EST_HUMAN	zcb6c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:327282 3'
10295	23220	36703	9.1	1.0E-01	AB046799.1	NT	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10295	23220	36704	9.1	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10502	23424		0.96	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10507	23429	36926	0.55	1.0E-01	T51952.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo sapiens cDNA
10694	23616	37110	0.99	1.0E-01	BE792760.1	EST_HUMAN	yb28a06.s1 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to
11018	23983		1.65	1.0E-01	AU159127.1	EST_HUMAN	contains Alu repetitive element
11370	24317	37844	2.25	1.0E-01	BF242946.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938096 5'
11370	24317	37845	2.26	1.0E-01	BF242946.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
11728	24614	38191	3.16	1.0E-01	BE790543.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
12365	25481		4.11	1.0E-01	BE537719.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
12588	25292		2.16	1.0E-01	7662166	NT	601582559F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
12604	25305		2.58	1.0E-01	X00654.1	NT	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12796	25425		1.45	1.0E-01	AA737961.1	EST_HUMAN	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12895	25481		4.47	1.0E-01	BE37716.1	EST_HUMAN	Drosophila melanogaster ftz gene
12943	25522		1.32	1.0E-01	BE159905.1	EST_HUMAN	nt11c08.s1 NCL CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255790 3'
12959	25891		0.14	1.0E-01	U66834.1	NT	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13016	25568		7.59	1.0E-01	AP001507.1	NT	QV4-HT0401-211299-064-g03 HT0401 Homo sapiens cDNA
2769	15781	28797	1.74	9.9E-02	AF274008.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
2768	15790	28808	1.71	9.9E-02	BE545554.1	EST_HUMAN	Bacillus halodurans genomic DNA, section 1/14
2798	15790	28809	1.71	9.9E-02	BE545554.1	EST_HUMAN	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds
3280	16334	29254	1.48	9.9E-02	AF099810.1	NT	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
							601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
							Homo sapiens neurexin III-alpha gene, partial cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3974	17014	29928	0.67	9.9E-02	A1821637.1	EST_HUMAN	z145c03.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3'
4707	17728	30622	1.02	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
7044	20066	33373	2.59	9.9E-02	BE613498.1	EST_HUMAN	601804252F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906084 5'
7163	18394	31239	7.77	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
8247	21216	34624	0.65	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
8247	21216	34626	0.66	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9612	22616	36068	1.23	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
565	13635		1.88	9.9E-02	X56338.1	NT	O saliva RAmv3C gene for alpha-amylase
3160	18216	29130	4.26	9.9E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4251	17280	30180	6.93	9.9E-02	AF257329.1	NT	Lepidophaeria maculans beta-tubulin mRNA, complete cds
4251	17280	30181	6.93	9.9E-02	AF257329.1	NT	Lepidophaeria maculans beta-tubulin mRNA, complete cds
7723	20678		0.94	9.9E-02	X64133.1	NT	Human HPTP della mRNA for protein tyrosine phosphatase della
8609	22613		1.21	9.9E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11788	23943	37485	1.83	9.9E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12330	25131		1.84	9.9E-02	8993751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1352	14387	27357	1.75	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1589	14621		1.33	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2270	15283	28309	2.78	9.7E-02	BE168660.1	EST_HUMAN	QV41-IT0516-070300-095-a04 HT0516 Homo sapiens cDNA
4008	17047		4.89	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5418	18521	31398	0.88	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III della prime subunit (dnaC) genes, complete cds
5418	18521	31399	0.88	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III della prime subunit (dnaC) genes, complete cds
6130	19207	32432	1.48	9.7E-02	AW954476.1	EST_HUMAN	EST386548 MAGC resequences, MAGC Homo sapiens cDNA
7517	20482	33843	3.36	9.7E-02	Z89119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
8315	21284	34697	1.09	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8315	21284	34698	1.09	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9201	22167	35597	1.52	9.7E-02	A1953984.1	EST_HUMAN	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
11629	24470		2.01	9.7E-02	U58337.1	NT	Mus musculus ligatin (lgt) mRNA, partial cds
2032	15051	28066	1.27	9.9E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares_NhiMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2032	15051	28067	1.27	9.6E-02	AJ080721.1	EST_HUMAN	0247d11 x1 Soares NIH-MPUs S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4372	17399	30279	6.7	9.6E-02	Z32686.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
5037	18050	30930	1.16	9.6E-02	AW968230.1	EST_HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
6225	19299		2.63	9.6E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8719	21687		0.65	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE105740 5'
9021	22854	36315	1.35	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
10231	23156		1.28	9.6E-02	BE84895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10399	23321	36805	1.27	9.6E-02	AJ24321.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10399	23321	36806	1.27	9.6E-02	AJ24321.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10479	23401	36898	0.44	9.6E-02	BF677270.1	EST_HUMAN	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10511	23433	36930	1.37	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10511	23433	36931	1.37	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10621	23543	37043	3.5	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECA-ACCELERATING FACTOR PRECURSOR (CD55)
11094	24054	37577	5.31	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
12028	24904	38498	1.53	9.6E-02	AA625755.1	EST_HUMAN	z919g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
12933	25515		1.81	9.6E-02	H14589.1	EST_HUMAN	ym18h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'
12996	25553	31719	1.51	9.6E-02	BE728219.1	EST_HUMAN	601563355F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3932908 5'
4128	17161	30050	2.86	9.5E-02	AW992395.1	EST_HUMAN	CM2-BND023-050200-087-f12 BND023 Homo sapiens cDNA
5748	18842	32025	0.81	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7294	20266	33601	0.51	9.5E-02	AA780728.1	EST_HUMAN	ac88a09.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:867736 3'
7522	20487	33849	4.14	9.5E-02	AB003473.1	NT	Timenesurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7818	20767	34144	7.16	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7863	18842	32025	0.89	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8212	21181	34591	2.85	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8212	21181	34592	2.85	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
11039	24003	37528	2.31	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
11039	24003	37529	2.31	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1850	14876	27571	4.07	9.4E-02	BF671083.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3894	16934	29844	4.91	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
5240	18248		0.96	9.4E-02	X98106.1	NT	Lactobacillus bacteriophage phig1e complete genomic DNA
6450	19515	32766	1.21	9.4E-02	AF097393.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7851	20797	34173	0.54	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vatl genes, complete cds, and lpf35 gene, partial cds
8947	21913		2.5	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cbbQ, lysS, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11280	20797	34173	2.22	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and ip35 gene, partial cds
12212	25828		10.73	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13087	25617	31692	1.37	9.4E-02	U27699.1	NT	Human pepHGT-1 betaine-GABA transporter mRNA, complete cds
3002	16060		1.71	9.3E-02	4809280	NT	Human sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3041	16099		7.39	9.3E-02	6812525	NT	Human sapiens nescopharyngeal epithelium specific protein 1 (NESG1), mRNA
3270	16324	29247	2.01	9.3E-02	BF575611.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4178	17210	30096	3.73	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4179	17210	30097	3.73	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4766	17786		2.29	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 5'
5745	18839		0.66	9.3E-02	AP001507.1	NT	Bacillus halodurens genomic DNA, section 1/4
8163	21091	34490	0.59	9.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8591	21659	34976	0.8	9.3E-02	AW566007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9480	22444		0.42	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
10068	22995	36454	2.32	9.3E-02	BE962831.2	EST_HUMAN	601655988F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865981 3'
10551	23473	36967	3.65	9.3E-02	Q18034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10551	23473	36968	3.65	9.3E-02	Q18034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10683	23605		3.59	9.3E-02	AW206117.1	EST_HUMAN	UH-B1-afx-h-05-0-UI.s1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12482	25750		2.56	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12831	25778		9.12	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), betat, 3-galactosyl transferase (betat, 3-galactosyl tr>
13040	25824		2.24	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26252	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26253	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26254	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2236	15280		2.72	9.2E-02	R54156.1	EST_HUMAN	y98f07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3194	16249	29167	3.72	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3316	16369	29289	0.99	9.2E-02	AA634354.1	EST_HUMAN	n79e01.s1 NCJ_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:926136 3'
3599	16844		1.27	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
4266	17295		1.24	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4337	17364		0.94	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4668	17669	30575	1.4	9.2E-02	X96402.1	NT	G.gallus Mla-CK gene
8342	21311	34725	1.87	9.2E-02	T49920.1	EST_HUMAN	y989c09.r1 Stralagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21485	34899	2.19	9.2E-02	X95256.1	NT	H.vulgaris xylase isomerase gene
12002	24879	38475	1.74	9.2E-02	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
13019	25986		1.31	9.2E-02	11469872	NT	Podospira anserina mitochondrion, complete genome
423	13118	26017	7.62	9.1E-02	X77695.1	NT	O. cuniculus k12 keratin gene
3684	16727		0.96	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4610	17635	30419	1.5	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5304	18307		0.98	9.1E-02	AB010896.1	NT	Ciona intestinalis endostyle-specific mRNA, complete cds
5819	18909	32093	1.27	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G8c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7528	26000		0.52	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7616	20576	33939	12.92	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781938 5'
7937	20879	34259	0.74	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7977	20916	34307	0.87	9.1E-02	U39073.1	NT	Mus musculus thymoporelin zeta mRNA, complete cds
9276	22242	35671	0.95	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10793	23714		1.84	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Strategene Homo sapiens cDNA clone FB19F10 3'end
10823	23744	37245	1.24	9.1E-02	S74059.1	NT	Tg616=Cyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 5275 nt]
10852	23772	37271	0.8	9.1E-02	Y1187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
12151	25009		3.93	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
12393	25919		2.15	9.1E-02	AA179901.1	EST_HUMAN	z338h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12468	25217		1.82	9.1E-02	AF052995.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12916	25771		1.78	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
746	13907	26747	6.38	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1640	14672	27645	6.7	9.0E-02	BE220482.1	EST_HUMAN	h339g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2815	15807	28826	6.5	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2815	15807	28827	6.5	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3347	16398	29321	1.11	9.0E-02	AF279135.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4328	17356	30243	0.83	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4328	17356	30244	0.83	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4448	17474	30363	1.25	9.0E-02	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
4695	17716	30611	2.37	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5261	18268	31137	0.93	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
6110	19189	32409	14.12	9.0E-02	W56037.1	EST_HUMAN	z68a12.1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
6880	19932		1.14	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element;
6931	20155	33473	0.86	9.0E-02	R62805.1	EST_HUMAN	Y11508.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
12762	25404		2.03	9.0E-02	AF022236.1	NT	Escherichia coli strain E234869 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1432	14466	27442	2.04	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1432	14466	27443	2.04	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2398	15403	28429	1.1	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251199-003-001 HT0339 Homo sapiens cDNA
4227	17256		2	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFio2 protein (AtranFio2) gene, partial cds
5950	19036	32230	2.64	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5950	19036	32231	2.84	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5966	19051	32252	3.5	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7399	20367	33720	1.49	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE]
7807	20757		2.02	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
8385	21354	34762	0.77	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
8488	21437	34855	0.7	8.9E-02	BF701665.1	EST_HUMAN	(CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8488	21437	34856	0.7	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8945	21911	35336	5.01	8.9E-02	AA309319.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
9978	22905	36369	0.62	8.9E-02	A1285627.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
9978	22905	36370	0.62	8.9E-02	A1285627.1	EST_HUMAN	MER10 repetitive element;
10090	23016	36492	0.67	8.9E-02	AA339356.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
12150	25743		1.3	8.9E-02	P30143	SWISSPROT	MER10 repetitive element ;
12211	25776		1.91	8.9E-02	P18624	SWISSPROT	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
12367	25154		9.08	8.9E-02	BF696918.1	EST_HUMAN	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
						SWISSPROT	MYOSIN-2 ISOFORM
						EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12530	26258		1.81	8.9E-02	6880220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12571	25282		1.5	8.9E-02	U28896.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
1374	14408	27378	1.25	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3921	16961	28874	1.03	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4065	17101		3.7	8.8E-02	O00288	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII130)
4267	17296		1.26	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4331	17359		2.3	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (amiridia, keratitis) (PAX6), isoform b, mRNA
7792	20744		0.86	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
9339	22304	35732	1.32	8.8E-02	AA151872.1	EST_HUMAN	zn99e05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11453	24396	37941	3.43	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11453	24396	37942	3.43	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11593	24331	38088	5.78	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_1 434 (synonym: htss3) Homo sapiens cDNA clone DKFZp434D1313 5'
12441	25204	31827	2.4	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
1654	14986	27681	1.55	8.7E-02	A187281.1	EST_HUMAN	ox85b01.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1661161 3'
3707	16750	28695	3.84	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3707	16750	28695	3.84	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4736	17756	30650	1.2	8.7E-02	AF178836.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5138	18147		1.02	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5166	18175	31053	0.97	8.7E-02	G563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
5387	18490	31365	6.04	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5387	18490	31366	6.04	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
7022	20147	33466	0.81	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7022	20147	33467	0.81	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7243	19978	33276	0.63	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
8860	21827	35250	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8860	21827	35251	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
11097	24030		2.15	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11641	24578	38144	1.79	8.7E-02	AJ007763.1	NT	Gluconobacter oxydans tRNA-Ile and tRNA-Ala genes

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12123	24892	38593	1.89	8.7E-02	Z74080.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL012c
12123	24892	38594	1.89	8.7E-02	Z74080.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL012c
12428	25186		1.6	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
1257	14292	27256	6.2	8.6E-02	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2256	16270	28295	1.96	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3639643 5'
3202	16257	29176	4.47	8.6E-02	LO5468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3658	16701		4.37	8.6E-02	AF153382.1	NT	Dictyostellum discoideum adenyl cyclase (acrA) gene, complete cds
3793	16834		0.66	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnpb) and prion-like protein (Prnd) genes, complete cds
4512	17537	30421	0.67	8.6E-02	U88179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
5170	18179		1.09	8.6E-02	L13419.1	NT	Chromatium vinosum tetraheme cytochrome c gene, 3' end, bacterial ankyrin homologue, flavocytochrome c
5276	18282		1.09	8.6E-02	AB011163.1	NT	heme subunit fccA (complete cds), and flavin subunit, fccB (3' end)
6213	19287	32520	4.24	8.6E-02	Y10826.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
6510	19574	32828	1.48	8.6E-02	J00440.1	NT	Homo sapiens LON1b gene
6510	19574	32828	1.48	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7834	20781	34159	1.01	8.6E-02	P14616	SWISSPROT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
8282	21231	34640	1.33	8.6E-02	5730066	NT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8282	21231	34641	1.33	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8405	21374	34782	0.66	8.6E-02	11427428	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8405	21374	34782	0.66	8.6E-02	11427428	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8469	21438		0.81	8.6E-02	U60168.1	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11006), mRNA
10084	23020	36495	1.04	8.6E-02	AF111170.3	NT	Dictyostellum discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
10131	23057		1.57	8.6E-02	AW692153.1	EST_HUMAN	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
10513	23435	36933	0.97	8.6E-02	AF026504.1	NT	h20c08.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2672846 3'
11578	24517	38072	2.47	8.6E-02	BF306606.1	EST_HUMAN	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11578	24517	38073	2.47	8.6E-02	BF306606.1	EST_HUMAN	601993437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11767	23922	37441	9.23	8.6E-02	AE001073.1	NT	601993437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
							Archaeoglobus fulgidus section 34 of 172 of the complete genome
							Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
11901	24782	38370	1.57	8.6E-02	AF283660.1	NT	cds
2406	15413	28437	2.86	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5752	18846	32028	0.71	8.5E-02	AA985491.1	EST_HUMAN	cc83b07.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gb:K01144 HLA
5793	18985		1.92	8.5E-02	P08089	SWISSPROT	CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
6127	19205	32428	6.34	8.5E-02	AF233885.1	NT	M PROTEIN, SEROTYPE 6 PRECURSOR
							Mus musculus phosphodiesterase C-like protein mRNA, partial cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8953	21919	35345	1.92	8.5E-02	8754779	NT	Mus musculus myosin XV (Myo15), mRNA
10196	23121	36607	3.17	8.5E-02	BE833064.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10196	23121	36608	3.17	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10338	23262	36742	0.44	8.5E-02	A1140618.1	EST_HUMAN	qeo5g05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738136 3'
10728	23650	37143	0.56	8.5E-02	X76731.1	NT	V. annimolydes gene for aminomethyltransferase C
10851	23771	37270	1	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11490	24433		8.1	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11507	24449	37999	4.05	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12985	25547		5.18	8.5E-02	AA362934.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2675	16901	28690	3.69	8.4E-02	W69230.1	EST_HUMAN	zd44et1.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343552 5'
4381	17409	30280	1.02	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4381	17409	30291	1.02	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5235	18243	31115	0.98	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5385	18488	31363	8.74	8.4E-02	BE267153.1	EST_HUMAN	601190438F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6847	19900	33194	1.86	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8363	21332	34744	7.84	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0790-260400-162-d05 BT0790 Homo sapiens cDNA
9194	22160	35588	1.02	8.4E-02	AF218860.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 2
10727	23649	37142	1.9	8.4E-02	A1735184.1	EST_HUMAN	as88g10.x1 Bartslead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
12351	26146	31853	1.46	8.4E-02	R79408.1	EST_HUMAN	O88312 GOB-4. ;
2027	15047	28060	0.97	8.3E-02	5935580	NT	y83h12.1.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2027	15047	28061	0.97	8.3E-02	5935580	NT	bodex hexagonus mitochondrion, complete genome
3608	16651	29568	6.11	8.3E-02	P75334	SWISSPROT	bodex hexagonus mitochondrion, complete genome
3634	16677	29590	0.66	8.3E-02	A1436787.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3634	16677	29591	0.66	8.3E-02	A1436787.1	EST_HUMAN	th82g08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6389	19457	32702	0.78	8.3E-02	A1942338.1	EST_HUMAN	th82g08.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6502	19596	32818	2.54	8.3E-02	AF052683.1	EST_HUMAN	wo79f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
8313	21282	34694	3.61	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
						NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds
8949	21315		1.19	8.3E-02	AA865285.1	EST_HUMAN	cg88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.1 L1 L1
8842	21610		1.54	8.3E-02	AA987873.1	EST_HUMAN	repetitive element ;
						EST_HUMAN	cg81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
9886	22849	36308	1.58	8.3E-02	AW589503.1	EST_HUMAN	ig05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
9309	22730		2.19	8.3E-02	AI161595.2	NT	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
						EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10706	23628		0.5	8.3E-02	AF020409.1	NT	Dictyostelium discoideum DocA (docA) mRNA, complete cds
12444	25924		1.48	8.3E-02	BE958458.1	EST_HUMAN	601844770F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3929883 5'
1379	14413		7.44	8.2E-02	Y06170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1494	14527	27499	1.77	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3089	16147		2.24	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C005
3815	16955		1.61	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4033	17071	29972	1.22	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C009
4313	17342	30222	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4313	17342	30223	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4313	17342	30224	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5108	18118	30992	1.29	8.2E-02	AF240776.1	NT	Mus musculus pepsinogen F (Pepf) mRNA, complete cds
5118	18128	31004	4.13	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5300	18128	31004	0.95	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5408	18511	31399	1.47	8.2E-02	BE997030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924823 5'
7221	20243	33577	2.84	8.2E-02	AF308555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8005	20944		0.6	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
8057	22023		0.45	8.2E-02	U29397.1	NT	Rattus norvegicus plasma membrane Ca ²⁺ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9124	22090	35518	2.75	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
9558	22985	36346	5.43	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
10121	23047	36526	2.38	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5'
12450	25209	31831	6.88	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12835	25710		5.74	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1493	14526	27498	1.05	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
5848	18938	32123	1.05	8.1E-02	AE004006.1	NT	Xylaria fastidiosa, section 152 of 228 of the complete genome
6516	19579	32836	1.38	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7403	20371		0.81	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7835	20782		0.9	8.1E-02	A1692881.1	EST_HUMAN	w866083.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8683	21651	35072	0.53	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8883	21651	35073	0.63	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
10272	23197		1.58	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
11827	24710	38294	1.53	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	15830	28028	4.82	8.0E-02	AW954653.1	EST_HUMAN	EST366723 MAGC resequences, MAGC Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1709	15875	27722	13.63	8.0E-02	D28535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1709	15875	27723	13.63	8.0E-02	D28535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1919	14943	27939	4.07	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2384	15392	28417	1.05	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2384	15392	28418	1.05	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2478	15482		4.69	8.0E-02	BF246744.1	EST_HUMAN	80186548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2831	14137	27088	0.99	8.0E-02	M23449.1	NT	Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2811	15969	28892	0.76	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3830	16870	29772	6.64	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGI resequences, MAGI Homo sapiens cDNA
4810	17827	30724	1.7	8.0E-02	AI434202.1	EST_HUMAN	831g02.x1 NCI_CGAP_Gac4 Homo sapiens cDNA clone IMAGE:2132114 3'
4818	17835	30733	0.99	8.0E-02	AF116556.1	NT	Arabidopsis thaliana putative transcription factor (HUA2) mRNA, complete cds
4852	17869		7.57	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5832	18922	32105	0.71	8.0E-02	AW651139.1	EST_HUMAN	EST363209 MAGI resequences, MAGA Homo sapiens cDNA
5993	19077	32274	3.28	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7386	19077	32274	1.44	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8465	21434	34851	3.74	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9744	22685	36139	1.21	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9744	22685	36140	1.21	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10519	23441		0.6	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11145	24105	37632	2.19	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12483	25230	31798	6.54	8.0E-02	AJ005375.1	NT	Drosophila oreana hunchback region
13036	18342		2.08	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2184	15199	28219	4.36	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
2992	16050	28971	8.43	7.9E-02	AI582029.1	EST_HUMAN	arg8c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:228876
3854	16903	29808	5.68	7.9E-02	6881044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3854	16903	29809	5.68	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4722	17742	30633	1.08	7.9E-02	BF348454.1	EST_HUMAN	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4849	17866		1.49	7.9E-02	AB008019.1	NT	60201970F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155401 5'
6855	19908		1.06	7.9E-02	BF368016.1	EST_HUMAN	Arabidopsis thaliana RXW24L mRNA, partial cds
8366	21335	34747	3.26	7.9E-02	U27832.1	NT	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
10388	23310	36788	4.89	7.9E-02	AI081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of MIF2 Sm14p (SMT4) gene, complete cds
							ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
							CE08611;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10388	23310	36789	4.89	7.9E-02	A1081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2 CE08611 ;
1215	14263	27210	1.69	7.8E-02	A1793275.1	EST_HUMAN	oc59d02.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.t3 L1 repetitive element ;
1215	14263	27211	1.69	7.8E-02	A1793275.1	EST_HUMAN	oc59d02.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.t3 L1 repetitive element ;
5123	16804		3.25	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
7279	20013	33317	1.29	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7279	20013	33318	1.29	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
9137	22103	35529	1.26	7.8E-02	BE987947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
9232	22198	35628	0.6	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
9408	22373	35808	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9408	22373	35809	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9716	22744	36195	1.23	7.8E-02	AA469354.1	EST_HUMAN	nc68b06.t1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:7717931
10161	23086	36593	0.65	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 3993281 to 4214814
12114	24984	38585	1.64	7.8E-02	BF025981.1	EST_HUMAN	601669378F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3953083 5'
1399	16867	27402	0.93	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3600	16845		2.05	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5622	18718	31877	0.61	7.7E-02	AF062636.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
8241	21210	34615	7.34	7.7E-02	AA402949.1	EST_HUMAN	zu63d11.t1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;
10195	23120	36606	3.76	7.7E-02	P30800	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10490	23412	36909	0.76	7.7E-02	A1318662.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10490	23412	36910	0.76	7.7E-02	A1318662.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
11352	24302	37829	4.65	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
12871	25785		1.91	7.7E-02	11436859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3398	16447	29373	2.43	7.6E-02	BE514432.1	EST_HUMAN	601319428F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3934903 5'
3419	16467	29387	1	7.6E-02	AA298447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
6216	19290	32823	0.72	7.6E-02	AJ061275.1	EST_HUMAN	en25g02.x1 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
6491	19556	32806	0.87	7.6E-02	BE379328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9725	22753	36206	1.35	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10257	23182		1.42	7.6E-02	AL13078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10590	23502	36994	0.47	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0845-020800-017-d08 HT0545 Homo sapiens cDNA
10714	23636		0.56	7.6E-02	BE659638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10952	23872	37384	0.67	7.6E-02	X92656.1	NT	L. esculentum mRNA for tissue phosphate translocator
10952	23872	37385	0.67	7.6E-02	X92656.1	NT	L. esculentum mRNA for tissue phosphate translocator
11988	24863	38459	1.9	7.6E-02	AW066645.1	EST_HUMAN	QV3-BN0048-150400-151-e04 BN0046 Homo sapiens cDNA
785	13845	26790	2.89	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
785	13845	26791	2.89	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1935	14959	27955	0.93	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4538	17559	30447	0.63	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, Intron 1 and exon 2
5952	19037	32233	0.71	7.5E-02	AJ948714.1	EST_HUMAN	wg24h09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
							wf62b02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8681	21649	35071	1.01	7.5E-02	AJ864367.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
8952	21819	35239	1.29	7.5E-02	AU116913.1	EST_HUMAN	7o61c05.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10392	23314		0.45	7.5E-02	BF221730.1	EST_HUMAN	MER27 repetitive element ;
10859	23779	37279	0.9	7.5E-02	BF208809.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10953	23873	37386	0.66	7.5E-02	X79460.1	NT	C.fiml DSM 20113 16S rDNA
478	13550	26478	1.24	7.4E-02	AW838547.1	EST_HUMAN	RC5L T0054-260100-011-H09 LT0054 Homo sapiens cDNA
1456	14849		1.08	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2585	15586		0.99	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pbx1), mRNA
3608	16653	29571	0.78	7.4E-02	AJ807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4733	17753	30646	1.09	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4833	17850	30750	3.24	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
4979	17984	30863	2.52	7.4E-02	6678492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrlp), mRNA
6643	18701		1.8	7.4E-02	R17477.1	EST_HUMAN	yg14g06.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:32339 5'
7707	20664	34031	0.79	7.4E-02	AA605132.1	EST_HUMAN	no71d02.e1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:112259 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8233	21202	34608	1.2	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3995264 5'
8846	21813	35233	1.01	7.4E-02	U56089.1	NT	Human periodic tyroptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9521	22484	35930	1.02	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCI CGAP_GUT Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9521	22484	35931	1.02	7.4E-02	AW629605.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9794	21117	34516	0.48	7.4E-02	A1672939.1	EST_HUMAN	hh67d11.y1 NCI CGAP_GUT Homo sapiens cDNA clone IMAGE:2346819 3'
9794	21117	34517	0.48	7.4E-02	A1672939.1	EST_HUMAN	hh67d11.y1 NCI CGAP_GUT Homo sapiens cDNA clone IMAGE:2346819 3'
10173	23098	36578	1.07	7.4E-02	U62293.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10301	23228	36708	0.53	7.4E-02	BF512678.1	EST_HUMAN	U1H-BW1-ang-g-06-0-U1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
12408	25181		1.47	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12665	25903		2.51	7.4E-02	AW379431.1	EST_HUMAN	CM4-H70243-081199-037-d11 HT0243 Homo sapiens cDNA
469	13542	26468	1.3	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
469	13542	26469	1.3	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
886	13748	26674	5.48	7.3E-02	AE001789.1	NT	Thermoboga maritima section 101 of 136 of the complete genome
1477	15669	27486	3.94	7.3E-02	AW900281.1	EST_HUMAN	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1862	15879		15.78	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3785	16828		0.72	7.3E-02	U66059.1	NT	Human geminine T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
5032	18046		1.06	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6595	19655	32927	1.04	7.3E-02	AA779977.1	EST_HUMAN	q24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7706	20663	34029	2.47	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7706	20663	34030	2.47	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8508	21476		1.2	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9565	22527		1.39	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11552	19665	32927	1.89	7.3E-02	AA779977.1	EST_HUMAN	q24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
12925	25510		1.33	7.3E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF (PL241c)
120	13229	26156	0.7	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039034 (section 88 of 148) of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
120	13229	26157	0.7	7.2E-02	AE000892.1	NT	Methanobacterium thermoautotrophicum from bases 1020155 to 1039934 (section 88 of 148) of the complete genome
1472	14505	27478	2.77	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1472	14505	27479	2.77	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2556	15558		2.98	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3900	16940	29851	0.74	7.2E-02	AW268322.1	EST_HUMAN	U1-H-BW0-aj1-a-05-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4373	17400	30280	4.57	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5360	18485	31336	2.81	7.2E-02	U67631.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5361	18486	31337	9.14	7.2E-02	P11120	SWISSPROT	CALMODULIN
6239	19312		0.73	7.2E-02	BF217596.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7374	20344	33696	1.78	7.2E-02	BF216088.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7391	20360	33712	0.6	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7417	20384		1.74	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8529	21497	34912	0.68	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8529	21497	34913	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9419	22384		0.62	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9934	22861		0.63	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9970	22897	36360	1.98	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAALG01 5'
10117	23043	36523	3.63	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10274	23199	36683	1.17	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
10362	23285	36762	2.28	7.2E-02	AW873187.1	EST_HUMAN	h24f11.x1 NCL_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120393 3' similar to TR:Q9Z340 Q9Z340
10552	23474	36989	0.64	7.2E-02	AA768204.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
							aa62c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10717	23639	37132	2.17	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10840	23760	37260	5.41	7.2E-02	BE595003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10894	23784		3.24	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
11258	24210	37733	4.17	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12311	25119	31842	1.58	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12350	25145		5.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12469	25218		3.99	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12484	25754		8.41	7.2E-02	AW900962.1	EST_HUMAN	GM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
12880	25933		1.45	7.2E-02	AF020439.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
12964	25633		1.85	7.2E-02	AA401779.1	EST_HUMAN	z157c12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1920	14944	27940	1.83	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D8) proviral structural capsid protein (gag) gene; partial cds
2300	15312	28332	6.39	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
8239	21208	34612	0.87	7.1E-02	A1126284.1	EST_HUMAN	gc92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
12193	25038		8.33	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
529	13600	26518	1.42	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1499	14632		1.82	7.0E-02	X98677.1	NT	Martellia Mitc-1 gene
1776	14805	27791	1.18	7.0E-02	AA056343.1	EST_HUMAN	z166104.s1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3042	16100	29015	1.76	7.0E-02	AW138152.1	EST_HUMAN	U1-H-B11-acy-c-07-b-UJ s1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3913	16953	29854	0.96	7.0E-02	AA815438.1	EST_HUMAN	al65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
4074	17110	30004	1.05	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4164	17195		1.24	7.0E-02	AW792992.1	EST_HUMAN	QV4-BT0407-280100-090-a10 BT0407 Homo sapiens cDNA
4242	17271	30156	1.28	7.0E-02	AF077821.1	NT	GM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4965	17981	30871	8.41	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5451	18553		1.03	7.0E-02	Y08143.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7630	20590	33953	0.9	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
7884	20808	34186	0.6	7.0E-02	Y19187.1	NT	AV689285 GK6 Homo sapiens cDNA clone GKGCAC06 5'
9454	22418	35856	1.2	7.0E-02	6628113	NT	Gallus gallus mRNA for partial aczonin, XL spliced variant (acz gene)
9856	22883	36345	1.21	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
10312	23236	36718	0.76	7.0E-02	U27266.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
11700	24665	38242	2.23	7.0E-02	AA724295.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
12939	25519	31710	1.88	7.0E-02	11421638	NT	ah09a05.e1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
515	13586	26504	11.2	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
515	13586	26505	11.2	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
						NT	Homo sapiens chromosome 21 segment HS21C010
						NT	Homo sapiens chromosome 21 segment HS21C010
1338	14370		1.68	6.9E-02	4507868	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3807	16947	29764	1.37	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3807	16947	29755	1.37	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5151	18161	31041	0.97	6.9E-02	AA670269.1	EST_HUMAN	ai25e08.s1 Soares_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:1032710 3'
6028	19109		0.57	6.9E-02	AF161364.1	NT	Homo sapiens HSPC101 mRNA, partial cds
7876	20820		0.67	6.9E-02	AF164967.1	NT	Canine distemper virus strain A75/17, complete genome
8387	21358		1.18	6.9E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8899	21865	35287	1.08	6.9E-02	BE567435.1	EST_HUMAN	601340861F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8899	21865	35288	1.08	6.9E-02	BE567435.1	EST_HUMAN	601340861F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9475	22439	35879	0.55	6.9E-02	U22987.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12343	25141		2.17	6.9E-02	X74315.1	NT	Xlaevis XFD2 mRNA for fork head protein
12519	25250		1.75	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFc HOMOLOG
13112	25631	31648	3.69	6.9E-02	BF352899.1	EST_HUMAN	IL3-HT0619-110700-210-C04 HT0619 Homo sapiens cDNA
1899	14924	27918	1.18	6.8E-02	AA496759.1	EST_HUMAN	ee30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1899	14924	27919	1.18	6.8E-02	AA496759.1	EST_HUMAN	ee30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1922	14948	27942	4.7	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3117	18174	29084	1.05	6.8E-02	AA781996.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3117	18174	29085	1.05	6.8E-02	AA781996.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
3117	18174	29086	1.05	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376826 3'
4583	17605		0.71	6.8E-02	BE141076.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376826 3'
5283	18289		0.76	6.8E-02	T03013.1	EST_HUMAN	MRO-H170069-071099-001-c05 HT0069 Homo sapiens cDNA
6776	19831		0.66	6.8E-02	P20792	SWISSPROT	FB20A6 Fetal brain, Stragelene Homo sapiens cDNA clone FB20A6 3'end
7084	20018		1.05	6.8E-02	BE061890.1	EST_HUMAN	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
7497	20462	33822	7.18	6.8E-02	AL163288.2	NT	RC1-BT0254-090300-017-c09 BT0254 Homo sapiens cDNA
7948	20889	34280	0.64	6.8E-02	U16856.1	NT	Homo sapiens chromosome 21 segment HS21C068
8631	21599	35020	5.44	6.8E-02	AJ248287.1	NT	Diclyostellum discoidium myosin heavy chain kinase A (MHCKA) mRNA, complete cds
8631	21599	35021	5.44	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
12140	25949		3.73	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
12274	25094		2.52	6.8E-02	AA758014.1	EST_HUMAN	FB4A8 Fetal brain, Stragelene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1
12832	25449		1.68	6.8E-02	AW975839.1	EST_HUMAN	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12894	25480		2.35	6.8E-02	9910585	NT	EST387948 MAGe resequences, MAGN Homo sapiens cDNA
1531	14584		1.93	6.7E-02	AF115536.1	NT	Mus musculus latent TGF beta binding protein (Tgfb) mRNA
1910	14934	27630	1.99	6.7E-02	AJ220285.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
3730	16772	29683	4.34	6.7E-02	P17278	SWISSPROT	gg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
8183	21153	34560	1.01	6.7E-02	X62695.1	NT	HOMEBOX PROTEIN HOX-D4 (HOXA)
							H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8183	21153	34581	1.01	6.7E-02	X62695.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8781	21748	35170	0.45	6.7E-02	AW082688.1	EST_HUMAN	xb51c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2590788 3'
9959	22886	36347	0.73	6.7E-02	AW137359.1	EST_HUMAN	UI-H-BH-act-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9959	22886	36348	0.73	6.7E-02	AW137359.1	EST_HUMAN	UI-H-BH-act-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1371	14405	27375	0.9	6.8E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2182	15207	28226	2.66	6.8E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3477	16523	29447	11.07	6.8E-02	R84306.1	EST_HUMAN	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3491	16637	29482	2.1	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3491	16637	29483	2.1	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4107	17141	30036	1.45	6.8E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5015	18029	30913	9.23	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5015	18029	30914	9.23	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6736	19792	33073	3.97	6.8E-02	X08411.1	NT	P.vulgaris mRNA for chalcone synthase
6967	19823	33105	0.55	6.8E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
6967	19823	33106	0.55	6.8E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
8152	21090	32106	0.57	6.8E-02	D14567.1	NT	Penicillium urticae mitochondrial rRNA (large rRNA) gene and its flanking region
8279	21248	34660	1.6	6.8E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8817	21784	35209	0.67	6.8E-02	AF008055.1	NT	Dichytellum discoidium darlin (darA) gene, complete cds
9273	22239	35666	0.67	6.8E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9273	22239	35667	0.67	6.8E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10311	23235	36717	0.52	6.8E-02	AI458752.1	EST_HUMAN	y97g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
10447	23369	36860	1.65	6.8E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rp22 and bsm22 genes
10481	23403		0.6	6.8E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
11310	24200	37788	4.9	6.8E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
12063	24938		1.73	6.8E-02	C05789.1	EST_HUMAN	C05789 Human pancreatic islet Homo sapiens cDNA clone hbc5156
12719	25373		2.53	6.8E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
13024	25572		1.31	6.8E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
594	13652	26566	2.67	6.8E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
989	14041	26996	1.95	6.8E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1392	14426	27395	3.5	6.8E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1749	14778	27763	2.08	6.8E-02	AE000784.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5638	18734	31896	1.71	6.8E-02	AA443991.1	EST_HUMAN	zv46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6693	19750	33027	0.93	6.8E-02	BF685340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN); 602118887F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276029 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7185	18396	31241	1.17	6.5E-02	U22661.1	NT	Azobacter vinelandii ATCC 30046 negative regulator MucB (mucB) gene, partial cds
10302	23227	36709	0.65	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865937 3'
10302	23227	36710	0.65	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865937 3'
10332	23753	37252	0.53	6.5E-02	BF106300.1	EST_HUMAN	60182361F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11002	23668	37482	4.51	6.5E-02	AA195648.1	EST_HUMAN	z32g05.s1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12164	25017		4.16	6.5E-02	M21496.1	NT	Rabbit microsomal epoxide hydrolase
12526	25255		7.31	6.5E-02	AF102993.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
577	13646	26539	1.74	6.4E-02	X94549.1	NT	A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene
1746	14775	27760	0.93	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
1746	14775	27761	0.93	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
4933	16085	29007	1.16	6.4E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5262	18270		2.56	6.4E-02	AA147572.1	EST_HUMAN	z51e04.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505470 5' similar to contains Alu repetitive element;
5525	18624	31559	1.19	6.4E-02	A191956.1	EST_HUMAN	q607b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element;
5982	19067	32265	1.16	6.4E-02	7305188	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6234	19307	32539	4.16	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6234	19307	32540	4.16	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6542	19604	32866	0.72	6.4E-02	A1672896.1	EST_HUMAN	w673g12.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6990	20213	33542	4.64	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
7693	20651	34015	0.52	6.4E-02	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8679	21647		2.79	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeita) (Cct6a), mRNA
9012	21978	35397	4	6.4E-02	AA093305.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9483	22447	35887	0.92	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9944	22871		0.61	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
10075	23002	36472	1.75	6.4E-02	AB011128.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10624	23546	37046	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10624	23546	37047	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12018	24895	38492	2.18	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12018	24895	38493	2.18	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12424	25881		5.38	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12476	25224	31783	5.88	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1769	14798	27784	2.78	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3818	16662		2.77	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6259	19332	32563	1.06	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7453	20419		1.39	6.3E-02	X67869.1	NT	H. sapiens gene encoding La autoantigen
8946	22590	36039	1.01	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
10374	23297	36773	2.98	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polypeptide (NS5A region), partial cds, strain: CMR-152
10634	23556		0.81	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
11070	19332	32563	2.76	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
4278	17307	30186	2.48	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4365	17392		1.12	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNP1) mRNA, complete cds
4812	17633		0.58	6.2E-02	Q62191	SWISSPROT	62 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6963	20188	33513	0.67	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7889	20833	34212	0.79	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8158	21096		0.58	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9299	26007		0.63	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9589	22852	36106	0.53	6.2E-02	AA778450.1	EST_HUMAN	af20a06.s1 Soares_tetrahymena_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9835	22771	36226	1.25	6.2E-02	6877888	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
12259	25979		15.66	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12596	25299		1.38	6.2E-02	BE793085.1	EST_HUMAN	601683773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
12676	25346	31784	3.54	6.2E-02	BF112039.1	EST_HUMAN	7137h08.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to
258	13663	26278	3.09	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
4017	17056		15.65	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
6043	19125	32330	0.62	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6043	19125	32331	0.62	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6235	19308		1.64	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8606	21574	34989	3.52	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8008	21974	35393	1.93	6.1E-02	BE971863.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9008	21974	35394	1.93	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
11082	24044	37596	3.44	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0818-110500-136-C06 HT0818 Homo sapiens cDNA
12216	25897		2.42	6.1E-02	X70989.1	NT	S Japonicum mRNA for serine-enzyme
12779	25774		1.35	6.1E-02	A188611.1	EST_HUMAN	ts5607.x1 NCL_CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2282901 3'
12912	25491		7.44	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1267	14302	27263	1.26	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2684	15680	28698	1.17	6.0E-02	AW968848.1	EST_HUMAN	EST380924 MAGE resequences, MAGJ Homo sapiens cDNA
2783	15775		1.98	6.0E-02	AB031288.1	NT	Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2948	13213	26137	1.47	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2948	13213	26138	1.47	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3243	16288	29222	1.52	6.0E-02	AA372376.1	EST_HUMAN	EST84256 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3243	16288	29223	1.52	6.0E-02	AA372376.1	EST_HUMAN	EST84256 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
5472	18573		0.76	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0283-011199-013-604 BT0283 Homo sapiens cDNA
6341	19410	32651	0.98	6.0E-02	AI807537.1	EST_HUMAN	wf48105.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 repetitive element
7180	18411	31212	2.79	6.0E-02	5174998	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7180	18411	31213	2.79	6.0E-02	5174998	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7394	20382	33714	2.08	6.0E-02	BF392349.1	EST_HUMAN	601816274F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4049226 5'
7508	20473	33833	0.57	6.0E-02	BF210488.1	EST_HUMAN	60187470F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101074 5'
7944	20886	34277	1.71	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764199 3'
8765	21732		0.52	6.0E-02	11466495	NT	Reclinomonas americana mitochondrion, complete genome
9627	22571	36020	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCL_CGAP_GC06 Homo sapiens cDNA clone IMAGE:2237362 3'
9627	22571	36021	1.17	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCL_CGAP_GC06 Homo sapiens cDNA clone IMAGE:2237362 3'
9761	22702	36159	2.03	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for immunoglobulin light chain variable region, exons 1-2
9761	22702	36160	2.03	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for immunoglobulin light chain variable region, exons 1-2
10285	23190	36675	0.66	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
10285	23190	36676	0.66	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
12475	25223	31792	3.08	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12845	25456		3.16	6.0E-02	AI809273.1	EST_HUMAN	wf69f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
232	13332	28255	5.34	5.9E-02	AW934719.1	EST_HUMAN	O60298 KIAA0351 PROTEIN ; RC1-DT0001-280100-012-e10 DT0001 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2996	16054	28975	3.42	5.9E-02	AF190269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4905	17922	30814	0.94	5.9E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7077	26874	33409	0.62	5.9E-02	AF145880.1	NT	Drosophila melanogaster LD23107 sllg (sting) mRNA, complete cds
8904	21830	33355	1.92	5.9E-02	9055249	NT	Mus musculus troquid related homeobox 5 (Drosophila) (hx5), mRNA
9806	21129		0.82	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4103994 5'
11138	24098		3.23	5.9E-02	6679870	NT	Mus musculus tollistatin-like (Fsf), mRNA
933	13986		0.03	5.8E-02	D80110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2872	15932		0.99	5.8E-02	AJ223821.1	NT	Populus trichocarpa CCoMT1 gene, exon 1 to exon 5
3676	16719	29633	1.32	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4382	17410	30282	5.33	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4382	17410	30283	5.33	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4578	17600	30495	4.73	5.8E-02	AJ247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4578	17600	30496	4.73	5.8E-02	AJ247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4604	17625		2.93	5.8E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6014	19097	32298	0.53	5.8E-02	AA190994.1	EST_HUMAN	zp88a11.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627088 3'
7941	20883	34273	2.52	5.8E-02	M99160.1	NT	Human polymorphic microsatellite DNA
7941	20883	34274	2.52	5.8E-02	M99160.1	NT	Human polymorphic microsatellite DNA
9014	21980	35399	0.59	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12655	25958		10.6	5.8E-02	AA604269.1	EST_HUMAN	no75e11.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3070	16127	29039	1.27	5.7E-02	AJ081644.1	EST_HUMAN	CE08811 ;
3086	16143	28055	1.61	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3814	16854	29781	2.47	5.7E-02	AW968791.1	EST_HUMAN	EST378865 MAGI resequences, MAGI Homo sapiens cDNA
5199	18208	31082	0.91	5.7E-02	AJ251973.1	NT	Homo sapiens partial cicerin-1 gene
5306	18309		1.18	5.7E-02	6754525	NT	Mus musculus low density lipoprotein receptor (Ldlr), mRNA
5979	19064		0.69	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7704	20661	34025	0.59	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7704	20661	34026	0.59	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7766	20739	34111	0.68	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7766	20739	34112	0.68	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8495	21463	34879	1.74	5.7E-02	AJ286090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
10209	23134	36621	0.65	5.7E-02	6681260	NT	Mus musculus ec2 oncogene (Ec2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10930	23850	37355	0.49	5.7E-02	Z49983.1	NT	L.mexicana cbp1 gene
11521	24482	38013	3.22	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11521	24462	38014	3.22	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11676	24642		1.89	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12573	25782		8.27	5.7E-02	D50320.1	NT	Pig DNA for SPA-2, complete cds
12784	25855		3.72	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12930	25958		5.65	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1529	14562	27533	1.85	5.8E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product
4671	17692	30578	1.92	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4725	17745	30636	1.21	5.6E-02	AA290599.1	EST_HUMAN	zs45c01.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:700416 3'
6917	19871	33160	5.93	5.6E-02	AW172708.1	EST_HUMAN	402c10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN. ;
7075	20097	33407	0.77	5.6E-02	AA866182.1	EST_HUMAN	cd47f12.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7358	20328	33677	2.94	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
8141	21078	34478	0.61	5.6E-02	AI89589.1	EST_HUMAN	qd84g11.x1 Scarsa testis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
8154	22120	35548	2.47	5.6E-02	BE542663.1	EST_HUMAN	601067168F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
8154	22120	35549	2.47	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10171	23096	36576	1.06	5.8E-02	AA482864.1	EST_HUMAN	nf49d07.s1 NCL_CGAP_AK1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C. ;
11891	24772		1.87	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2663	15660	28678	8.23	5.6E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
3228	16283	29207	3.44	5.9E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4244	17273	30157	1.13	5.8E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5742	18836	32017	3.09	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6141	18836	32017	3.81	5.8E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7603	20564	33925	1.85	5.8E-02	6755902	NT	Mus musculus tuftsin 1 (Tuft1), mRNA
8457	21426	34842	0.69	5.6E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8457	21426	34843	0.69	5.6E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10013	22940	36405	0.63	5.6E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10013	22940	36408	0.83	5.9E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10107	23033	36510	1.46	5.9E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
11360	24309	37836	6.48	5.8E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
13089	25920	31303	1.89	5.9E-02	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
3032	16090		1.02	5.4E-02	AJ277468.1	NT	Oryza sativa rbb13-1 gene for putative Bowman Birk trypsin inhibitor
3433	18323		6.97	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3931	16971	29885	0.7	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8462	21431		1.05	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395281 to 2613730
9428	22390	35828	0.53	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
11057	24020	37543	1.54	5.4E-02	U20780.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
1056	14102	27052	1.91	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1056	14102	27053	1.91	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1506	14539	27511	16.63	5.3E-02	T94759.1	EST_HUMAN	ye3712.11 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506
2504	15507	28533	2.12	5.3E-02	AJ278408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2953	16011	28937	0.95	5.3E-02	M58417.1	NT	Pseudomonas putida tgsS gene
2953	16011	28938	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3167	16222	29137	5.38	5.3E-02	AJ278408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
4841	17682	30550	0.9	5.3E-02	AJ011048.1	NT	Pseudomonas putida tgsS gene
5125	18134	31011	8.41	5.3E-02	M80463.1	NT	Arabidopsis thaliana ell5 gene, exons 1-11
5392	18495	31372	1.8	5.3E-02	AE000627.1	NT	Mus musculus caudal type homeobox-1 (Cbx-1) gene, complete cds
5392	18495	31373	1.8	5.3E-02	AE000627.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6222	19296	32530	3.03	5.3E-02	M85289.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
7088	20090	33398	3.94	5.3E-02	U695413	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7299	20271	33806	1.23	5.3E-02	U32832.1	NT	Lymphocystis disease virus 1, complete genome
7595	20546		2.12	5.3E-02	S78221.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
8209	21108	34507	0.51	5.3E-02	P38742	SWISSPROT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8748	21716		0.5	5.3E-02	U10098.1	NT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
9481	22445	35886	2.05	5.3E-02	X03127.1	NT	Mus musculus 129/Sv cytactin C (cst3) gene, complete cds
10491	23413	36911	0.61	5.3E-02	AB022605.1	NT	Podospira anserina mitochondrial epsilon-sen DNA
10491	23413	36912	0.61	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10491	23413	36912	0.61	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10618	23540		0.6	5.3E-02	Y07907.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenesis, 20-28 hpf)
10695	23617	37111	0.69	5.3E-02	X68432.1	NT	B. rerio pou(g) mRNA for transcription factor
12092	24963	38558	2.06	5.3E-02	X68435.1	NT	H. sapiens mRNA for HMG-CoA-synthase
2293	15305		89.73	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3131	16188	29097	1.98	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3131	16188	29098	1.98	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3960	17000	29815	0.73	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
3962	17002		0.97	5.2E-02	6671757	NT	Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA
4307	17336	30214	3.36	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nco-1 mRNA, complete cds
6025	19108	32310	0.66	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6228	19302		1.22	5.2E-02	A1830965.1	EST_HUMAN	w80e04.x1 NCL_OGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element;
7489	20454	33813	1.07	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8537	21606		2.16	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10087	23014	36487	1.77	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
10087	23014	36488	1.77	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
11888	24769	38357	5.42	5.2E-02	F32386.1	EST_HUMAN	HSPD25097 HM3 Homo sapiens cDNA clone s3000039A02
11888	24769	38358	5.42	5.2E-02	F32386.1	EST_HUMAN	HSPD25097 HM3 Homo sapiens cDNA clone s3000039A02
12893	25358		1.55	5.2E-02	Q03030	SWISSPROT	OXAALACETATE DECARBOXYLASE ALPHA CHAIN
2372	15380		0.97	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073.1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547D073 5'
5041	18054		0.94	5.1E-02	AB031740.1	NT	Homo sapiens PB11 gene for salivary proline-rich protein P-B, complete cds
6830	18884	33175	0.68	5.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
7039	18371	31258	1.76	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8598	21594	34978	0.77	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8598	21594	34979	0.77	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8690	21658	35081	1.26	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
9237	22203	35634	0.61	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9237	22203	35635	0.61	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10168	23093	36571	7.1	5.1E-02	AF012868.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10542	23464	36859	1.66	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN GEX)
11179	24135	37665	2.19	5.1E-02	AF063930.1	NT	Homo sapiens ES18 mRNA, partial cds
11179	24135	37666	2.19	5.1E-02	AF063930.1	NT	Homo sapiens ES18 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12639	25359		1.75	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
12961	25531		1.6	5.1E-02	AA534104.1	EST_HUMAN	nt7302.61 NCL_CGAP_P110 Homo sapiens cDNA clone IMAGE:998139
483	13556	26481	2.16	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
835	13988	28938	4.55	5.0E-02	Z33896.1	NT	O virginianus (HEL37) microsatellite DNA
1209	14247	27205	4.03	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2007	15028	28036	4.94	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2829	14040	26995	1.62	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3348	16399		1.34	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3609	16654		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3696	18739	28652	13.52	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
6253	18326	32567	0.77	5.0E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6441	19306		1.25	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7181	18412	31214	0.6	5.0E-02	P36616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7785	20738	34110	12.03	5.0E-02	P36616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
8008	20946		0.52	5.0E-02	AW062494.1	EST_HUMAN	MRO-CT0094-100899-002-g10 CT0064 Homo sapiens cDNA
10560	23482	36977	1.26	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
11820	24703	38286	2.47	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12226	25918		6.4	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
226	13325		27.61	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
369	13455	26384	2.96	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
369	13455	26385	2.96	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3302	16355	28274	1.84	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3584	16829		0.7	4.9E-02	AA188940.1	EST_HUMAN	Zq48a12.e1 Stratagene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3605	16650	29566	0.96	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3605	16650	29567	0.96	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4877	17894	30783	2.11	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL_CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2632386 3'
4877	17894	30784	2.11	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL_CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2632386 3'
5444	18546	31458	1.71	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5444	18546	31459	1.71	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7349	20319	33698	2.83	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8963	21929		0.91	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
9107	22073	35500	0.8	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69

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10656	23578	37075	0.53	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11730	24616	38183	3.44	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12878	25473		6.66	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
330	13420	26344	1.06	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
331	13420	26344	2.41	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
489	13592	26486	12.99	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2281	15294	28318	2.24	4.8E-02	W51983.1	EST_HUMAN	z049b02.s1 Soares senescent fibroblasts, NBHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3222	16277	29202	1.93	4.8E-02	X17144.1	NT	Tetrahymena rosirata histone H3II and histone H4II intergenic DNA
4698	17719		1.24	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5174	18183	31060	0.63	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8477	21446	34863	1.55	4.8E-02	AW389497.1	EST_HUMAN	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
9485	22449	35889	0.76	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9485	22449	35890	0.76	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
12505	26242		1.35	4.8E-02	8632893	NT	Streptococcus thermophilus bacteriophage Sf19, complete genome
7004	20130	33445	3.77	4.7E-02	W01153.1	EST_HUMAN	yz9709.r1 Soares melanocyte 2Nblm-Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element;
7069	20091	33399	0.88	4.7E-02	BF686625.1	EST_HUMAN	602143554FT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7089	20081	33400	0.88	4.7E-02	BF686625.1	EST_HUMAN	602143554FT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7103	20037	33340	1.56	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8594	21582	34976	8.56	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9305	22270	35701	1.65	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9327	22292		2.51	4.7E-02	AB026678.1	NT	Gallus gallus Wpki-8 gene, complete cds
9582	22544	35995	7.94	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
10005	22932	36395	0.55	4.7E-02	BF305237.1	EST_HUMAN	601802692FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
10082	23018		0.56	4.7E-02	AI873042.1	EST_HUMAN	we78c10.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2347314 3'
12783	25970		1.97	4.7E-02	P52951	SWISSPROT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
13022	25570		1.56	4.7E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
270	13366	26292	1.08	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
741	13802	26741	3.47	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1361	14395	27366	3.62	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW/C01 5'

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2498	15499	28525	4.32	4.6E-02	AW236023.1	EST_HUMAN	xt24f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
2819	13366	26292	1.03	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1;
3020	16078	28999	0.67	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3342	16078	28999	0.67	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3507	16078	28999	0.91	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4149	17180		1.24	4.6E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II/Gu (ddx21) gene, complete cds
5252	18260	31129	0.94	4.6E-02	AA079167.1	EST_HUMAN	zn92c10.s1 Stragene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:X03212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
5823	18913	32066	1.42	4.6E-02	AF076962.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6357	19426	32668	4.48	4.6E-02	X61624.1	NT	C.reinhardtii alp2 (alpB) mRNA
6357	19426	32669	4.48	4.6E-02	X61624.1	NT	C.reinhardtii alp2 (alpB) mRNA
6968	20191	33518	1.51	4.6E-02	A1149574.1	EST_HUMAN	qc60506.x1 Soares_placenta_8to9weeks_2NLR-HP8to9W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1 t3 L1 repetitive element;
8134	21071	34470	0.68	4.6E-02	6978720	NT	Rattus norvegicus Cathepsin H (Ctsh), mRNA
9003	21989	35391	2.89	4.6E-02	BE154006.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11731	24617	38194	5.31	4.6E-02	AA913328.1	EST_HUMAN	cl27h09.s1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12761	25987		1.99	4.6E-02	L11692.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
12992	25552		8.41	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
447	13520	26453	1.9	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1222	14260	27217	0.78	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1222	14260	27218	0.78	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1821	14848	27841	4.23	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2119	15136	28156	3.34	4.5E-02	AE003984.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3736	16778	28691	4.42	4.5E-02	AL103278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6359	19427	32670	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6656	19713	32990	0.94	4.5E-02	AL103280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7062	20084	33392	0.98	4.5E-02	L26487.1	NT	Methanococcus marisnigri carbon monoxide dehydrogenase large subunit (cdhA) gene, carbon monoxide dehydrogenase small subunit (cdhB) gene, complete cds
7062	20084	33393	0.98	4.5E-02	L26487.1	NT	Methanococcus marisnigri carbon monoxide dehydrogenase large subunit (cdhA) gene, carbon monoxide dehydrogenase small subunit (cdhB) gene, complete cds
8736	21704	35128	2.34	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds

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10309	23293	36715	4.58	4.5E-02	AA325210.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' and similar to similar to neuro-D4 protein
10460	23382	36875	0.43	4.5E-02	X95508.1	NT	A.europaeum mRNA for legumini-like protein
10577	23499	36991	0.81	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12440	25203	31826	2.95	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
12823	25863	31440	7.3	4.5E-02	AA191097.1	EST_HUMAN	z43f11.r1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
222	13322		4.84	4.4E-02	BE972733.1	EST_HUMAN	601852154Ft NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2107	15124		6.38	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2498	15501	28527	2.11	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3654	16697	28612	2.01	4.4E-02	AF159160.1	NT	Mycobacterium xanthus serine/threonine kinase Pln10 (pln10) gene, complete cds
4657	17678	30563	1.25	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4657	17678	30564	1.25	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7721	17791		0.94	4.4E-02	AJ222869.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7325	20208	33639	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7325	20208	33640	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
9105	22071	35497	2.17	4.4E-02	AA736969.1	EST_HUMAN	hw13h03.st NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11409	24353	37886	3.75	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11533	24474	38025	2.56	4.4E-02	AA498739.1	EST_HUMAN	ac33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12159	25014		2.22	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12346	25980		1.83	4.4E-02	BF241245.1	EST_HUMAN	601878746Ft NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
781	13841	26786	5.93	4.3E-02	AF003249.1	NT	Macrone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2575	15576	28595	1.4	4.3E-02	AF704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3443	16490	28409	8.93	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3671	16714		1.25	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6844	19702	32977	4.62	4.3E-02	P30427	SWISSPROT	PLECTIN
6844	19702	32978	4.62	4.3E-02	P30427	SWISSPROT	PLECTIN
6896	16948	33245	0.73	4.3E-02	AA652266.1	EST_HUMAN	ns69c12.st NCL_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188886
8858	21826	35248	0.9	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9163	22119	35548	0.95	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
9163	22119	35547	0.96	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
823	13881	26832	1.85	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
867	13923		2.58	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
897	13952	26910	0.83	4.2E-02	AW003645.1	EST_HUMAN	wk34g01.x1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR.Q63291 Q63291
1733	14763		1.54	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 MRNA ;contains L1.t3 L1 L1 repetitive element ;
1763	14822	27806	1.02	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
3677	16720	28634	2.18	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4774	17794	30686	0.73	4.2E-02	BF342995.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
							602017105F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'
5699	18794	31967	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31968	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7175	18406	31205	0.73	4.2E-02	BE268285.1	EST_HUMAN	601124566F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2989319 5'
7769	20722	34094	4.52	4.2E-02	AF276762.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7763	20745	34118	0.61	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9162	22128	35556	3.74	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10525	23447	36945	1.19	4.2E-02	Q16850	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-58)
11379	24326	37855	1.58	4.2E-02	AA976118.1	EST_HUMAN	on33b1.1.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1559461 3' similar to gb:M65290
11637	24574	38138	2.65	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11637	24574	38139	2.65	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12694	25908		5.62	4.2E-02	AI983494.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12980	25550		1.69	4.2E-02	D14711.1	NT	w49g10.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
511	13582	26503	0.75	4.1E-02	AF200629.1	NT	Staphylococcus aureus HSP10 and HSP60 genes
2655	15681	28699	1.16	4.1E-02	AE002330.2	NT	Homo sapiens HPS1 gene, intron 5
4499	17524		7.84	4.1E-02	AW893484.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
5302	18305	31166	0.62	4.1E-02	5902103	NT	QV1-NN0012-180400-164-f06 NN0012 Homo sapiens cDNA
5726	18820	31999	1.08	4.1E-02	BE251894.1	EST_HUMAN	Homo sapiens SRV (sex-determining region Y)-box 10 (SOX10), mRNA
5726	18820	32000	1.08	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7066	20088		0.9	4.1E-02	X75881.1	NT	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7306	20277	33615	1.19	4.1E-02	AE002132.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7756	20709	34078	2	4.1E-02	7662347	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7880	20804	34180	0.7	4.1E-02	L02110.1	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
							Mus musculus proviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8042	20979	34375	2.63	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
8549	21617	34935	0.58	4.1E-02	P97857	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8990	21958	35381	0.57	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9509	22472	35916	0.83	4.1E-02	AA372388.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13013	25909	31423	4.48	4.1E-02	AJ271909.1	NT	Braessia napus gln gene for plastid glutamine synthetase, exons 1-12
13102	25625	31679	1.33	4.1E-02	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
1649	14681	27654	1.21	4.0E-02	AF675392.1	EST_HUMAN	wb98h01.x1 NCL CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2313746 3'
3258	16312	28233	2.57	4.0E-02	AB040604.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5453	18555	31466	5.39	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6339	19408	32849	1.43	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75299 O75298 R29124.1;
7954	20895	34288	6.1	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
8026	20963	34376	0.68	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
8043	20980	34377	0.85	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
9087	22033	35456	2.78	4.0E-02	P08640	SWISSPROT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
10002	22929	36423	0.71	4.0E-02	BF679376.1	EST_HUMAN	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
10027	22954	36423	2.95	4.0E-02	AJ000941.1	NT	60215384F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284724 5'
10344	23268	37118	0.92	4.0E-02	D43949.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
12068	24941	37118	1.48	4.0E-02	AJ001018.1	NT	Human mRNA for KIAA0082 gene, partial cds
12331	25730	31614	3.52	4.0E-02	AJ001058.1	NT	Kluyveromyces fragilis gene for Ca++ ATPase
1122	14166	27118	3.13	3.9E-02	BF516149.1	EST_HUMAN	Ovis aries mRNA for acetyl-coA carboxylase
1348	14383	27351	1.9	3.9E-02	P41047	SWISSPROT	U1H-BW1-ank-h-08-0-UJ.st NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1978	14999	28001	2.82	3.9E-02	AJ403388.1	NT	FAS ANTIGEN LIGAND
2715	15709		2.12	3.9E-02	4508682	NT	M.musculus DNA for desmin-binding fragment DesD7
5191	18200	31072	0.65	3.9E-02	AW392417.1	EST_HUMAN	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
							RC6-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5573	18669	31630	0.74	3.9E-02	D50608.1	NT	Rat gene for cholesteryltransferin type-A receptor (CCKAR), complete cds
5573	18669	31631	0.74	3.9E-02	D50608.1	NT	Rat gene for cholesteryltransferin type-A receptor (CCKAR), complete cds
5820	18970	32094	1.08	3.9E-02	BE968841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933842 5'
5957	19042	32241	0.71	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7259	19994	33291	1.1	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049890 5'
8167	21105	34504	0.53	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8172	21142	34548	1.07	3.9E-02	BF230613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8395	21364	34772	0.63	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8395	21364	34773	0.63	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11737	21105	34504	1.61	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12184	25872		14.17	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12949	25794		5.15	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
1989	14990	27893	1.13	3.8E-02	BE985137.1	EST_HUMAN	601510391F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
2129	15146		1.1	3.8E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
4906	17923	30815	0.92	3.8E-02	BE933275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5'
4906	17923	30818	0.92	3.8E-02	BE933275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5'
4955	17980	30870	1.4	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
6616	18616	31848	1.2	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6208	19280	32513	1.04	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOXB-4 (HOXB-2.6)
7540	20503	33862	1.43	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
9011	21977		1.28	3.8E-02	M80875.1	NT	Human von Willebrand factor gene, exons 23 through 34
11014	23979	37505	2.04	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12008	24886	39481	1.53	3.8E-02	P01641	SWISSPROT	IG KAPPA CHAIN V-V REGION MOPC 173B PRECURSOR
12009	24886	39482	1.53	3.8E-02	P01641	SWISSPROT	IG KAPPA CHAIN V-V REGION MOPC 173B PRECURSOR
694	14045	26999	4.76	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1389	14423	27392	0.96	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2246	15280	28287	4.98	3.7E-02	A1984806.1	EST_HUMAN	wr85q03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
3093	16120	29034	1.27	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3095	16122	29035	4.14	3.7E-02	BF312963.1	EST_HUMAN	601866233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3488	16514		1.03	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
5279	18285	31148	0.76	3.7E-02	AF168106.1	NT	Bubo virginianus cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7281	25998		0.79	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
7956	20897	34290	0.64	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
10375	23298		0.89	3.7E-02	AA782516.1	EST_HUMAN	ai55c09.s1 Soares parathyroid_tumor_NBHPA Homo sapiens cDNA clone 1360912 3'
12225	25061	38628	5.94	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024873 5'
12883	25762	31520	2.34	3.7E-02	11418392	NT	Homo sapiens scute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3667	16710	29625	1.04	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3674	16717	29631	0.75	3.6E-02	AL096808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5253	18281	31130	2.27	3.6E-02	AL096810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5501	18601	31514	0.8	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5501	18601	31530	0.8	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5578	18674	31638	0.68	3.6E-02	AF181722.1	NT	Homo sapiens RU2AS (RU2) mRNA, complete cds
6865	19918	33212	4.97	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6865	19918	33213	4.97	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7150	18382	31270	0.5	3.6E-02	U67575.1	NT	Methanococcus jannaschii section 117 of 150 of the complete genome
7291	20263	33597	1.7	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cx2 precursor (sgp2) gene, complete cds
7527	20491	33853	2.75	3.6E-02	AA714521.1	EST_HUMAN	hw20e05.s1 NOI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2
7895	20838	34218	1.08	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8746	22687	36142	1.85	3.6E-02	U20608.1	NT	MRO-HT0188-030200-003-b08 HT0188 Homo sapiens cDNA
8746	22687	36143	1.85	3.6E-02	U20608.1	NT	Dictyostellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9746	22887	36143	1.85	3.6E-02	U20608.1	NT	Dictyostellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9971	22898	36361	0.68	3.6E-02	BF347596.1	EST_HUMAN	602020453F1 NOI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156116 5'
886	13951	26909	0.9	3.5E-02	U09506.1	NT	Drosophila melanogaster tigglin mRNA, complete cds
1010	14059	27011	1.38	3.5E-02	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1566	14599	27574	1.3	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1566	14599	27575	1.3	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4241	17270	30155	1.95	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4344	17371	30253	3.67	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5285	18273		1.04	3.5E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION
6347	19418	32857	1.74	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAC1), complete cds
8310	21279		0.78	3.5E-02	H29951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5H-R Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8970	21836	35362	2.87	3.5E-02	BE958970.1	EST_HUMAN	60164-4701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
10378	23301	36777	1.99	3.5E-02	X76642.1	NT	Llactis MG1363 grE and dhak genes
10425	23347	36832	0.47	3.5E-02	BE661042.1	EST_HUMAN	60134-4661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11823	24706	38288	1.61	3.5E-02	AW861841.1	EST_HUMAN	PM1-CT0326-291289-002-h03 CT0328 Homo sapiens cDNA
11823	24706	38288	1.61	3.5E-02	AW861841.1	EST_HUMAN	PM1-CT0326-291289-002-h03 CT0328 Homo sapiens cDNA
12877	25806		5.77	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
580	13649	26562	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
580	13649	26563	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
581	13649	26562	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
581	13649	26563	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1053	14099	27049	2.4	3.4E-02	AW274020.1	EST_HUMAN	x26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1211	14249		6.51	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2401	15408	28432	2.51	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3444	16491	28410	1.19	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3942	16882	29897	3.71	3.4E-02	AW784952.1	EST_HUMAN	RC6-UJ0015-210200-021-A10 UM0015 Homo sapiens cDNA
4628	17649	30537	3.05	3.4E-02	X59789.1	NT	M.musculus S-antigen gene promoter region
5100	18110		2.48	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5114	18124	30999	1.93	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6330	19400		0.63	3.4E-02	BF131628.1	EST_HUMAN	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
7032	18364	31251	3.97	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8604	21572		3.14	3.4E-02	A1869629.1	EST_HUMAN	wf99d04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'
9100	22066	35492	1.66	3.4E-02	AA664886.1	EST_HUMAN	nu7008.s1 NCI_CGAP_AJ1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ;
							zq04f11.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9298	22234		6.2	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRNFTEITAENLTKESVTADAGRYEITAAANSSGTTKAFINIVLDRPG
10136	23082		0.64	3.4E-02	A1092719.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGGQSVTYNLLKRETSVAVWTEVSATVARTMMKVMKL ... ;

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
372	13458		9.24	3.3E-02	AA398735.1	EST_HUMAN	z75e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1171	14212	27169	14.49	3.3E-02	AB035867.1	NT	Cricetus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1645	14677	27650	1.73	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1753	14782		1.29	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2096	15113		1.76	3.3E-02	R09112.1	EST_HUMAN	yf25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
2458	15402	28485	1.31	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Trat), mRNA
3372	16422	28347	8.85	3.3E-02	H02389.1	EST_HUMAN	yf35h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4206	14677	27650	2.36	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4494	17519	30407	1.81	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Trat), mRNA
4848	17865	30759	0.66	3.3E-02	AW275696.1	EST_HUMAN	xp40b04.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742799 3'
6570	19630	32896	20.14	3.3E-02	BF245995.1	EST_HUMAN	601833910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6570	19630	32897	20.14	3.3E-02	BF245995.1	EST_HUMAN	601833910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9671	22630	36084	0.71	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9677	22630	36085	0.71	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9779	22720	36174	0.72	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
9779	22720	36175	0.72	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
10984	23884		0.46	3.3E-02	H38709.1	EST_HUMAN	yf511f1.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190989 3'
11455	24398	37945	2.47	3.3E-02	BF691107.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12425	25193		3.71	3.3E-02	T96645.1	EST_HUMAN	yf48f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
12547	25270		1.69	3.3E-02	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
12577	25286		3.04	3.3E-02	M81890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
132	13237	26168	1.27	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1128	14171	27122	10.01	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1128	14171	27123	10.01	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2127	15144		3.6	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
3151	16208	29122	9.61	3.2E-02	BE867393.1	EST_HUMAN	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
4246	17275		16.99	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4801	17818	30712	3.75	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5303	18306		1.34	3.2E-02	Y08624.1	NT	P.falciptarm mRNA for AARP2 protein
5613	18709	31866	1.56	3.2E-02	X68709.1	NT	S.griseocaneum whiG-Stv gene
5613	18709	31867	1.56	3.2E-02	X68709.1	NT	S.griseocaneum whiG-Stv gene

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6673	19730	33006	2.23	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W88.14
6676	19733		30.53	3.2E-02	T89387.1	EST_HUMAN	yd33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6763	19817	33097	4.01	3.2E-02	AF173845.1	NT	Alu repetitive element/contains LTR1 repetitive element ;
8039	20876	34372	0.82	3.2E-02	11424049	NT	Saguius oedipus tissue kallikrein gene, complete cds
8843	21611	35033	2.84	3.2E-02	6680555	NT	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
9293	22259		0.7	3.2E-02	AF109718.1	NT	Mus musculus khesin family member 3c (Kif3c), mRNA
9580	22542	35992	1.02	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9580	22542	35993	1.02	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1892063 3'
10417	23339		4.18	3.2E-02	AA719786.1	EST_HUMAN	zg54b12.s1 Soares_pineal_pland_N3HPG Homo sapiens cDNA clone IMAGE:1882063 3'
10723	23645	37138	0.98	3.2E-02	U68782.1	NT	gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
12812	25976		1.43	3.2E-02	V00574.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1265	14300		2.28	3.1E-02	4503416	NT	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-res-1) with four exons
1308	14344	27309	1.67	3.1E-02	P18845	SWISSPROT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1909	14933	27929	1	3.1E-02	6671584	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1991	16012		1.16	3.1E-02	Z50097.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5338	18441	31184	1.28	3.1E-02	U78104.1	NT	Drosophila melanogaster mRNA for headcase protein
5434	18536		2.26	3.1E-02	AA278478.1	EST_HUMAN	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5731	18825	32006	0.81	3.1E-02	BF687742.1	EST_HUMAN	z381a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5803	25645	32078	0.52	3.1E-02	AJ391284.1	NT	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
10391	23313	36783	2.66	3.1E-02	AF034779.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flhC-homologs, unknown genes) and flanking genes, strain FAM18
1627	14660		2.21	3.0E-02	AF187125.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
2590	15591	28608	0.97	3.0E-02	AA402242.1	EST_HUMAN	Pityokines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3579	16624	29545	0.91	3.0E-02	M94176.1	NT	z165h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3666	16709	29624	2.77	3.0E-02	AF247644.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3758	18789		0.98	3.0E-02	AW820223.1	EST_HUMAN	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3969	17009		1.45	3.0E-02	AA364003.1	EST_HUMAN	QV2-ST0298-150200-040-e09 ST0298 Homo sapiens cDNA
5092	18102	30977	7.41	3.0E-02	AF281074.1	NT	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5092	18102	30978	7.41	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5465	18567		2.99	3.0E-02	AB046793.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6383	19451	32593	0.58	3.0E-02	N99815.1	EST_HUMAN	z39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element ;
6383	19451	32594	0.58	3.0E-02	N99815.1	EST_HUMAN	z39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element ;
6957	20182	33505	3.17	3.0E-02	A124205.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
7091	20025	33327	2.8	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7091	20025	33328	2.8	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7274	20009	33310	2.29	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7274	20009	33311	2.29	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7442	20408	33760	1.29	3.0E-02	M86524.1	NT	Human dystrophin gene
7838	20783		0.75	3.0E-02	BF246361.1	EST_HUMAN	601864081F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8463	21432		0.48	3.0E-02	BF679706.1	EST_HUMAN	602154384F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4295664 5'
8988	21954	35378	0.74	3.0E-02	BF333889.1	EST_HUMAN	IL5-HT0704-290800-108-c04 HT0704 Homo sapiens cDNA
9145	22111		1.62	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10828	23747	37248	1.89	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
11568	24506	38063	2.38	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11897	24874	38470	7.84	3.0E-02	AA483216.1	EST_HUMAN	ne8704.st NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:3911263
12529	25960	31316	2.02	3.0E-02	R92019.1	EST_HUMAN	yh63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12868	25470		2.06	3.0E-02	AW895555.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12908	25954		1.96	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2442	15893	28467	1	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3005	16063	28982	1.14	2.9E-02	BE566544.1	EST_HUMAN	601339428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3005	16063	28983	1.14	2.9E-02	BE566544.1	EST_HUMAN	601339428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3573	16618	29540	0.8	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
3950	16960	29906	0.72	2.9E-02	H72805.1	EST_HUMAN	yu07a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
6181	19256	32489	1.13	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6424	19491	32743	7.33	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855598 5'
7142	20118	33431	0.52	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (thaB- and thac-homologs, unknown genes) and flanking genes, strain FAM18
7460	20426	33782	10.95	2.8E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7657	20817	33982	0.67	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8169	21107	34506	0.53	2.9E-02	AE003332.1	NT	Xylolla fastidiosa, section 78 of 229 of the complete genome
8331	21300	34716	0.83	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8331	21300	34717	0.83	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
10016	22943	36409	2.26	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10016	22943	36410	2.26	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10233	23158		0.67	2.9E-02	AW976597.1	EST_HUMAN	EST388706 MAGe resequences, MAGN Homo sapiens cDNA
10710	23832	37127	1.07	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomis DNA, section 777
11388	16618	29540	1.6	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12531	25870		1.46	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5'
567	13637		1.93	2.8E-02	AW970153.1	EST_HUMAN	EST332234 MAGe resequences, MAGK Homo sapiens cDNA
3380	16428	29355	1.27	2.8E-02	AF060603.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
3380	16428	29356	1.27	2.8E-02	AF060603.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
4341	17368		0.67	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Map1), mRNA
5206	18215	31090	3.2	2.8E-02	N87073.1	EST_HUMAN	L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-
5294	18299		0.93	2.8E-02	M58493.1	NT	GUANINE TRANSGLYCOSYLASE
5565	18662	31622	10.89	2.8E-02	BE741083.1	EST_HUMAN	Dengue virus type 2 non-structural protein 1 (NS1) gene, partial cds
6981	20204	33533	1.13	2.8E-02	T78960.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
8871	21638	35063	2.24	2.8E-02	AJ006920.1	NT	y421b08.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'
9371	22336	35766	0.82	2.8E-02	AA280762.1	EST_HUMAN	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9563	22625	35974	1.03	2.8E-02	AF187872.1	NT	z39606.f1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9667	22620	36071	0.71	2.8E-02	AE001092.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
10960	23900	37413	0.42	2.8E-02	BF52744.1	EST_HUMAN	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12809	25801		1.6	2.8E-02	R06966.1	EST_HUMAN	602039477F2 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177267 5'
12816	26438		1.57	2.8E-02	X06322.1	NT	Y12h02.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5'
						NT	Yeast CNG3C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV25S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
1485	14518	27491	1.07	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3445	16492	29411	1.88	2.7E-02	AL161494.2	NT	y86h12.f1 Soares multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:280487 5'
4230	17259	30143	2.01	2.7E-02	N47258.1	EST_HUMAN	

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	17269	30144	2.01	2.7E-02	N47258.1	EST_HUMAN	y88h12.r1 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
5319	18425	31176	0.52	2.7E-02	BF245672.1	EST_HUMAN	60186481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5516	18616	31549	1.09	2.7E-02	R12245.1	EST_HUMAN	y33c09.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6005	19088	32288	0.68	2.7E-02	X61670.1	NT	T. aestivum pTTH20 mRNA for wheat type V thionin
6087	19167	32379	0.51	2.7E-02	AB004789.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6754	19808		1.03	2.7E-02	X97580.1	NT	A.bisporus pgkA gene
7269	20004	33304	1.93	2.7E-02	AA933571.1	EST_HUMAN	ot9eh03.s1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
8140	21077		0.53	2.7E-02	AK024456.1	NT	Homo sapiens G21 protein (G21), mRNA
8160	21098	34497	0.59	2.7E-02	9256542	NT	Mus musculus G21 protein (G21), mRNA
8697	21865		1.23	2.7E-02	A377036.1	EST_HUMAN	tc28g08.x1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
573	13642	26556	1.25	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2374	15382	28404	2.54	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2376	15384	28406	3.05	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2376	15384	28407	3.05	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2926	15984		1.52	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
3988	17028		0.91	2.6E-02	AW181945.1	EST_HUMAN	x98i09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2662409 3'
4942	17958	30848	3.25	2.6E-02	L12032.1	NT	Chicken dorsalis-1 mRNA, complete cds
5104	18114	30987	1.8	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5128	18137	31014	3.05	2.6E-02	AW241154.1	EST_HUMAN	xe52b04.x1 NCI_CGAP_Ser4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
5944	19030		0.6	2.6E-02	AL161563.2	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5992	19076		0.55	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6345	19414		6.36	2.6E-02	A1206030.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6565	19625	32890	1.88	2.6E-02	BE621748.1	EST_HUMAN	qg27f11.x1 NCI_CGAP_Kd3 Homo sapiens cDNA clone IMAGE:1762317 3'
7001	20127	33441	0.82	2.6E-02	Z99064.1	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
7001	20127	33442	0.82	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth
7095	20029	33333	6.03	2.6E-02	6981271	NT	Vaccinia virus ORF1L, strain Wyeth
7516	20481	33842	0.55	2.6E-02	P21894	SWISSPROT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
8850	21817	35237	0.71	2.6E-02	AA860946.1	EST_HUMAN	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
9715	22743	38194	1.27	2.6E-02	11432020	NT	ak22f04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
							Homo sapiens KIAA1070 protein (KIAA1070), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10072	22989	36485	0.7	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	22989	36469	0.7	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10768	23689	37186	4.31	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11717	24680		2.02	2.6E-02	AA279351.1	EST_HUMAN	z884c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
11889	24770	38359	1.61	2.6E-02	AW500547.1	EST_HUMAN	U1-HF-BN0-alk-10-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
12457	25944	31313	1.96	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150944 5'
533	13604	26522	1.85	2.6E-02	AI793130.1	EST_HUMAN	on2606.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
533	13604	26523	1.85	2.6E-02	AI793130.1	EST_HUMAN	on2606.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
810	13668	26817	9.19	2.6E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
870	13928	26884	6.9	2.6E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2773	15765		2.26	2.6E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2988	16026	28949	3.43	2.6E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2988	16026	28950	3.43	2.6E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4075	18316	30005	1.02	2.6E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4075	18316	30006	1.02	2.6E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4233	17262	30146	8.52	2.6E-02	AW592114.1	EST_HUMAN	h36h08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5799	18691	32073	0.65	2.6E-02	AI732776.1	EST_HUMAN	z883c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810354 3'
6317	19388		4.71	2.6E-02	BE870128.1	EST_HUMAN	7630e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.t1 L1 repetitive element;
6334	19403		4.42	2.6E-02	BE746888.1	EST_HUMAN	601578933F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6470	19535	32783	0.97	2.6E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7927	20870	34258	1.48	2.6E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213408 5'
7927	20870	34259	1.48	2.6E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213408 5'
8137	21074	34474	0.54	2.6E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (PHF2) gene, complete cds
9177	22143	35570	0.82	2.6E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9315	22280	35710	0.46	2.6E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516370 3'
10426	23348		0.55	2.6E-02	X71303.1	NT	D. radiatum 28S ribosomal RNA, D2 domain
10947	23667	37381	0.67	2.6E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus NbHPU Homo sapiens cDNA clone IMAGE:1699982 3'
11161	24119	37646	2.15	2.6E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11161	24119	37647	2.15	2.6E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11227	24180		3.01	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds;
12059	24932		1.47	2.5E-02	AB007548.1	NT	butyrophilin-like (NG9), butyrophilin-B
12418	28985		3.35	2.5E-02	11420078	NT	Homo sapiens gene for LECT2, complete cds
12598	25751		1.47	2.5E-02	11433220	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC93634), mRNA
12686	25353		2.24	2.5E-02	U60169.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12709	25365	31770	3.42	2.5E-02	BE973327.1	EST_HUMAN	Dichostellium discoloratum putative protein kinase Mica (mka) gene, complete cds
175	13276	26203	0.69	2.4E-02	A376582.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935573 3'
1802	14834	27610	2.24	2.4E-02	H65884.1	EST_HUMAN	IC72c07.x1 Soares_NhiHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
2060	16884	28088	1.73	2.4E-02	P01901	SWISSPROT	y75f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
2060	15884	28088	1.73	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4396	17424	30308	1.43	2.4E-02	J05110.1	NT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4549	17572	30461	1.43	2.4E-02	P01901	SWISSPROT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4549	17572	30462	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5227	18235		0.9	2.4E-02	AL161595.2	NT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6340	19409	32650	0.97	2.4E-02	W86680.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
6496	19560	32811	0.65	2.4E-02	M31650.1	NT	zh83h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
6496	19560	32812	0.65	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7431	20398	33750	1.38	2.4E-02	Z20573.1	EST_HUMAN	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7448	20414	33767	1.05	2.4E-02	X12925.1	NT	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7448	20414	33768	1.05	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8159	21097	34495	0.52	2.4E-02	P98092	SWISSPROT	Rat gene for uncoupling protein (UCP)
8159	21097	34496	0.52	2.4E-02	P98092	SWISSPROT	HEMOCYTIN PRECURSOR (HUMORAL LECTIN)
8222	21191		0.57	2.4E-02	AW813007.1	EST_HUMAN	HEMOCYTIN PRECURSOR (HUMORAL LECTIN)
8276	21244		0.58	2.4E-02	M16780.1	NT	RC3-ST0186-230300-019-h08 ST0186 Homo sapiens cDNA
							Human retrotransposon 3' long terminal repeat
8784	21751		0.53	2.4E-02	H78376.1	EST_HUMAN	y412c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element
8876	21843	35265	11.43	2.4E-02	N69442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294566 3' similar to gb K02909 RA7SR7K Rat (RNA); contains A3R.b1 A3R repetitive element
9338	22303	35731	0.49	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
							z491c06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
9363	22328	35767	0.81	2.4E-02	AA625660.1	EST_HUMAN	XTR repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10050	22877	36443	0.46	2.4E-02	AF124160.1	NT	Arabidopsis thaliana methylglutathione synthase sulphurase (cns5) gene, complete cds
10050	22977	36444	0.46	2.4E-02	AF124160.1	NT	Arabidopsis thaliana methylglutathione synthase sulphurase (cns5) gene, complete cds
10165	23090	36968	2.57	2.4E-02	AF692854.1	EST_HUMAN	AV692854 GK Homo sapiens cDNA clone GKCDSC03 5'
10340	23264	36743	2.76	2.4E-02	AA493894.1	EST_HUMAN	h07b12.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element;
10976	23896		1.35	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902 5'
11900	24781	38368	1.81	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, Mus homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11900	24781	38369	1.81	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, Mus homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
12209	25050		2.39	2.4E-02	9627809	NT	Bacteriophage phi67, complete genome
12383	25152	31856	1.7	2.4E-02	6763636	NT	Mus musculus DmB homolog 1 (E. coli) (Dmb1), mRNA
12418	25188	31823	3.48	2.4E-02	BE928869.1	EST_HUMAN	MR0-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA
12474	25222	31791	1.59	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12474	25222	31833	1.59	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12643	25327		7.88	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1888	14913		5.26	2.3E-02	W05340.1	EST_HUMAN	z84g08.t1 Scarsa_fetal Jung_NbHL 19W Homo sapiens cDNA clone IMAGE:299284 5'
1904	14928		8.44	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2358	15366	28388	3.16	2.3E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
3694	16737	29650	4.2	2.3E-02	Z00377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
4176	17207	30083	0.8	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4176	17207	30094	0.8	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4450	17476	30364	1.52	2.3E-02	AW899107.1	EST_HUMAN	GM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4477	17503	30388	0.78	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4477	17503	30389	0.78	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4478	18317	30390	1.23	2.3E-02	AW593693.1	EST_HUMAN	xs25408.x1 NCI CGAP_U2 Homo sapiens cDNA clone IMAGE:2770671 3'
4478	18317	30391	1.23	2.3E-02	AW593693.1	EST_HUMAN	xs25408.x1 NCI CGAP_U2 Homo sapiens cDNA clone IMAGE:2770671 3'
4625	17646	30334	2.89	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
4625	17646	30335	2.89	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5203	18212	31086	1.19	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5203	18212	31087	1.19	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5449	18551	31463	3.35	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcdB) homolog gene, partial cds
6363	19432	32575	0.55	2.3E-02	BF108464.1	EST_HUMAN	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042828 3'
6774	19828	33112	4.22	2.3E-02	AL161605.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7172	18403	31201	0.84	2.3E-02	BE141475.1	EST_HUMAN	MRQ-HT0080-011099-002-c09 HT0080 Homo sapiens cDNA
7695	20853	34016	0.52	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
8208	21178	34686	6.65	2.3E-02	U63610.1	NT	Human plectin (PLECT) gene, exons 3-32, and complete cds
8815	21782	35207	0.87	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8815	21782	35208	0.87	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9044	22010	35431	0.74	2.3E-02	AI685380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9044	22010	35432	0.74	2.3E-02	AI685380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9493	22457	35897	0.89	2.3E-02	P41996	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0290.5 IN CHROMOSOME III PRECURSOR
10218	23143	36632	0.77	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10390	23312	36791	1.47	2.3E-02	AE000169.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10390	23312	36792	1.47	2.3E-02	AE000169.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11135	24095	37624	1.71	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12336	25738	37555	7.99	2.3E-02	BE278331.1	EST_HUMAN	601170958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12742	25392	31755	1.5	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12742	25392	31756	1.5	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12843	25453	31724	3.2	2.3E-02	U36394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12897	25983		2.48	2.3E-02	U11077.1	NT	Dicystostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
13100	25833		1.82	2.3E-02	11428388	NT	Homo sapiens deod ring (Drosophila)-like 1 (DRIL1), mRNA
739	13800	26739	4.3	2.2E-02	AF018267.1	NT	Columbia lilia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1762	14781		1.59	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2031	16050	28065	1.68	2.2E-02	Z82001.1	NT	S.pneumoniae popA gene and open reading frames
3448	16495		2.15	2.2E-02	AA577785.1	EST_HUMAN	nn24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3660	16703		3.48	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3887	16906	28814	1.26	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3941	16981	28806	0.74	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5105	18115	30888	1.17	2.2E-02	Z75597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241a
7458	20424	33780	3.37	2.2E-02	AV689721.1	EST_HUMAN	AV689721 GKB Homo sapiens cDNA clone GKBAND03 3'
8714	21682	35109	2.28	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8714	21682	35110	2.28	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9161	22127	35555	0.77	2.2E-02	X79468.1	NT	P.vulgate alpha tub 2 mRNA
10045	22972	38438	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10045	22972	38439	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10565	23487		0.91	2.2E-02	6878140	NT	Mus musculus Sjogren syndrome antigen A1 (Saa1), mRNA
11540	24481	38033	1.8	2.2E-02	BE797401.1	EST_HUMAN	6015843039F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938571 5'
12602	26304		6.72	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:500541 3' similar to contains Alu repetitive element
419	13492		5.37	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
449	13522		8.77	2.1E-02	AF029726.1	NT	Dicystosellium discoideum histidine kinase C (dhkC) mRNA, complete cds
1268	14303	27264	8.3	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1387	14420	27389	0.98	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1387	14420	27390	0.99	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1787	14826	27811	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1797	14826	27812	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1797	14826	27813	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1980	15001	28004	1.01	2.1E-02	AF190899.1	NT	Tegula aureolinea major acrosomal protein precursor (TMAP) mRNA, complete cds
2050	15069	28089	0.9	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2050	15069	28090	0.9	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2591	15582	28609	1.04	2.1E-02	AA225095.1	EST_HUMAN	nc21g03.r1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:1008820
2827	13839	28784	4.45	2.1E-02	N29266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:284541 5'
3164	15069	28089	1.02	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3164	15069	28090	1.02	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3597	16642	28661	0.98	2.1E-02	AA461271.1	EST_HUMAN	z63b09.r1 Soares total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4028	17066	29667	0.97	2.1E-02	BF203457.1	EST_HUMAN	601865890F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:4098407 5'
4157	17188	30076	0.94	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4339	17366	30249	1.4	2.1E-02	BF343555.1	EST_HUMAN	602016305F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4473	17499	30384	2.15	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4483	17508	30397	1.13	2.1E-02	AI768127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4739	17759	30654	5.69	2.1E-02	Y06501.1	NT	A.thaliana mitochondrial genome, part A
4761	17781	30877	1.5	2.1E-02	AA665737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
5265	18264	31133	1.07	2.1E-02	BF026405.1	EST_HUMAN	60167141F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3964410 5'
5723	18817	31996	0.75	2.1E-02	AW379529.1	EST_HUMAN	GM4-HT0244-111199-040-h05 HT0244 Homo sapiens cDNA
7268	20003	33303	0.65	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8864	21831	35264	0.66	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9861	22797	36250	0.51	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element contains element MER11 repetitive element;
9889	22916	36381	2.63	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9959	22916	36382	2.63	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10343	23267	36746	1.13	2.1E-02	L29324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
10421	23343	36829	0.68	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element contains element MER11 repetitive element;
12584	18345		8.95	2.1E-02	Y18213.1	NT	Homo sapiens putative psilHbA pseudogene for hair keratin, exons 2 to 7
12624	25735	31617	1.4	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
13003	25557	31693	3.5	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds
19	13139	26037	1.39	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13 MER1 repetitive element;
20	13140	26038	10.78	2.0E-02	AW895665.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
259	13356	26280	3.29	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
295	13389	26317	2.85	2.0E-02	AA456538.1	EST_HUMAN	eat15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
799	13858	26805	1.27	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1089	14133	27085	1.03	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p38.33] of Homo sapiens
1204	14243	27201	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1204	14243	27202	0.78	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1890	14915	27909	2.08	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1890	14915	27910	2.08	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2810	15802		4.57	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3096	13139	26037	1.61	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13 MER1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3159	16216		1.83	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8B (Sema8b), mRNA
3241	18296		1.8	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4032	17070	29971	1.4	2.0E-02	M18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5153	18163		0.7	2.0E-02	AI271995.1	EST_HUMAN	qj83503.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1866076 3'
5175	18184	31061	0.94	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5718	18812	31091	0.59	2.0E-02	U34778.1	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
6000	19063	32282	0.73	2.0E-02	L35321.2	NT	Dicysteleium discoidium class VII unconventional myosin (myoI) gene, complete cds
7799	20751	34128	1.09	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt, position (477)
7799	20751	34127	1.09	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt, position (477)
10236	23161		1.99	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10726	23648	37141	1.54	2.0E-02	AI640342.1	EST_HUMAN	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
11005	23971	37495	1.64	2.0E-02	Z73966.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11699	24664	38241	2.26	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
12148	18351	31298	3.03	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12621	15802		1.99	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13076	25608		3.4	2.0E-02	T80037.1	EST_HUMAN	yd04c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24675 5'
894	13758	26686	2.55	1.9E-02	AA572784.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.t1 L1 repetitive element;
1619	14652	27628	1.03	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2055	15074	28093	3.04	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2055	15074	28094	3.04	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2514	15517	28540	1.07	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2916	15974	28897	8.5	1.9E-02	AA713859.1	EST_HUMAN	mw04f05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2964	16022	28947	1.46	1.9E-02	AV648669.1	EST_HUMAN	AV048669 GLC Homo sapiens cDNA clone GLOCBLH07 3'
3273	16327		0.72	1.9E-02	AB033611.1	NT	Utricularia talpoides mitochondrial gene for cytochrome b, complete cds
3625	16668		1.36	1.9E-02	N62250.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosis_2NBHMP Homo sapiens cDNA clone IMAGE:284331 3'
3718	16761		8.23	1.9E-02	BE739088.1	EST_HUMAN	601572692F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839504 5'
3727	16769	29681	0.69	1.9E-02	AI301183.1	EST_HUMAN	qn04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;
4077	17112	30008	1.59	1.9E-02	AF141940.1	NT	Mycoplasma limicola VihA1 precursor (VihA1) and VihA2 precursor (VihA2) genes, partial cds
4222	17251	30137	1.82	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4222	17251	30138	1.62	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	17594	30488	3.65	1.9E-02	AI452999.1	EST_HUMAN	U46404.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5048	15517	28540	2.68	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5389	18492	31369	0.91	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5544	18641	31581	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
5985	18974		1.24	1.9E-02	AB019507.1	NT	Drosophila kanakl gene for glycerol-3-phosphate dehydrogenase, complete cds
7308	20279	33617	1.34	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7308	20279	33618	1.34	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8917	21983		1.2	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9886	22639	36036	0.78	1.9E-02	BF316129.1	EST_HUMAN	601898130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
10071	22968	36487	0.43	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10405	23327	36811	1.09	1.9E-02	BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10510	23432	36929	0.45	1.9E-02	N39160.1	EST_HUMAN	y46h08.s1 Soares multiple sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:276639 3'
10614	23636	37034	0.5	1.9E-02	D64001.1	NT	Synechocystis sp. PCC8803 complete genome, 20/27, 2539000-2644794
12372	25742	31620	3.14	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gliadin mRNA, complete cds
13026	25574	31696	1.4	1.9E-02	X68271.1	NT	H. sapiens MUC18 gene exon 16
346	13435	26357	1.35	1.8E-02	AW771104.1	EST_HUMAN	h152c06.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
686	13749	26675	1.39	1.8E-02	BF308122.1	EST_HUMAN	MER29 repetitive element;
1164	14205	27159	1.87	1.8E-02	X17664.1	NT	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
2687	15683	28701	1.78	1.8E-02	AE004544.1	NT	H.francisci mRNA for myelin basic protein (MBP)
3224	16279		1.06	1.8E-02	AI805829.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3902	16942	29853	1.01	1.8E-02	AW879122.1	EST_HUMAN	le52a09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3902	16942	29854	1.01	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4113	17147		1.04	1.8E-02	AA891446.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4461	17487	30374	1.49	1.8E-02	AW936363.1	EST_HUMAN	ak24h04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4992	18007	30895	0.98	1.8E-02	O60810	SWISSPROT	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
5287	18263	31154	0.68	1.8E-02	AF255711.1	NT	HYPOTHETICAL PROTEIN DJB45O24.2
6524	19587	32845	0.59	1.8E-02	AE002518.1	NT	Oryza sativa putative histone deacetylase HD2 mRNA, complete cds
6524	19587	32846	0.59	1.8E-02	AE002518.1	NT	Neisseria meningitidis serogroup B strain MC58 section 160 of 206 of the complete genome
6982	20205	33534	4.59	1.8E-02	P14310	SWISSPROT	Neisseria meningitidis serogroup B strain MC58 section 160 of 206 of the complete genome
7699	20657	34021	0.65	1.8E-02	BF125690.1	EST_HUMAN	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7722	20657	34021	0.58	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
8467	21436	34854	0.77	1.8E-02	U37091.1	NT	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
							Mus musculus carbonic anhydrase IV gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8811	21778	35203	0.79	1.8E-02	AW805327.1	EST_HUMAN	QV2-NN1073-220400-159-H09 NN1073 Homo sapiens cDNA
8857	21824	35247	0.75	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9849	22785	36238	0.5	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9849	22785	36239	0.5	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
10000	22927						q182f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:U11672 ZINC FINGER PROTEIN 91 (HUMAN);
10423	23345	36830	1.65	1.8E-02	AA897543.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3566963 5'
10586	23508	37000	1.2	1.8E-02	X86833.1	NT	L. stagnalis mRNA for myomodulin neuropeptide precursor
11765	23920	37438	1.7	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11765	23920	37439	1.7	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11935	24816	38413	2.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (617)
11948	24827	38422	3.16	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
13105	25626	31680	1.35	1.8E-02	R40255.1	EST_HUMAN	y680d01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28985 3' similar to gb:M62783 ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (HUMAN);
13105	25626	31681	1.35	1.8E-02	R40255.1	EST_HUMAN	y680d01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28985 3' similar to gb:M62783 ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (HUMAN);
907	13952	26918	0.8	1.7E-02	BE394869.1	EST_HUMAN	601310828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1806	14834	27823	2.15	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element;
1806	14834	27824	2.15	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element;
1887	14912		4.23	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2121	15138		11.19	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitoguanin29, complete cds
2301	15313	28333	1.03	1.7E-02	S74186.1	NT	[Microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
2648	15846		1.18	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3011	16089	28990	0.98	1.7E-02	A1147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3523	16559						hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
4198	17229						ac19f04.s1 Stralagene ovary (#837217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4228	17257						y88f08.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124647 5'
4482	17507	30396	0.7	1.7E-02	A1305279.1	EST_HUMAN	qm08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4557	17580	30471	1.52	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains
4744	17764	30658	1.54	1.7E-02	V00641.1	NT	L1.11 L1 repetitive element;
4851	17868		7.05	1.7E-02	AJ015076.1	EST_HUMAN	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
5105	18116	30869	0.74	1.7E-02	6981289	NT	ov61a02.x1 Soares_basla_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5229	18237		0.91	1.7E-02	AJ229041.1	NT	Rattus norvegicus N-arginine dibasic convertase 1 (Nrd1), mRNA
6248	19321	32551	1.63	1.7E-02	AJ769247.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6618	19676		0.64	1.7E-02	Z28383.1	NT	wg35f03.x1 Soares_NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6731	19787	33065	1.37	1.7E-02	AJ038280.1	EST_HUMAN	T.niveum (ATCC34921) simA gene for cyclosporine synthetase
7251	19986	33284	1.31	1.7E-02	AF190930.1	NT	ov65h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7411	20378	33729	1.95	1.7E-02	8400716	NT	Mecaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7681	20543	33902	0.86	1.7E-02	L07898.1	NT	Homo sapiens nebulin (NEB), mRNA
7681	20543	33903	0.85	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
8016	20954		1.98	1.7E-02	AJ010770.1	NT	Human apolipoprotein (a) gene, exon 1
9791	21114	34514	0.91	1.7E-02	U21854.1	NT	Homo sapiens hyperion gene, exons 1-50
10057	22984	39453	1.31	1.7E-02	AL040554.1	EST_HUMAN	Caenorhabditis elegans cCAF1 protein gene, complete cds
12084	24956	38551	1.59	1.7E-02	5902007	NT	DKFZp434i0314_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434i0314 5'
12810	25910	31424	3.15	1.7E-02	AW903482.1	EST_HUMAN	Homo sapiens serum constituent protein (MSE55), mRNA
13059	25595	31687	1.31	1.7E-02	AA846926.1	EST_HUMAN	CM4-NN1030-040400-130-106 NN1030 Homo sapiens cDNA
512	13583		2.22	1.8E-02	AL021929.1	NT	oe08d04.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1 repetitive element;
1665	14697	27673	0.91	1.6E-02	Y18889.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
2572	16573	28693	0.95	1.6E-02	AJ008345.1	NT	Treponema maltophilum flaB2, flaB3 and flilD genes for flagellin subunit proteins and CAP protein homologue
2661	16648	28671	1.46	1.6E-02	AA484872.1	EST_HUMAN	Homo sapiens KYLQ11 gene
2704	15700		1.37	1.6E-02	AB014534.1	NT	ne81d08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
3537	16583	29506	4.46	1.6E-02	AW850652.1	EST_HUMAN	Homo sapiens mRNA for KIA0634 protein, partial cds
4204	17235		2.14	1.6E-02	AF110520.1	NT	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
4329	17357	30245	0.96	1.6E-02	AW875407.1	EST_HUMAN	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5172	18181		0.76	1.6E-02	N80156.1	EST_HUMAN	QV2-PT0012-140100-030-107 PT0012 Homo sapiens cDNA
5325	18431	31183	0.49	1.6E-02	AI281385.1	EST_HUMAN	z665e07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:297444 3'
							qu42b09.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967417 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6705	18800	31977	1.33	1.6E-02	6871715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6799	19853	33139	2.07	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7117	20051	33354	0.93	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7117	20051	33355	0.93	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7978	20917	34308	1.08	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8458	21427	34844	0.72	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8519	21487		1.5	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10400	23322		1.98	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10785	23706	37206	1.2	1.6E-02	AA572818.1	EST_HUMAN	P28294 TELOKIN. [1];
10785	23706	37207	1.2	1.6E-02	AA572818.1	EST_HUMAN	nt19g03.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
11255	25705	37730	1.83	1.6E-02	Z94828.1	NT	P28294 TELOKIN. [1];
11547	24488	38042	1.7	1.6E-02	AL161508.2	NT	G.gallus microsatellite DNA (LEI0280 (=T16iIE11))
11547	24488	38043	1.7	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11839	24722	38307	1.66	1.6E-02	AJ373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
12347	18334	31172	1.39	1.6E-02	Q64176	SWISSPROT	q298610.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
12347	18334	31173	1.39	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
752	13813		20.75	1.6E-02	8823734	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2152	15168	28184	4.44	1.5E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
2185	15200	28220	1.82	1.5E-02	AL161594.2	NT	y27607.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
3074	16131	29043	2.54	1.5E-02	AJ006216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3074	16131	29044	2.54	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3737	16779	29692	1.06	1.5E-02	BF092942.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
6426	19493	32745	1.33	1.5E-02	Q09711	SWISSPROT	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
7541	20504		1.59	1.5E-02	11467282	NT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
7631	20591	33954	1.38	1.5E-02	11418713	NT	Cyanophora paradoxa cyanelle, complete genome
8208	21176	34585	1.5	1.5E-02	AL163303.2	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8213	21182	34593	4.62	1.5E-02	11417739	NT	Homo sapiens chromosome 21 segment HS21C103
9182	22148	35575	0.93	1.5E-02	BF345554.1	EST_HUMAN	Homo sapiens valyl-RNA synthetase 2 (VARS2), mRNA
9823	22672		0.58	1.5E-02	AF096774.1	NT	602019135F1 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4154504 5'
9929	22812	36286	1.58	1.5E-02	D44808.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
10170	23095	36574	0.95	1.5E-02	R32667.1	EST_HUMAN	Saccharomyces cerevisiae chromosome VI plasmid GapC
							yh54p10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10170	23095	36575	0.95	1.8E-02	R3287.1	EST_HUMAN	yt54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
11503	24445	37997	2.75	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11537	24478	38028	2.52	1.8E-02	AL111238.1	NT	Borhyis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
12564	25783		2.04	1.5E-02	AW75034.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
13078	25610		1.3	1.5E-02	AI763127.1	EST_HUMAN	wi08h03.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element; contains element MER26 MSR1 repetitive element ;
417	13490		1.99	1.4E-02	AE002230.2	NT	Chlamydomonas reinhardtii AR39, section 58 of 94 of the complete genome
1120	14164	27115	5.44	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1261	14296		1.74	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1301	14337		3.4	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1520	14552		1.03	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAH11 5'
3226	16281	28204	2.04	1.4E-02	AF160869.2	NT	Bifidobacterium longum Nav/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosaminylxylase repressor protein (nagC/xylR) gene, partial cds
3409	16458	29380	0.88	1.4E-02	AW074212.1	EST_HUMAN	xb09d09.x1 NCL_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2575793 3'
3498	16543	29467	6.29	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3498	16543	29468	6.29	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3669	16712	29627	6.69	1.4E-02	6966918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4516	17541	30427	6.1	1.4E-02	AW962888.1	EST_HUMAN	EST374761 MAGG Homo sapiens cDNA
4516	17541	30428	6.1	1.4E-02	AW962888.1	EST_HUMAN	EST374761 MAGG Homo sapiens cDNA
4911	17928	30818	8.08	1.4E-02	BE733142.1	EST_HUMAN	601667403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4911	17928	30819	8.08	1.4E-02	BE733142.1	EST_HUMAN	601667403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5130	18139	31017	1.01	1.4E-02	AW949453.1	EST_HUMAN	GM0-FN0041-120500-370-h09 FN0041 Homo sapiens cDNA
5888	25992		0.95	1.4E-02	X91338.1	NT	H.sapiens La/SS-B pseudogene 3
6555	19615	32890	4.9	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6555	19615	32881	4.9	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
8478	21447		1.61	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9249	22215	35645	0.77	1.4E-02	M81702.1	NT	Candida biddini methanol oxidase (AOD1) gene, complete cds
9510	22473	35917	0.9	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9755	22696	39153	2.15	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10923	23843		0.58	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment H521C018

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12254	25080	38172	2.14	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12616	25312		1.47	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12882	25474		1.98	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1972	14983	27994	2.05	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3227	18282	29205	2.31	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3227	18282	29206	2.31	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3993	17033		1.38	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
4964	17979	30869	1.06	1.3E-02			Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
5317	18423	31225	1.79	1.3E-02	U66061.1	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5317	18423	31228	1.79	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6289	19360	32597	1.21	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
6322	19393	32634	0.7	1.3E-02	M82662.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7164	18386	31228	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7154	18386	31229	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7829	20777	34155	4.86	1.3E-02	AI031593.1	EST_HUMAN	ox04g05.x1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8826	21793	35216	1.48	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10567	23483	36981	2.18	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10641	23563	37059	0.63	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10988	23608	37421	0.44	1.3E-02	AA707741.1	EST_HUMAN	zh24a07.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:412980 3'
11336	24286	37809	3.74	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11336	24286	37810	3.74	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12622	25923		1.4	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12714	25368		2.51	1.3E-02	9633069	NT	Human herpesvirus 8B, complete genome
12886	25718		16.88	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
214	13314		0.67	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
355	13443	26368	4.67	1.2E-02	AA059299.1	EST_HUMAN	zf65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element:
453	13526	26456	1.81	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR53REGION
740	13801	26740	3.32	1.2E-02	AI183522.1	EST_HUMAN	qd08e12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element:
2187	15202	28222	1.82	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2190	15205	28225	1.44	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2449	15454	28476	1.65	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2859432 3'
2505	15508	28534	0.99	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2505	15508	28535	0.99	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2643	15454	28476	1.31	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2859432 3'
3118	16175		6.56	1.2E-02	AA075418.1	EST_HUMAN	zn188603.r1 Stratagene ovarian cancer (#537219) Homo sapiens cDNA clone IMAGE:545020 5'
3301	16354	29273	2.62	1.2E-02	R62805.1	EST_HUMAN	yt1108.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4917	17934	30826	8.36	1.2E-02	6754367	NT	Mus musculus interferon regulatory factor 5 (irf5), mRNA
4953	17968	30858	1.66	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5080	18090		1.54	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CplUbiqT mRNA, partial cds
5121	18131	31008	2.09	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5259	18287	31135	1.01	1.2E-02	AF185576.1	NT	Mus musculus POZ/zinc finger transcription factor ODA-8 mRNA, complete cds
5769	18661		0.5	1.2E-02	AA758018.1	EST_HUMAN	ai29f10.s1 Soares testis_NHT Homo sapiens cDNA clone 1344235 3'
5946	18936	32120	1.72	1.2E-02	D78589.1	NT	Rana rugosa mRNA for catreticul, complete cds
6238	19311	32543	0.58	1.2E-02	AF045555.1	NT	Homo sapiens wbcscr1 (WBCSCR1) and wbcscr5 (WBCSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7203	20227	33560	5.57	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7510	20475	33836	1.07	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7534	20497	33858	8.5	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
7805	20755	34131	0.54	1.2E-02	BF216860.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8330	21299	34715	2.29	1.2E-02	Q11205		CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8534	21502	34918	1.31	1.2E-02	AF163612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8534	21502	34920	1.31	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
9242	22208		1.1	1.2E-02	T76987.1	EST_HUMAN	y472c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9997	22924	36389	2.63	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
10030	22957	36425	1.29	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12310	25118	31841	2.74	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU) (HPER)
12898	25482		5.61	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujiiwara) Homo sapiens cDNA clone GEN-557G06 5'
1274	14309	27270	1.14	1.1E-02	AA070364.1	EST_HUMAN	zn69e1.1.s1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1719	14749	27734	1.8	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1719	14749	27735	1.8	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2054	16073	28092	4.08	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5'
2889	15948		3.91	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:295040 5'
3535	16591	29505	2.75	1.1E-02	AI653508.1	EST_HUMAN	iq95b10.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW_XPF_HUMAN
4051	17088		1.52	1.1E-02	BE144837.1	EST_HUMAN	Q92899 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4133	17165		0.71	1.1E-02	AW813768.1	EST_HUMAN	PM3-HT0175-300999-001-h08 HT0175 Homo sapiens cDNA
4867	17884	30772	2.22	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp586E0924_s1 586 (synonym: huter) Homo sapiens cDNA clone DKFZp586E0924
6272	19345	32578	1.02	1.1E-02	U60480.1	NT	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), YnaK (ynbK), YnaL (ynbL), YnaM (ynbM), YnaN (ynbN), YnaO (ynbO), YnaP (ynbP), YnaQ (ynbQ), YnaR (ynbR), YnaS (ynbS), YnaT (ynbT), YnaU (ynbU), YnaV (ynbV), YnaW (ynbW), YnaX (ynbX), YnaY (ynbY), YnaZ (ynbZ)
7855	20800	34176	2.47	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
8105	21042	34441	3.79	1.1E-02	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
8987	21953	35377	0.7	1.1E-02	AW996160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
9174	22140	35568	0.66	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (YNakanura) Homo sapiens cDNA clone 3NHC4040
9253	22219	36650	7.21	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10289	23214	36698	2.1	1.1E-02	AA082578.1	EST_HUMAN	zn24e01.r1 Stralagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10454	23376	36869	3.79	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Cdon carchoma (HCC) cell line II Homo sapiens cDNA 5' end
11324	24274	37802	2.01	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
12194	25039		3.52	1.1E-02	AA68239.1	EST_HUMAN	ab77f11.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12660	17165		1.67	1.1E-02	AW813768.1	EST_HUMAN	Alu repetitive element
7	13127	26027	6.08	1.0E-02	AW848120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1528	14559	27530	1.07	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
2578	15579		1.26	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3106	16163	29075	2.7	1.0E-02	BE835556.1	EST_HUMAN	cc22f08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3276	16330	29251	1.33	1.0E-02	BE988999.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
							601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'

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3520	16566		0.65	1.0E-02	AW845621.1	EST_HUMAN	MRO-CT0080-081099-003-h10 CT0080 Homo sapiens cDNA
3895	16935	28845	0.75	1.0E-02	AI065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
3911	16951	28862	1.06	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4811	17828	30725	4.97	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4851	17898	30787	5.01	1.0E-02	R06567.1	EST_HUMAN	y954h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
5036	18048	30929	0.63	1.0E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5490	18590	31501	0.88	1.0E-02	H52681.1	EST_HUMAN	y03h11.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'
5840	18930	32114	0.82	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6237	19310	32542	1.02	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6305	19376	32614	2.49	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6305	19376	32615	2.49	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6928	20150	33470	2.15	1.0E-02	Z28642.1	NT	Zmays U3snRNA pseudogene
9748	22889	36145	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9748	22889	36146	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11594	24532		1.96	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11595	24560	38238	2.05	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDG10 5'
12091	24962		1.47	1.0E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12276	25990		1.99	1.0E-02	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12337	25757	31518	3.9	1.0E-02	AW935521.1	EST_HUMAN	RC2-DT0007-120200-018-h02 DT0007 Homo sapiens cDNA
12356	25816		5.66	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12722	25789		2.07	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12873	25873		4.78	1.0E-02	X62654.1	NT	H. sapiens gene for Me491/CD63 antigen
13094	25620	31676	1.7	1.0E-02	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
894	13949	26907	1.77	9.0E-03	AI798126.1	EST_HUMAN	wh4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element *
1269	14304		1.88	9.0E-03	BE781899.1	EST_HUMAN	MER22 MER22 repetitive element ;
1476	14510	27485	0.97	9.0E-03	AE001270.1	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2405	15412	28436	2.87	9.0E-03	AL161559.2	NT	Trepone pallidum section 86 of 87 of the complete genome
2413	15420	28444	0.95	9.0E-03	AF099934.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2917	15975	28898	0.69	9.0E-03	AI251744.1	EST_HUMAN	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2917	15975	28899	0.69	9.0E-03	AI251744.1	EST_HUMAN	qh9009.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3682	16725	29638	0.87	9.0E-03	J05184.1	NT	qh9009.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5061	18071	30850	1.01	9.0E-03	T70044.1	EST_HUMAN	S. acidocaldarius thermophilus gene, complete cds
							yc17b08.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'

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5061	18071	30951	1.01	9.0E-03	T70044.1	EST_HUMAN	yc17b08.s1 Stragelene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
5260	18268	31136	0.95	9.0E-03	6753521	NT	Mus musculus corticotroph releasing hormone receptor 2 (Chr2), mRNA
5908	18994		1.2	9.0E-03	A1809792.1	EST_HUMAN	wf77f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
6785	19840		4	9.0E-03	BE745988.1	EST_HUMAN	601673438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7698	20656	34020	0.63	9.0E-03	A1242219.1	EST_HUMAN	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7712	20669	34036	0.81	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8207	21177		0.99	9.0E-03	AL039991.1	EST_HUMAN	DKFZp434L0412_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5'
8592	21560		0.55	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10221	23146	36635	1.42	9.0E-03	P20808	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
11331	24261		1.6	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
12690	25985		2.12	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12989	25549		15.47	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-409 HT0462 Homo sapiens cDNA
502	13574		3.01	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element;
991	14043	26997	19.52	8.0E-03	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2166	15182	28202	1.66	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3321	16372	29293	1.12	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-609 HT0545 Homo sapiens cDNA
3370	16420	29345	0.93	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3689	16732	29644	1.25	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3689	16732	29645	1.25	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4285	17314	30193	1.08	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4410	17438	30328	5.3	8.0E-03	BF363327.1	EST_HUMAN	CM4-NN0119-300600-223-505 NN0119 Homo sapiens cDNA
4747	17767	30662	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4747	17767	30663	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5501	18597	31668	2.68	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacri21 gene, partial>
6323	25658	32635	1.39	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (217)
6913	19966	33281	4.24	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
7104	20038		1.4	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7415	20362	33733	1.88	8.0E-03	M17197.1	NT	A.californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7760	20743		1.81	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds

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9235	22201	35631	0.58	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9261	22227	36657	3.77	8.0E-03	AW808592.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
9270	22236	35885	0.52	8.0E-03	AL139075.2	NT	MR1-ST0111-111199-011-P06 ST0111 Homo sapiens cDNA
9831	22296	35728	0.58	8.0E-03	9789956	NT	Campylobacter jejuni NCTC11168 complete genome, segment 2/6
10308	23232		5.16	8.0E-03	BE086509.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA
11118	24078	37692	1.99	8.0E-03	BE788441.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
11330	24280		2.66	8.0E-03	Z49652.1	NT	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
11649	24586	38156	2.59	8.0E-03	BF363327.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR152w
11710	24875	38252	1.55	8.0E-03	AA828817.1	EST_HUMAN	GM4-NN0119-300600-223-505 NN0119 Homo sapiens cDNA
11710	24875	38253	1.55	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCL_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1374232
12024	24900	38495	3.74	8.0E-03	AF064589.1	NT	cd80a09.s1 NCL_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1374232
12205	25047		2.04	8.0E-03	M69035.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12249	25077		2.6	8.0E-03	AB038161.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
695	13757	26687	18.14	7.0E-03	AF097183.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
695	13757	26688	18.14	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
978	14029	26983	4.66	7.0E-03	AF243376.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1118	14162	27113	4.38	7.0E-03	AV731712.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1366	14400		1.16	7.0E-03	Q61060	SWISSPROT	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1396	14430	27399	3.03	7.0E-03	AA668298.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3/FFI) TRANSCRIPTION FACTOR GENESIS (HEPATOCYTE
1502	14535	27506	3.04	7.0E-03	AW303589.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFH-2)
1756	14785	27769	1.03	7.0E-03	AW950556.1	EST_HUMAN	ab79609.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1756	14785	27770	1.03	7.0E-03	AW950556.1	EST_HUMAN	x21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2267	15888	28307	2.08	7.0E-03	P04929	SWISSPROT	EST362626 MAGE resequences, MAGA Homo sapiens cDNA
3571	16616	29537	0.67	7.0E-03	A1150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3778	16820	29728	0.93	7.0E-03	AW444463.1	EST_HUMAN	qf34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1761955 3'
3925	16965	29769	1.45	7.0E-03	AF196344.1	NT	UI-H-B13-akb-c-10-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4048	16820	29728	0.83	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4366	17393		0.66	7.0E-03	U60086.1	NT	UI-H-B13-akb-c-10-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'

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4565	17588		1	7.0E-03	AW117711.1	EST_HUMAN	xe34f09.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987
4629	17650		1.47	7.0E-03	AW630888.1	EST_HUMAN	ACIDIC 82 KDA PROTEIN. ;
5024	18038		1.81	7.0E-03	AL163278.2	NT	hh89a05.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969936 5'
5228	18234	31108	1.4	7.0E-03	AV724419.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5228	18234	31109	1.4	7.0E-03	AV724419.1	EST_HUMAN	AV724419 HTB Homo sapiens cDNA clone HTBCEE08 5'
5918	18004		0.83	7.0E-03	H71106.1	EST_HUMAN	AV724419 HTB Homo sapiens cDNA clone HTBCEE08 5'
6233	25656		6.11	7.0E-03	AW861059.1	EST_HUMAN	yr82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gbX14723 CLUSTERIN PRECURSOR (HUMAN);
6447	19512	32782	1.38	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6687	18744	33019	3.16	7.0E-03	AA327128.1	EST_HUMAN	z333f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
6717	19773	33052	0.91	7.0E-03	BE657385.1	EST_HUMAN	EST30674 Colon I Homo sapiens cDNA 5' end
7284	20061	33387	1.92	7.0E-03	BE928133.1	EST_HUMAN	7q34b10.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 Q13387 HYPOPHYSEAL PROTEIN 384D8_2 ; contains TAR1.12 TAR1 repetitive element ;
7763	20716	34098	5.31	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7763	20716	34098	5.31	7.0E-03	Z35838.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077w
8180	21150	34558	0.45	7.0E-03	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8448	21417	34830	2.46	7.0E-03	BE175667.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8961	21927	35354	0.49	7.0E-03	AF281074.1	NT	RC6-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
9752	22693		0.71	7.0E-03	AF111168.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9953	22860	36344	0.85	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
10078	23005	36475	2.84	7.0E-03	P48982	SWISSPROT	yy49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains Alu repetitive element;
10078	23005	36476	2.84	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10688	23690		1.08	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10853	23773		0.95	7.0E-03	AJ789734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
11176	24132	37682	2.23	7.0E-03	AB008852.1	NT	AV687379 GKX Homo sapiens cDNA clone GKCAFC07 5'
11248	24201	37722	1.51	7.0E-03	AJ004862.1	NT	wc37e09.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2320840 3'
11248	24201	37723	1.51	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
12734	25977		1.53	7.0E-03	H94065.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12741	26391		1.91	7.0E-03	BE263253.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12834	26451		1.99	7.0E-03	Y17455.1	NT	yy15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains Alu repetitive element;
						EST_HUMAN	801145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160478 5'
						NT	Homo sapiens LSFR2 gene, penultimate exon

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1245	14282	27244	9.96	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXN_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR;
1245	14282	27245	9.96	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXN_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR;
2782	15774	28793	1.32	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2901	15960	28879	4.82	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2901	15960	28880	4.82	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3260	16314		2.26	6.0E-03	H75690.1	EST_HUMAN	y77h04.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3393	16442	29368	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3393	16442	29369	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3557	16803		1.28	6.0E-03	W37985.1	EST_HUMAN	zc13a11.r1 Soares_papillary thyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3672	16715	29629	4.48	6.0E-03	BF510966.1	EST_HUMAN	UIH-B14-apm-c-06-Q-U1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3708	16751	29687	1.21	6.0E-03	BE077358.1	EST_HUMAN	RC1-BT0606-260400-014-a07 BT0606 Homo sapiens cDNA
3760	16831	29737	1.19	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3944	16984	28900	0.87	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA
3979	17019		0.9	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4391	17419		1.81	6.0E-03	A1016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4724	17744	30635	5.97	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
6276	25657	32581	0.9	6.0E-03	9627521	NT	Varicella virus, complete genome
6969	20212	33541	0.87	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
7034	18366	31253	0.64	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7461	20427	33783	0.83	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7461	20427	33784	0.83	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7908	20851	34238	0.63	6.0E-03	AF128964.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
8100	21036	34436	0.62	6.0E-03	P17964	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
8136	21073	34473	0.5	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
8191	21161	34571	6.56	6.0E-03	A1033980.1	EST_HUMAN	ow13a04.x1 Soares_papillary thyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
8307	21276	34687	2.64	6.0E-03	AW799337.1	EST_HUMAN	RCO-UN0051-210300-032-g02 UM0051 Homo sapiens cDNA
8381	21360		1.51	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
9912	22733	36188	8.57	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10403	23325		2.08	6.0E-03	AI432681.1	EST_HUMAN	U22022.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10523	23445	36843	0.87	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ; Bacillus subtilis fenD gene
10659	23581		1.03	6.0E-03	AF084555.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10769	23690	37187	0.68	6.0E-03	X68366.1	NT	M.thermophilum complete plasmid pFV1 DNA
11096	24056	37580	1.61	6.0E-03	AW062164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
11162	24120		1.55	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
11327	24277		3.99	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11328	24278	37805	2.65	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12319	25123		2.28	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12422	25812		1.52	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
12446	25744		5.26	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429162 to 450296 (section 39 of 148) of the complete genome
12525	25807		2.71	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12576	25285		1.48	6.0E-03	Q62209	SWISSPROT	SYNAPTOMEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12850	25459		2.16	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
12869	25471		1.53	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
13043	25584		1.76	6.0E-03	BF110298.1	EST_HUMAN	7n36b1.1.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566564 3'
670	13735	26861	2.34	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
670	13735	26862	2.34	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
671	13735	26861	3.43	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
671	13735	26862	3.43	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1114	14158	27109	1.03	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1574	14607		1.02	5.0E-03	AJ138977.1	EST_HUMAN	q079005.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2690	15686	28703	2.63	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2947	16005	28930	3.66	5.0E-03	BE266057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538789 5'
3153	16210	29125	3.96	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:22395 3'
3169	16224		3.05	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3181	16236	28153	1.22	5.0E-03	R71794.1	EST_HUMAN	y86g02.s1 Scores breast 2NtHBat Homo sapiens cDNA clone IMAGE:155666 3'
3281	16344		0.94	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3679	16722	29635	0.97	5.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3713	16756	29670	4.03	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3771	16813	29722	1	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3995	17035		2	5.0E-03	AA239675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4333	17361	30246	0.69	5.0E-03	H78355.1	EST_HUMAN	y179g10.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240066 5'
4335	16813	28722	1.02	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4601	17622	30515	1.02	5.0E-03	U46691.1	NT	Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds
4638	17659	30546	1.13	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4749	17769	30865	1.34	5.0E-03	A1752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
4970	17985	30875	1.08	5.0E-03	P15285	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5222	18230	31105	1.69	5.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp), mRNA
5893	18981	32172	5.69	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
6162	19237	32468	2.97	5.0E-03	O00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6198	19272		0.89	5.0E-03	AE002234.2	NT	Chlamydia pneumoniae AR39, section 62 of 94 of the complete genome
6747	19801		7.44	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2560871 3'
7023	19355	31274	7.12	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7240	19975		0.82	5.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7295	20267	33602	0.57	5.0E-03	6753651	NT	Mus musculus dynein, exon, heavy chain 11 (Dnaic11), mRNA
7727	20683	34047	0.62	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCE83 similar to EST containing Alu repeat
7858	20801		1.17	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-107 CT0255 Homo sapiens cDNA
8044	20981	34378	6.8	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8097	21033	34431	0.49	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8097	21033	34432	0.49	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8581	21549	34967	2.12	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8959	21925		5.83	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9159	22125	35554	1.08	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
9282	22258	35688	0.61	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10199	23124	36911	0.97	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
10330	23254	36732	0.68	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10518	23440	36938	0.44	5.0E-03	AA533143.1	EST_HUMAN	h46h10.s1 NCL CGAP_P18 Homo sapiens cDNA clone IMAGE:995587
10896	23618	37112	0.47	5.0E-03	7662557	NT	Homo sapiens PRO0471 protein (PRO0471). mRNA
10844	23784		0.51	5.0E-03	AA653261.1	EST_HUMAN	ag48c10.s1 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
11075	24037		4.17	5.0E-03	T18598.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
11287	24237	37764	2.15	5.0E-03	AW170334.1	EST_HUMAN	xt59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element ;
11287	24237	37765	2.15	5.0E-03	AW170334.1	EST_HUMAN	xt59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element ;
11381	24328	37657	1.55	5.0E-03	T49163.1	EST_HUMAN	y609e04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'
11659	24995		3.62	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCL CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291622 5'
12463	25938		5.42	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12595	25298		3.7	5.0E-03	AF067263.1	NT	Brugia malayi Y chromosome marker
12688	25355		3.19	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12718	26372		1.89	5.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:309548 3' similar to SW-DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12743	25752		5.67	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12822	25498	31702	3.21	5.0E-03	AW449109.1	EST_HUMAN	UJH-B19-akf-f08-0-UJ.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
236	13335	26269	2.6	4.0E-03	AW500196.1	EST_HUMAN	UJH-BN0-akc-h-04-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
321	13413	26337	2.12	4.0E-03	R48482.1	EST_HUMAN	y951e04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
443	13516	26449	1.15	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PI3K)
606	13672	26586	4.63	4.0E-03	AA839339.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
878	13933	26893	1.9	4.0E-03	R48482.1	EST_HUMAN	y951e04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
912	13967		3.64	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1153	14185	27147	27.01	4.0E-03	AA099777.1	EST_HUMAN	z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1173	14214	27168	1.92	4.0E-03	AW794740.1	EST_HUMAN	RC9-LJM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1306	14342	27306	1.5	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1690	14622		1.64	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAK806 5'
1758	14787	27772	2.38	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
2034	15053	28070	11.42	4.0E-03	AA099777.1	EST_HUMAN	z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2259	15273		1.68	4.0E-03	BE410598.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2286	15299	28323	1.53	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2579	15580	28598	1.75	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2579	15580	28599	1.75	4.0E-03	U52111.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2701	15597	28712	3.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2701	15597	28713	3.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2701	15702	28716	1.68	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3239	16294	28217	1.04	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3239	16294	28218	1.04	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3541	16587	29510	0.8	4.0E-03	AW188426.1	EST_HUMAN	X98104.X1 NCI_CGAP_Cot8 Homo sapiens cDNA clone IMAGE:2665279 3'
3541	16587	29511	0.8	4.0E-03	AW188426.1	EST_HUMAN	X98104.X1 NCI_CGAP_Cot8 Homo sapiens cDNA clone IMAGE:2665279 3'
3639	16882	29597	0.64	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4020	17058		2.14	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
							ab18a08.x5 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4643	17664	30553	1.1	4.0E-03	AI732754.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4805	17822	30717	3.73	4.0E-03	AL163284.2	NT	Xe83d03.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.t1 L1 L1 repetitive element;
5173	18182	31059	0.98	4.0E-03	AW103719.1	EST_HUMAN	Xe83d03.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.t1 L1 L1 repetitive element;
5220	18228	31102	0.63	4.0E-03	AA699995.1	EST_HUMAN	z69b01.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436009 3'
5272	18278	31142	0.93	4.0E-03	J02187.1	NT	Foot and mouth disease virus serotype A-12 119ab capsid protein VP3
5348	18453	31324	1.56	4.0E-03	AF005859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5473	18574	31482	23.1	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5891	18978	32171	2.72	4.0E-03	P04196	SWISSPROT	(HPRG)
5895	18983	32173	1.63	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
5883	19088	32266	0.87	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7811014_r1.761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7811014 5'
6203	19277		3.56	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6381	19430	32673	1	4.0E-03	AW590572.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948652 3'
6442	19507	32757	1.78	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6827	19881	33172	0.87	4.0E-03	AA813222.1	EST_HUMAN	aj32111.s1 Soares testis_NHT Homo sapiens cDNA clone 1392045 3'
6942	20168	33489	1.5	4.0E-03	U76408.1	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7273	20008	33308	1.22	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7273	20008	33309	1.22	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7404	20372	33723	4.12	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7665	20624	33988	0.99	4.0E-03	AI681483.1	EST_HUMAN	bc37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7667	20626	33990	0.72	4.0E-03	BE670170.1	EST_HUMAN	7a31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7767	20720		0.68	4.0E-03	X92109.1	NT	H. sapiens hcgIX gene
8274	21243	34655	0.49	4.0E-03	Q9TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8383	21352	34781	6.06	4.0E-03	AF111944.1	NT	Dicystellum discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
8545	21513	34930	1.92	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9064	22030	35453	7.41	4.0E-03	AI539883.1	EST_HUMAN	7a49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element;
9241	22207		4.72	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9250	22216	35646	3.66	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10287	23212	36695	0.57	4.0E-03	H30684.1	EST_HUMAN	yp42g12.1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
10742	23664	37159	0.76	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11176	24133	37663	1.65	4.0E-03	AW513635.1	EST_HUMAN	xx47h04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707159 3'
11464	24407	37954	4.53	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
12431	25956		1.62	4.0E-03	BE816173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12454	25213		3.2	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12533	25259		2.13	4.0E-03	AW504273.1	EST_HUMAN	U1-HF-BN0-alp-g-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12755	25400		7.22	4.0E-03	BF224125.1	EST_HUMAN	7a74c06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12801	25866		3.31	4.0E-03	AW614586.1	EST_HUMAN	hh02a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2983932 3' similar to contains element LTR5 repetitive element;
12814	25437		2.73	4.0E-03	AW819141.1	EST_HUMAN	RC3-5T0281-240400-015-03 ST0281 Homo sapiens cDNA
13093	25619	31675	6.48	4.0E-03	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
371	13457	26387	1.69	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
880	13935	26894	3.09	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1669	14701	27676	5.52	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:762984 similar to contains Alu repetitive element;
2268	16281		1.58	3.0E-03	AF065066.1	NT	Homo sapiens MHC class 1 region
2302	15314		8.06	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2303	15315	28334	1.3	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2303	15315	28335	1.3	3.0E-03	U48858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3006	16084		0.8	3.0E-03	Y09006.1	NT	Arabidopsis thaliana rpm1 gene
3099	16156	29069	4.09	3.0E-03	BE379296.1	EST_HUMAN	601237882F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608933 5'
3166	16221	29136	2.54	3.0E-03	AW802887.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3428	16476	29355	1.62	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3439	16486		6.72	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4002	17041	28949	7.18	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4002	17041	28950	7.18	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4067	17103	28995	1.47	3.0E-03	AI792278.1	EST_HUMAN	an0409.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4177	17208		1.08	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
4424	17451	30342	3.8	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4546	17669	30468	5.58	3.0E-03	AI636141.1	EST_HUMAN	xu8.P10.H3 concnrm Homo sapiens cDNA 3'
4871	17888	30776	1.74	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4990	17907	30796	5.49	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5338	18443	31196	3.42	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5935	18731	31893	1.22	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5708	18803	31980	0.95	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6705	19761	33040	10.04	3.0E-03	AA458701.1	EST_HUMAN	aa13f10.r1 Soares_NH-MIPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7224	20246	33580	0.65	3.0E-03	D37977.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7412	20379	33730	1.37	3.0E-03	AJ011419.1	NT	Xluweromyces marizianus pcp3 gene for purine-cytosine permease
7765	20718	34091	3.16	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
8145	21082	34481	0.49	3.0E-03	P28659	SWISSPROT	DNA REPAIR HELICASE RAD15 (RHP3)
8270	21239	34650	0.91	3.0E-03	BF333068.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8270	21239	34651	0.91	3.0E-03	BF333068.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8498	21464	34880	1.31	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_NbH-PA Homo sapiens cDNA clone IMAGE:304783 3'
8658	21626		0.77	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8804	21771	35197	1.16	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8827	21794	35217	1.34	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8933	21899		1.25	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8943	22308		10.07	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.11 L1 repetitive element
9400	22366	35797	4.01	3.0E-03	AL161569.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9424	22388	35827	4.74	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X67138_mai1 HISTONE H2B.2 (HUMAN);
9434	22398	35836	0.83	3.0E-03	BF338078.1	EST_HUMAN	60203580F1 NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4183938 5'
9764	22705		0.95	3.0E-03	D90001.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9802	21125	34529	0.81	3.0E-03	BE154670.1	EST_HUMAN	PM3-HT0344-071299-003-d07 HT0344 Homo sapiens cDNA
9994	22921		0.82	3.0E-03	P03355	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
10065	22992		5.33	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
10255	23180	36867	1.56	3.0E-03	P11399	SWISSPROT	ENDONUCLEASE
10355	23279	36755	1.15	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10499	23421	36920	4.39	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11194	24149		1.82	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11708	24673	38250	1.47	3.0E-03	AF090222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11775	23930	37451	1.86	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11810	24695	38275	2.27	3.0E-03	AF094481.1	NT	Homo sapiens triniticoida repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11810	24695	38278	2.27	3.0E-03	AF094481.1	NT	Homo sapiens triniticoida repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
11881	24763	38348	1.47	3.0E-03	P11399	SWISSPROT	ENDONUCLEASE
12199	25765		4.08	3.0E-03	AI525056.1	EST_HUMAN	promna-5.ED7.r bvtumor Homo sapiens cDNA 5'
12232	25084	38162	1.83	3.0E-03	AA993154.1	EST_HUMAN	cl77b10.s1 Soares_tota_fetus_Nb2HF9_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER26 repetitive element;
12292	25895		2.42	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12478	26226	31794	2.01	3.0E-03	AJ292822.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
516	13587	26506	0.82	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
516	13587	26507	0.92	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
788	15851		12.84	2.0E-03	T70874.1	EST_HUMAN	yd15h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1365	14399	27370	1.9	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1368	14402	27372	1.34	2.0E-03	AA661605.1	EST_HUMAN	nu8801.s1 NCL_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1217593
1376	14410	27380	12.34	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
							PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN
1486	14519	27492	1.83	2.0E-03	P48509	SWISSPROT	SFA-1 (CD151 ANTIGEN)
							Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1519	14551	27522	3.03	2.0E-03	4557836	NT	type VI) (PLOC) mRNA

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1519	14551	27523	3.03	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1595	14627		8.7	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1786	14815	27800	1.26	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
2011	15032	28042	1.52	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2261	15275	28299	1.02	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2584	15585		4.02	2.0E-03	AW137782.1	EST_HUMAN	ULH-BI1-adi-g-10-Q-UJ.e1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3427	16475	29394	4.82	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3434	16481	29400	0.8	2.0E-03	BF68855.1	EST_HUMAN	602183860T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3980	16723	29636	6.1	2.0E-03	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IAPP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
3973	17013	29927	0.65	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4140	17171	30059	2.1	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP38]
4203	17234	30122	1.29	2.0E-03	AA179693.1	EST_HUMAN	zp13n01.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:509361 5'
4248	17277		9.31	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4458	17484		1.01	2.0E-03	AW297380.1	EST_HUMAN	ULH-BWO-air-g-03-Q-UJ.e1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4462	17488	30375	1.11	2.0E-03	A1084748.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4577	17599	30493	1.99	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4577	17599	30494	1.99	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4735	17755	30649	1.09	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4740	17760		1.84	2.0E-03	R87773.1	EST_HUMAN	yo45e02.e1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
5054	18066	30945	0.75	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5163	18172	31051	1.02	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
5281	18287	31149	2.26	2.0E-03	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
5564	18661	31607	1.33	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5709	25643	31981	2.18	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5795	18867	32068	0.61	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-402 UM0025 Homo sapiens cDNA
5795	18867	32069	0.61	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-402 UM0025 Homo sapiens cDNA
5797	18889	32071	1.73	2.0E-03	U63711.1	NT	Xenopus laevis xefilin mRNA, complete cds
6231	19305	32536	3.79	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6231	19305	32537	3.79	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6480	19545	32793	15.16	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6480	19545	32794	15.16	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6482	18547	32796	7.38	2.0E-03	BF308187.1	EST_HUMAN	601987434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6521	19684	32842	2.26	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6522	19585	32843	0.77	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6554	19814	32879	1.38	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)
6756	19810		1.25	2.0E-03	AI991089.1	EST_HUMAN	wu36h09.x1 Soares Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914.60S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element; 213a11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
6794	19848	33133	0.71	2.0E-03	AA677831.1	EST_HUMAN	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7151	18393	31271	1.08	2.0E-03	AB038502.1	NT	CM4-BT0366-061299-054-401 BT0366 Homo sapiens cDNA
7287	20064	33371	2.86	2.0E-03	BE067866.1	EST_HUMAN	qns8d1.1.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7351	20321	33688	0.64	2.0E-03	AI298883.1	EST_HUMAN	yt77g10.r1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
7511	20476	33837	0.77	2.0E-03	T86569.1	EST_HUMAN	PROTEOLYCLIN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7677	20821	34198	1.55	2.0E-03	P07354	SWISSPROT	h137d06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY.:
8386	21355	34763	1.95	2.0E-03	AW592004.1	EST_HUMAN	yx42g08.s1 Soares melanocytes 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element:
8560	21528	34947	6.01	2.0E-03	N20287.1	EST_HUMAN	yx42g08.s1 Soares melanocytes 2NbHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element:
8560	21528	34948	6.01	2.0E-03	N20287.1	EST_HUMAN	yx42g08.s1 Soares melanocytes 2NbHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element:
8607	21575	34890	0.57	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C8G9.05 IN CHROMOSOME I
8629	21587	35018	1.23	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8684	21652	35074	0.77	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8684	21652	35075	0.77	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8709	21677	35102	0.81	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8782	21729		0.67	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9550	18887	32068	0.66	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
9550	18887	32069	0.66	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
9595	22557	35007	0.66	2.0E-03	AF224693.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9884	22837	36291	0.97	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:194296 3'
9884	22837	36292	0.97	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:194296 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9916	22737	36190	3.31	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
10028	22953	36421	1.02	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10026	22953	36422	1.02	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10081	23008	36479	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10081	23008	36480	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10275	23200	36684	0.94	2.0E-03	AW894269.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA
10402	23324		6.44	2.0E-03	AA251376.1	EST_HUMAN	ze10a08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754.3
10781	23702	37200	0.45	2.0E-03	BF367386.1	EST_HUMAN	MR2-GN0030-140900-001-e05 GN0030 Homo sapiens cDNA
10969	23889	37401	0.43	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
10969	23889	37402	0.43	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
11356	24306		2.4	2.0E-03	M86524.1	NT	Human dystrophin gene
11817	20821	34198	2.2	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11870	24752		1.87	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11876	24758	38342	10.47	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12180	25028		2.99	2.0E-03	A1625745.1	EST_HUMAN	ly65h03.x1 NCL_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2283989.3 similar to SW.VATG_MANSE
12197	25042	38623	2.41	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds
12220	25057	38627	1.75	2.0E-03	A1084325.1	EST_HUMAN	oy43g06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634.3 similar to TR.P97535 P97535 PS-PLA1 PRECURSOR ;
12241	18349		11.57	2.0E-03	AJ245167.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
12459	25932		2.03	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCXGD05.5
12550	25273	31777	1.93	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12663	25341		1.33	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12710	25795		1.55	2.0E-03	A1375037.1	EST_HUMAN	t66f02.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051.3 similar to contains Alu repetitive element;
12826	25445		1.6	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
13002	25745		1.95	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCXGD05.5
13095	25621		1.44	2.0E-03	P04797	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)
439	13573	26444	1.72	1.0E-03	H98471.1	EST_HUMAN	y98c08.r1 Soares_pineal_gland_N81PG Homo sapiens cDNA clone IMAGE:232334.5

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830	13887	26842	2.09	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barslead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
830	13887	26843	2.09	1.0E-03	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOL-COA HYDRATASE. ;
1097	14141	27081	3.37	1.0E-03	AI865788.1	EST_HUMAN	as70b08.x1 Barslead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1117	14161	27112	1.69	1.0E-03	AI964672.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOL-COA HYDRATASE. ;
							wk86a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
							wk93a10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1170	14211	27166	1.5	1.0E-03	AI692616.1	EST_HUMAN	wk88a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element.
2042	15061	28082	3.08	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
2163	15179	28199	9.01	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2893	16051	28972	1.42	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3205	16260	29179	2.08	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3205	16260	29180	2.08	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3313	16366	29286	1.23	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3553	16599	29524	0.92	1.0E-03	U68061.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3553	16599	29525	0.92	1.0E-03	U68061.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3678	16721		1.49	1.0E-03	AB044400.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							Human MUC2 gene, promoter region
							Human MUC2 gene, promoter region
							Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3946	16986	29901	0.64	1.0E-03	AW170552.1	EST_HUMAN	Xr63d07.x1 Soares_NHGeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.1f TAR1 repetitive element ;
3954	16994	29910	1.11	1.0E-03	Z49649.1	NT	S. cerevisiae chromosome X reading frame ORF YJR149w
4464	17490	30377	2.27	1.0E-03	BE939162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
							TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4502	17527	30412	4.39	1.0E-03	BE246536.1	EST_HUMAN	sepiens cDNA clone TCBAP4909
4692	17713	30808	0.79	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4861	17878	30765	2.07	1.0E-03	AJ073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4861	17878	30766	2.07	1.0E-03	AJ073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4862	17878		4.33	1.0E-03	BE154067.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5113	18123	30998	9.53	1.0E-03	O48409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5202	18211	31085	1.03	1.0E-03	AV685870.1	EST_HUMAN	AV685870 GKO Homo sapiens cDNA clone GKCDME11 5'
5381	18485	31360	1.74	1.0E-03	AA290951.1	EST_HUMAN	z544f01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5476	18577	31486	2.98	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQ11 gene
5531	18629	31586	1.77	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG878 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds

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5531	18929	31566	1.77	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IP2 domain encoding nuclear protein EBNA2, complete cds
5652	18748	31916	0.93	1.0E-03	BE796491.1	EST_HUMAN	60189841F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3943954 5'
5658	18754	31921	1.76	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5716	18810	31988	0.7	1.0E-03	N41974.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element:
5716	18810	31989	0.7	1.0E-03	N41974.1	EST_HUMAN	y07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element:
5995	19078	32276	0.56	1.0E-03	AA773352.1	EST_HUMAN	ab65g12.s1 Straglene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:845734 3'
6018	19101		0.52	1.0E-03	BF541639.1	EST_HUMAN	602068042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068907 5'
6136	19213		2.57	1.0E-03	X07669.1	NT	Mouse nucleolin gene
6177	19252	32485	1.06	1.0E-03	BE963939.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6316	19387		8.39	1.0E-03	11528178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6468	19533	32781	1.05	1.0E-03	T87761.1	EST_HUMAN	y093a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6549	19810		1.69	1.0E-03	AW802585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6919	19970	33266	1.18	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7359	20329	33678	2.43	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7728	20885		2.36	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7901	20844	34228	1.71	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7975	20914	34305	3.18	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
8033	20970	34364	0.87	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5'
8221	21190	34589	0.55	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8282	21251	34663	5.32	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8483	21451	34859	1.01	1.0E-03	AA122270.1	EST_HUMAN	zk97c09.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.11 L1 repetitive element;
8586	21554	34970	2.42	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8773	21740	35161	0.7	1.0E-03	U28397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8941	21907	35331	0.63	1.0E-03	AA001613.1	EST_HUMAN	zh82e06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8941	21907	35332	0.53	1.0E-03	AA001613.1	EST_HUMAN	zh82e06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
9295	22261		1.37	1.0E-03	Y11204.1	NT	V carten gene encoding veloxopsin
9321	22266	35716	0.6	1.0E-03	AW840353.1	EST_HUMAN	CM3-LT0079-170200-092-607 LT0079 Homo sapiens cDNA

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9435	22399		0.66	1.0E-03	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9474	22438	35877	3.71	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH6) chi subunit mRNA, complete cds
9474	22438	35878	3.71	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH6) chi subunit mRNA, complete cds
9955	22882		0.45	1.0E-03	A1247482.1	EST_HUMAN	qf56d01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848673 3' similar to gb:M97988 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9966	22893	36354	1.77	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (eglA) gene, complete cds
9966	22893	36355	1.77	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (eglA) gene, complete cds
10179	23104	36585	0.8	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSFG)
10524	23446	36944	1.55	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10529	23451		0.79	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10679	23601	37096	1.12	1.0E-03	A1024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1
11025	23690	37516	1.65	1.0E-03	AW362393.1	EST_HUMAN	MER39 MER39 repetitive element;
11025	23690	37517	1.65	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11102	24082	37585	2.91	1.0E-03	BE170859.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11172	24129		2.21	1.0E-03	A1583847.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11491	24434		2.59	1.0E-03	AV759949.1	EST_HUMAN	h73a12.x1 NCJ_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248446 3' similar to TR:Q26195 Q26195 PVA1 GENE.;
11862	24598	38171	6.18	1.0E-03	AA122270.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
12176	25024	38621	6.74	1.0E-03	BE894488.1	EST_HUMAN	zik97c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1 H L1 repetitive element;
12853	25915		1.53	1.0E-03	A1347355.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12753	25936	31311	7.37	1.0E-03	BE780572.1	EST_HUMAN	ic05h11.x1 NCJ_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
5765	18857		1.76	9.0E-04	P06727	SWISSPROT	601488878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
6388	19456		0.81	9.0E-04	A1006345.1	NT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6633	19691	32870	1.08	9.0E-04	P02381	SWISSPROT	Homo sapiens KVLQ11 gene
10001	22928		1.39	9.0E-04	AB037203.1	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VARI
1484	14517		1.04	8.0E-04	X98469.1	NT	Glycylrhiza glabra GgBAS1 mRNA for beta-amylin synthase, complete cds
3939	16979	28894	0.94	8.0E-04	R07008.1	EST_HUMAN	Xlaevis mRNA for C4SR protein
4209	17238		4.49	8.0E-04	P08547	SWISSPROT	yf12ht10.1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:126691 5'
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4768	17815	30709	2.7	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11480	24423		2.01	8.0E-04	AA777084.1	EST_HUMAN	z124c10.s1 Soares fetal heart NHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11627	24566		2.02	8.0E-04	AI571090.1	EST_HUMAN	tr85a08.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
1844	14870	27868	1.17	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2408	15415	28439	1.01	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2726	15720	28737	1.22	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3293	16346	29266	1.13	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6215	19289	32522	1.02	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1.L1 repetitive element :
6862	19719		2.3	7.0E-04	AI768331.1	EST_HUMAN	ng36f09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7438	20405		0.78	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
10163	23088	36585	0.48	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10163	23088	36586	0.48	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11892	24773		1.98	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11920	24801	38392	2.41	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12921	25497		4.1	7.0E-04	R17336.1	EST_HUMAN	yg13c06.r1 Soares infant brain N1B Homo sapiens cDNA clone IMAGE:32288 5'
12952	25627		3.97	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2706	16701		1.03	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCL CGAP_Bri64 Homo sapiens cDNA clone IMAGE:4149297 5'
3984	17024	29935	1.78	6.0E-04	AI862525.1	EST_HUMAN	wf18a11.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4214	17243	30128	3.15	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7830	20778	34156	0.69	6.0E-04	Q16034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
8198	21198		3.18	6.0E-04	P48408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 8, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
8349	21318		0.69	6.0E-04	H92947.1	EST_HUMAN	y94c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231958 3' similar to contains LOR1 repetitive element :
10339	23263		3.99	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp586M2024
10440	23362	36852	2.18	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10704	23628		0.65	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds
11814	24699	38280	2.11	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11893	24774	38360	3.12	6.0E-04	AW013847.1	EST_HUMAN	U1-H-B10-aab-09-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
12364	25820		5.73	6.0E-04	AW380519.1	EST_HUMAN	RC1-H-T0269-261199-012-d08 HT0269 Homo sapiens cDNA
652	13718	26640	8.71	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 293 KD PROTEIN (ORF92)
1501	14534		1.88	6.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021089-030-a07 CT0225 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3424	16472	29391	1.28	5.0E-04	AA548931.1	EST_HUMAN	nt27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
3728	16770	29682	0.95	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR(A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5549	18546	31588	2.37	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6784	19839	33124	5.84	5.0E-04	AA156080.1	EST_HUMAN	z033b08.t1 Stratiene colon (#337204) Homo sapiens cDNA clone IMAGE:586563 5'
7802	20563	33924	10.72	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
							qd13f06.x1 Soares_piacenta_8to6weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN);contains Alu repetitive element
8289	21258	34669	4.95	5.0E-04	AI188382.1	EST_HUMAN	ob98602.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element
8546	21614	35036	0.92	5.0E-04	AA814519.1	EST_HUMAN	MER22 repetitive element;
9632	22576	36026	1.57	5.0E-04	AA846545.1	EST_HUMAN	aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9726	22754	36207	0.62	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9876	22829	36283	0.54	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYL A PRECURSOR
9868	22895	36358	4.55	5.0E-04	AW270938.1	EST_HUMAN	xs06a02.x1 NCI_CGAP_K111 Homo sapiens cDNA clone IMAGE:2768858 3'
10640	23562		0.47	5.0E-04	U60871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
11320	24270		1.94	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024.t1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586M2024
12022	18646	31598	10.61	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12296	25753		4.4	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
674	13738	26655	1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
848	13904	26852	1.6	4.0E-04	AI70263.1	EST_HUMAN	as70b08.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
848	13904	26853	1.6	4.0E-04	AI70263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOL-COA HYDRATASE. ;
1461	14494	27468	2.76	4.0E-04	AW763356.1	EST_HUMAN	as70b08.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2095	15112	28133	1.57	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2143	15160		0.99	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2635	15634	29659	1.66	4.0E-04	O96616	SWISSPROT	DKFZp434D059.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D059 5'
3178	16233	29150	1.8	4.0E-04	AF281074.1	NT	SERPIN-2 (SILK GUM PROTEIN 2)
							Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4351	17378	30257	3.23	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4351	17378	30258	3.23	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4568	17591	30484	1.4	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5124	18133	31010	4.37	4.0E-04	BE560660.1	EST_HUMAN	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:592670 3'
5288	16921		1.02	4.0E-04	AL163287.2	NT	601345895F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3678910 5'
7483	20449	33808	1.26	4.0E-04	P48442	SWISSPROT	Homo sapiens chromosome 21 segment HS21C067
7780	20733		0.78	4.0E-04	AL161566.2	NT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7987	20926	34321	0.56	4.0E-04	AU122078.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
8881	21848	35289	1.07	4.0E-04	BF240712.1	EST_HUMAN	AU122078 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8889	21855	35275	1.56	4.0E-04	N25507.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
10049	22876	36442	3.11	4.0E-04	AJ025699.1	EST_HUMAN	y939e12.r1 Soares melanocyte 2Yb1M Homo sapiens cDNA clone IMAGE:264142 5'
10200	23125		1.11	4.0E-04	AF022855.1	NT	ov87h03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1844341 3'
12684	25729		2.42	4.0E-04	AF254822.1	NT	Mus musculus neuropilin-2(17) mRNA, alternatively spliced, complete cds
157	13260	26187	3.45	3.0E-04	AL119426.1	EST_HUMAN	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
197	13298	26226	1.65	3.0E-04	P49259	SWISSPROT	DKFZp781J221_r1 781 (synonym: harny2) Homo sapiens cDNA clone DKFZp781J221 5'
881	13936	26895	1.64	3.0E-04	U83991.1	NT	160 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
1858	14882	27878	1.65	3.0E-04	AJ262100.1	EST_HUMAN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1871	14896		1.43	3.0E-04	AJ39674.1	EST_HUMAN	q228d03.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
3319	16371	29291	3.17	3.0E-04	P25147	SWISSPROT	h23a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
3987	17027	29938	2.72	3.0E-04	P48448	SWISSPROT	INTERNALIN B PRECURSOR
4086	17120		1.21	3.0E-04	AJ271735.1	NT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4120	17153		1.33	3.0E-04	BE140609.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
4854	17871		5.29	3.0E-04	BE153778.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
5248	18258		1.02	3.0E-04	AJ271735.1	NT	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
6266	19339		5.73	3.0E-04	AL163281.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6993	20119	33432	1.62	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C081
7183	18414	31216	0.71	3.0E-04	AW893981.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
7847	20794	34171	0.77	3.0E-04	P23468	SWISSPROT	RC4-NN0027-060400-011-608 NN0027 Homo sapiens cDNA
8602	21670	34086	5.18	3.0E-04	P22607	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
10280	23205	36689	1.44	3.0E-04	AA454055.1	EST_HUMAN	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
							zx48d08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
							VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10538	23460	36957	0.58	3.0E-04	AI692139.1	EST_HUMAN	wf75a11.x1 Soares_thymus_NHFTn Homo sapiens cDNA clone IMAGE:2513276 3'
10825	23746	37247	7.72	3.0E-04	AA781201.1	EST_HUMAN	ej24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S
12245	25657	31315	3.98	3.0E-04	AA228301.1	EST_HUMAN	nc38a04.r1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
12623	25802	31525	5.33	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
13014	25564		4.33	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547L185 5'
177	13278	26204	1.29	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helix-coiled-coil protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
479	13551	26479	3.55	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBBT1 Homo sapiens cDNA clone HEMBB1001253 3'
908	13683	26919	4.01	2.0E-04	M86524.1	NT	Human dystrophin gene
908	13683	26920	4.01	2.0E-04	M86524.1	NT	Human dystrophin gene
1183	14224		2.52	2.0E-04	AI286021.1	EST_HUMAN	q198e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1190	14230		2.5	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1849	14875		1.19	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pib3 gene
2194	16209		1.03	2.0E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2581	15582	28601	4.05	2.0E-04	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV11S1A1T, HVB reho, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
3000	16058	28977	1.13	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3449	16496	29413	2.44	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0836-070500-194-b07 BT0836 Homo sapiens cDNA
3932	16972	29888	1.21	2.0E-04	AW978441.1	EST_HUMAN	EST390550 MAGE resequences, MAGP Homo sapiens cDNA
4187	17198		5.41	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4698	17717	30812	1.21	2.0E-04	H86285.1	EST_HUMAN	y01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4698	17717	30813	1.21	2.0E-04	H86285.1	EST_HUMAN	y01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4834	17851		1.46	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5070	18080	30961	1.21	2.0E-04	H85683.1	EST_HUMAN	ys88b08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218927 5' similar to contains L1 repetitive element;
5098	18108	30961	1.85	2.0E-04	AB037997.1	NT	Danio rerio hagarano gene, exons 1 to 6, partial cds
5623	18719	31878	1.23	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5636	18732	31894	1.78	2.0E-04	AI690862.1	EST_HUMAN	iq03b11.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'

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5843	18933	32117	1.15	2.0E-04	AA296552.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6057	19138	32349	0.88	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6366	19435	32678	0.8	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7440	20407		2.54	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7546	20509		0.81	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA
7882	20826		15.1	2.0E-04	P08549	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7892	20835	34215	1.21	2.0E-04	P54286	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8170	21109	34508	0.53	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2023 5'
8170	21109	34508	0.53	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2023 5'
8288	21257	34667	2.13	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8288	21257	34668	2.13	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8627	21595	35015	1.21	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8627	21595	35016	1.21	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8911	21877	35303	1.9	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9095	22081	35486	0.56	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9689	22642	36100	0.51	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3'
9774	22716	36170	0.66	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF26.1
10334	23258	36735	1.21	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA
10377	23300	36776	2.74	2.0E-04	AA405777.1	EST_HUMAN	zu68c11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
11197	24152	37683	3.56	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
11310	24451		2.59	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11635	24572	38136	2.95	2.0E-04	AJ440282.1	EST_HUMAN	q01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
11755	24683	38282	2.49	2.0E-04	AW136740.1	EST_HUMAN	UI-H-BT1-adm-c-04-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
768	13827	26771	0.81	1.0E-04	H95646.1	EST_HUMAN	yz26c09.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.t1 L1 repetitive element;
951	14004	26956	2.03	1.0E-04	P48725	SWISSPROT	PERICENTRIN
1076	14121	27072	2.61	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1116	14160	27110	4.21	1.0E-04	AW013847.1	EST_HUMAN	UI-H-BI0-aab-e-09-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1116	14160	27111	4.21	1.0E-04	AW013847.1	EST_HUMAN	U1-H-B10-aab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1335	14369		3.08	1.0E-04	U62918.1*	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1632	14665	27640	3.19	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1632	14665	27641	3.19	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1678	14903	27903	2.37	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2698	15694	28710	1.05	1.0E-04	BE218833.1	EST_HUMAN	h145c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
2698	15694	28711	1.05	1.0E-04	BE218833.1	EST_HUMAN	h145c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176369 3'
3287	16350	29270	1.14	1.0E-04	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPlicing FACTOR 3A SUBUNIT 2) (SF3A66)
3748	16780	29702	0.93	1.0E-04	A1440282.1	EST_HUMAN	h01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
4089	17123	30017	2.07	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4109	17143	30037	1.04	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB004 3'
5132	18141	31020	1.87	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5137	18146	31026	0.82	1.0E-04	A1357166.1	EST_HUMAN	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5960	19045	32244	1.19	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6033	19116	32319	0.52	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6033	19116	32320	0.52	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6579	19639	32905	0.9	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:262
7012	20138	33455	0.66	1.0E-04	AA664651.1	EST_HUMAN	n125a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb-M97252
7392	20361	33713	12.86	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7821	20361	33713	12.73	1.0E-04	A1251980.1	EST_HUMAN	q157d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
8328	21297	34712	0.89	1.0E-04	AA630453.1	EST_HUMAN	q157d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
9692	22645	36102	2.18	1.0E-04	A1806220.1	EST_HUMAN	ab94g08.s1 Streptococcus pneumoniae (9337210) Homo sapiens cDNA clone IMAGE:854654 3'
9703	22655	36111	1.47	1.0E-04	O88969	SWISSPROT	w126e08.x1 Scars_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9780	22721		0.63	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
10004	22931	36394	1.89	1.0E-04	10863876	NT	y072e08.r1 Scars fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 5'
10539	23461		9.91	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10576	23498	36990	0.91	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11967	24803		1.74	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11961	24840	38433	1.5	1.0E-04	AB032958.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11989	24876	38472	1.46	1.0E-04	AW265061.1	EST_HUMAN	U43912.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12032	24908	38502	1.81	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12032	24908	38503	1.81	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12413	25770		2.4	1.0E-04	BE076399.1	EST_HUMAN	7f28a10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296068 3' similar to contains L1.13 L1
13061	25597		1.38	1.0E-04	BE700353.1	EST_HUMAN	repetitive element ;
699	13761	26693	2.39	9.0E-05	AAT18933.1	EST_HUMAN	PM4-NN0091-180700-004-f11 NN0091 Homo sapiens cDNA
2020	15041	28092	1.09	9.0E-05	AW860218.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
6074	19155	32387	1.58	9.0E-05	Q60716	SWISSPROT	QV4-SN0023-070400-166-b04 SN0023 Homo sapiens cDNA
7828	20776	34163	0.67	9.0E-05	AW204958.1	EST_HUMAN	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7828	20776	34164	0.67	9.0E-05	AW204958.1	EST_HUMAN	U1-H-B1-aer-d-05-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9831	22880		2.89	9.0E-05	D85606.1	NT	U1-H-B1-aer-d-05-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9833	22882	36137	3.13	9.0E-05	AF120882.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
11472	24415	37894	2.03	9.0E-05	AW073078.1	EST_HUMAN	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11938	19155	32387	3.21	9.0E-05	Q60716	SWISSPROT	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
							repetitive element ;
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12465	25832		3.02	9.0E-05	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds, and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
822	13980	26831	1.79	8.0E-05	AJ251846.1	NT	Plasmodium sativum mRNA for beta-1,3 glucanase (gns2 gene)
865	13921		7.38	8.0E-05	AJ251846.1	NT	Plasmodium sativum mRNA for beta-1,3 glucanase (gns2 gene)
2861	16019		0.91	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4507	17532	30415	0.87	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
9101	22067	35493	0.48	8.0E-05	Y11886.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11485	24428	37679	3.08	8.0E-05	M69187.1	NT	Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
13050	25815		2.74	8.0E-05	AA279333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu
347	13436	26358	6.11	7.0E-05	AW847445.1	EST_HUMAN	repetitive element; contains element MSR1 repetitive element ;
347	13436	26359	6.11	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
589	13639	26553	1	7.0E-05	L49075.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
589	13639	26554	1	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST_HFD072014
							HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST_HFD072014

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1058	14104	27055	1.47	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2730	15724	28740	4.26	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3172	16227	28143	4.21	7.0E-05	AB009080.1	NT	Dicotyledonum discoldeum gene for TRFA, complete cds
3714	16767		0.8	7.0E-05	AI432413.1	EST_HUMAN	ig73c09.x1 Soares_NhiHMPu_S1 Homo sapiens cDNA clone IMAGE:2114416 3'
4400	17428	30313	1.53	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4962	17977	30867	0.89	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
8687	21535	34955	1.27	7.0E-05	AA505582.1	EST_HUMAN	nt93p01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966096 3'
9911	22732	36187	3.34	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBED60
10982	23902	37415	0.44	7.0E-05	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
10982	23902	37416	0.44	7.0E-05	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
11485	24438		9	7.0E-05	10935046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2041	15060	28080	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2041	15060	28081	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2594	15595	28613	1.05	6.0E-05	AI655241.1	EST_HUMAN	wb54h06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2694	15690	28707	1.3	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2694	15690	28708	1.3	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2825	13743	28689	3.23	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5107	18117	30990	0.93	6.0E-05	AV722942.1	EST_HUMAN	AV722942 HTB Homo sapiens cDNA clone HTBED12 5'
5107	18117	30991	0.93	6.0E-05	AV722942.1	EST_HUMAN	AV722942 HTB Homo sapiens cDNA clone HTBED12 5'
6019	19102	32303	3.08	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GPI35)
6019	19102	32304	3.06	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GPI35)
6543	19605	32887	1.45	6.0E-05	N72829.1	EST_HUMAN	y50g11.f1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:246212 5'
7119	20053	33387	0.77	6.0E-05	AA897880.1	EST_HUMAN	q80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8421	21390	34800	0.71	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
8421	21390	34801	0.71	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
8786	21753	35175	0.68	6.0E-05	AA150482.1	EST_HUMAN	z08c08.s1 Soares_pregnant uterus_NhiHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
8791	21758	35180	2.37	6.0E-05	AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8927	21893	35321	0.61	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9607	22611	36063	1.11	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9607	22611	36064	1.11	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9879	22832	36296	1.05	6.0E-05	T94149.1	EST_HUMAN	y28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'

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10079	23006	36477	0.71	6.0E-05	AW627985.1	EST_HUMAN	h37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
11100	24060	37684	2.27	6.0E-05	R75639.1	EST_HUMAN	y59a08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
11847	24730	38318	2.71	6.0E-05	AA044015.1	EST_HUMAN	z68f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12670	25813	31529	16.08	6.0E-05	AW650110.1	EST_HUMAN	MR0-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA
1403	14436	27404	16.34	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241189-040-h11 ST0234 Homo sapiens cDNA
1880	14905		1.15	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
4004	17043	26951	3.54	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5603	18699	31670	11.74	5.0E-05	X88955.1	NT	Human ML C1emb gene for embryonic myosin alkaline light chain, 3'UTR
6107	19185	32405	3.22	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCMA06 3'
6292	18364	32603	0.84	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7553	20516		1.18	5.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
12462	25371		5.88	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12717	25371		4.8	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2818	13329		4.95	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4508	17533	30416	1.68	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4508	17533	30417	1.68	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4910	17827		0.99	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
7127	20060	33366	0.71	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9881	22834		8.43	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10360	23283	36760	0.51	4.0E-05	P11369	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10771	23692	37189	0.66	4.0E-05	P23780	SWISSPROT	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element;
11120	24080	37604	3.91	4.0E-05	AW627946.1	EST_HUMAN	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
12423	25192		2.49	4.0E-05	AW117580.1	EST_HUMAN	z01te11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:748252 3'
13081	25612		2.29	4.0E-05	AA417756.1	EST_HUMAN	qf64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
684	13744	28671	0.78	3.0E-05	AJ248081.1	EST_HUMAN	contains Alu repetitive element; contains element KER repetitive element;
1061	14107	27057	1.89	3.0E-05	AW273851.1	EST_HUMAN	601461463F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:2814100 3'
1133	14176	27125	0.82	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3865142 5'
1133	14176	27126	0.82	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3865142 5'
4409	17437	30324	8.15	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4409	17437	30325	8.15	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4493	17518	30405	2.41	3.0E-05	AA368878.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to p53-associated protein
4493	17518	30406	2.41	3.0E-05	AA368878.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to p53-associated protein
4620	17841		0.7	3.0E-05	AL183302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5637	18733	31895	1.78	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
6921	18971	33287	1.18	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6921	18971	33288	1.18	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8230	21199	34606	2.48	3.0E-05	BE733157.1	EST_HUMAN	601667451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8565	21663	35087	1.68	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9244	22210	35641	1.54	3.0E-05	AW770982.1	EST_HUMAN	hi94e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
9248	22214	35644	1.37	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9252	22218	35649	0.59	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9486	22450		0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9675	22628	36081	1.2	3.0E-05	AA372562.1	EST_HUMAN	EST784476 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
10021	22948		3.24	3.0E-05	AJ769331.1	EST_HUMAN	wg3609.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387208 3'
10901	23821	37330	0.89	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10901	23821	37331	0.89	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12353	25147		1.49	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
2332	15343	28365	1.32	2.0E-05	AJ286021.1	EST_HUMAN	qh98a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2587	15588	28605	2.2	2.0E-05	M13792.1	NT	MER3.b2 MER3 repetitive element ;
2725	16719		7.98	2.0E-05	AA160562.1	EST_HUMAN	Human adenosine deaminase (ADA) gene, complete cds
3154	16211	28126	1.15	2.0E-05	BE08038.1	EST_HUMAN	zq46a12.1 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element ;
3359	16409	28331	0.88	2.0E-05	AF184614.1	NT	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3382	16431	28369	1.35	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3505	16552		0.7	2.0E-05	X95465.1	NT	H. sapiens DNA for endogenous retroviral like element
3820	16860		0.69	2.0E-05	AL039107.1	EST_HUMAN	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4720	17740		1	2.0E-05	BE378471.1	EST_HUMAN	DKFZp6661064.J1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp6661064 5'
5852	18943	32128	1.57	2.0E-05	AJ011712.1	NT	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
6034	19107		0.65	2.0E-05	AF028308.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6082	19162	32373	0.86	2.0E-05	Q13183	SWISSPROT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6082	19162	32374	0.86	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)-DICARBOXYLATE COTRANSPORTER)
6281	19353	32589	0.68	2.0E-05	A1149272.1	EST_HUMAN	q72a02.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:1715114 3'
6356	19425	32687	0.49	2.0E-05	P35085	SWISSPROT	similar to contains L1.13 L1 repetitive element ;
6778	19833	33116	2.32	2.0E-05	AA714330.1	EST_HUMAN	CALCIUM-BINDING PROTEIN
7086	20020	33322	1.52	2.0E-05	Y08928.1	NT	hw06d12.61 NCI_CGAP_SST1 Homo sapiens cDNA clone IMAGE:1238519 3'
7089	20033	33336	0.94	2.0E-05	A1492860.1	EST_HUMAN	P.falciptarum mRNA for AARP1 protein, partial
7108	20042		8.62	2.0E-05	A1991025.1	EST_HUMAN	Q02711 PRO-POL-DUTPASE POLYPROTEIN ;
							wu35h07.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7360	20330	33679	2.22	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7360	20330	33680	2.22	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7392	20553		0.81	2.0E-05	AF128847.1	NT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
8157	21095	34494	0.5	2.0E-05	U69061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HV8 relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
8217	21186	34596	1.25	2.0E-05	A1381040.1	EST_HUMAN	ig20h05.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109389 3'
9477	22441	35881	0.52	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9477	22441	35882	0.52	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9622	22566	36015	0.57	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9622	22566	36016	0.57	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10283	23208	36693	0.57	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10484	23416	36914	0.87	2.0E-05	BF055939.1	EST_HUMAN	7175g09.y1 NCL_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:3340578 5'
10954	23874	37387	2.1	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:259570 5'
10954	23874	37388	2.1	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:259570 5'

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11006	20042		2.01	2.0E-05	A1991026.1	EST_HUMAN	w135h07.x1 Soares_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11781	23836	37457	1.8	2.0E-05	BE175801.1	EST_HUMAN	RCS-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
12473	26740		6.5	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
12626	25727		1.54	2.0E-05	AF275948.1	NT	Q12832 GLYCOPHORIN HEP2; Homo sapiens ABCA1 (ABCA1) gene, complete cds
12768	25409	31759	1.48	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2705	15902	28715	3.2	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3663	16708	29621	1.86	1.0E-05	AF088273.1	NT	Drosophila melanogaster atrain Larito 120 Suppressor of Hairless (Su(H)) gene, partial cds
3826	16866		1.17	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3991	17031	29940	10.43	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4201	17232	30119	1.52	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4306	17336	30213	1.77	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4887	17904	30793	1.82	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5005	18019	30807	0.94	1.0E-05	Z18943.1	NT	H.sapiens repeat region
6915	19367	33262	1.03	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7028	18360	31281	0.52	1.0E-05	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7286	20063	33370	3.02	1.0E-05	AA641846.1	EST_HUMAN	ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1
7288	20260	33594	8.81	1.0E-05	4505844	NT	L1 repetitive element;
7921	20864	34262	0.86	1.0E-05	BF222646.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
8057	20994		1.5	1.0E-05	P19474	SWISSPROT	7p57d01.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3649345 3' similar to contains MER10.b3
9266	22232		2.45	1.0E-05	AL163227.2	NT	MER10 repetitive element;
9415	22380	35818	2.22	1.0E-05	AA452578.1	EST_HUMAN	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9842	22586	36035	14.03	1.0E-05	AA236110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9721	22749	36201	0.82	1.0E-05	AV732190.1	EST_HUMAN	zx35h12.s1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:1.02032 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
10198	23123	36609	0.79	1.0E-05	AW510902.1	EST_HUMAN	zs05e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element;
10198	23123	36610	0.79	1.0E-05	AW510902.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFBH01 5'
10276	23201	36685	1.11	1.0E-05	AW291521.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element;
							hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element;
							UI-H-B12-agg-e-08-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10278	23201	36686	1.11	1.0E-05	AW291521.1	EST_HUMAN	UH-B12-agk-e-08-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10544	23466		1.95	1.0E-05	AW468995.1	EST_HUMAN	ha07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1 L2 L1 repetitive element;
11284	24216	37740	1.79	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11284	24216	37741	1.79	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12841	25900	31421	1.43	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2680	15676	28687	5.9	9.0E-06	AI583811.1	EST_HUMAN	IT73806.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3112	16169	29079	4.25	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8tc6weeks_2NbpHP81c6W Homo sapiens cDNA clone IMAGE:1759191 3'
3624	16667		2.82	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6008	19091	32291	2.31	9.0E-06	L234716.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7047	20059	33375	0.73	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-e07 BT0313 Homo sapiens cDNA
7674	20632	33996	0.94	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8053	20990	34398	11.84	9.0E-06	AI034370.1	EST_HUMAN	α20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
8907	21774	35200	1.18	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9334	22299	35728	2.51	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9334	22299	35728	2.51	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9577	22539	35990	4.44	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11286	24236	37793	3.65	9.0E-06	Q10384	SWISSPROT	POTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2535	15896	28559	2.23	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
10998	23818	37326	0.64	9.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10998	23818	37327	0.64	9.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
980	14031		2.14	7.0E-06	AA669729.1	EST_HUMAN	ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains repetitive element;
1433	14467	27444	3.05	7.0E-06	7662177	NT	MER20.t1 MER20 repetitive element;
2884	15943		7.94	7.0E-06	AI368252.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA qw16g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1981286 3' similar to contains Alu repetitive element;

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3578	16621		0.78	7.0E-06	AA385542.1	EST_HUMAN	EST09205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5780	18872		5.16	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-101 OT0062 Homo sapiens cDNA
5902	18939	32179	0.81	7.0E-06	N98845.1	EST_HUMAN	Y65c07.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:278412 5'
9141	22107	35533	0.7	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
10260	23185		0.54	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	25927	31307	2.83	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2928	15986	28907	1.27	6.0E-06	BE089189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3706	16749	28664	1.08	6.0E-06	BE089189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4785	16010	28636	2.35	6.0E-06	Q01458	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4794	17811	30703	2.54	6.0E-06	A1040099.1	EST_HUMAN	ox09e02.x1 Soares_fetal_liver_spleen_TNFRSF_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element ;
5422	18525	31403	1.41	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5483	18583	31495	1.05	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
10215	23140		1.52	6.0E-06	AW801912.1	EST_HUMAN	IL5-JM0070-110400-063-g02 UM0070 Homo sapiens cDNA
13041	26582	31700	1.74	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
6179	19254	32487	3.86	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6471	19536	32784	3.98	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7444	20410	33762	1.14	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8803	21770	35185	0.49	5.0E-06	AW859972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8803	21770	35198	0.49	5.0E-06	AW859972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10482	23384	38877	7.1	5.0E-06	AA313620.1	EST_HUMAN	EST185406 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
12101	24972	38569	2	5.0E-06	Q28039	SWISSPROT	SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSPORTER 1 (GLYT-1)
12928	25512	31709	2.14	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
648	13714	28635	6.59	4.0E-06	R16267.1	EST_HUMAN	ya48c03.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;
847	13903	28861	6.33	4.0E-06	AW103354.1	EST_HUMAN	xx69p12.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ;
1337	14371	27340	4.22	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1337	14371	27341	4.22	4.0E-06	A1334928.1	EST_HUMAN	tb33e09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1470	14503	27477	2.58	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2274	15287	28313	3.05	4.0E-06	AW015401.1	EST_HUMAN	UHH-B10-aat-f-05-0-U1.e1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3076	16133	29046	0.94	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3909	16949	29860	1.1	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4846	17863	30756	2.18	4.0E-06	A188939.1	EST_HUMAN	w94c10.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
8844	21811	35230	0.98	4.0E-06	O15393	SWISSPROT	MER22 repetitive element;
9152	22118	35545	3.6	4.0E-06	AF009660.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
10066	22993	36462	1.14	4.0E-06	AJ272265.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11778	23933	37454	2.91	4.0E-06	AB007855.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
2173	15189	28209	1.9	3.0E-06	AA700582.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2173	15189	28210	1.9	3.0E-06	AA700582.1	EST_HUMAN	z134b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to
2276	16288		1.89	3.0E-06	AF202635.1	NT	contains L1.t1 L1 repetitive element;
2833	15991	28911	0.95	3.0E-06	AA868218.1	EST_HUMAN	contains L1.t1 L1 repetitive element;
3279	16333		2.32	3.0E-06	A1857779.1	EST_HUMAN	Homo sapiens PP1200 mRNA, complete cds
3797	16837	28743	1.12	3.0E-06	BE047094.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408252 3' similar to contains L1.T1 t3
3797	16837	28744	1.12	3.0E-06	BE047094.1	EST_HUMAN	W122a03.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425516 3' similar to TR:O60734 O60734
4501	17526	30411	0.87	3.0E-06	T50268.1	EST_HUMAN	LINE-1 LIKE PROTEIN; contains L1.t2 L1 repetitive element;
4594	17615	30509	4.02	3.0E-06	X54816.1	NT	hg64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6284	19356	32592	0.74	3.0E-06	AU169412.1	EST_HUMAN	hg64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6874	20197	33525	0.56	3.0E-06	Z79478.1	NT	hg64d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6974	20197	33528	0.56	3.0E-06	Z79478.1	NT	y678b10.r1 Stralagena ovary (#837217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1
7439	20406		1.9	3.0E-06	P08548	SWISSPROT	repetitive element
8419	21388	34798	0.76	3.0E-06	BE562964.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
9032	21998	35417	0.84	3.0E-06	P07743	SWISSPROT	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
12631	25317		6.4	3.0E-06	AW385262.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
203	13304		3.24	2.0E-06	P64366	SWISSPROT	H. sapiens flow-sorted chromosome 6 TaqI fragment, SC9pA9E5
1572	14605		5.6	2.0E-06	P21414	SWISSPROT	H. sapiens flow-sorted chromosome 6 TaqI fragment, SC9pA9E5
2387	15395	28420	2.84	2.0E-06	A1672138.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2474	15478	28501	2.73	2.0E-06	P04929	SWISSPROT	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
							PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
							RCQ-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
							HOMEOBOX PROTEIN GOOSECOID
							POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
							w04a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1
							MER30 repetitive element;
							HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2573	15574	28594	1.94	2.0E-06	P08719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3531	16577	29500	1.29	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05.3'
3774	16816	29725	1.56	2.0E-06	AA173518.1	EST_HUMAN	z02e05.r1 Stralagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232.6'
3763	16824	29732	0.67	2.0E-06	AW450215.1	EST_HUMAN	U1-H-B19-alky-g-05-Q-UI.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2736176.3'
3789	16830	29738	1.74	2.0E-06	AB030886.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6208	18282		0.9	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558809.3' similar to contains Alu repetitive element
6241	19314	32544	0.93	2.0E-06	AI539448.1	EST_HUMAN	ts51f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241.3' similar to TR:Q13537
6581	19841	32608	5.37	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
8250	21219		0.81	2.0E-06	AW868223.1	EST_HUMAN	W50b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063.3'
8426	21395	34806	0.63	2.0E-06	T12238.1	EST_HUMAN	MR3-SND067-120400-002-f02 SNC067 Homo sapiens cDNA
9188	22154		0.81	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9200	22166	35596	1.83	2.0E-06	H62051.1	EST_HUMAN	zh27c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300.3' similar to
9571	22533	35983	0.87	2.0E-06	AF003529.1	NT	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9571	22533	35984	0.87	2.0E-06	AF003529.1	NT	YU37c04.r1 Soares ovary tumor N3HOT Homo sapiens cDNA clone IMAGE:235974.5' similar to gb:X74929
9591	22553		0.48	2.0E-06	AI473450.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
10059	22986	38454	0.92	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10278	23204		0.81	2.0E-06	AV748969.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12111	24981	38581	2.21	2.0E-06	O15553	SWISSPROT	ij176g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730.3'
12111	24981	38582	2.21	2.0E-06	O15553	SWISSPROT	yw66e03.s1 Soares_placenta_8tc9weeks_2NblP8to9W Homo sapiens cDNA clone IMAGE:257212.3'
12540	26928	31308	2.97	2.0E-06	P23249	SWISSPROT	AV748969 NPC Homo sapiens cDNA clone NP-CAXD05.5'
36	13156	26057	3.02	1.0E-06	O76082	SWISSPROT	PYRIN (MARENOSTRIN)
638	13724	26549	1.96	1.0E-06	AF084394.1	NT	PYRIN (MARENOSTRIN)
1445	14478	27454	1.61	1.0E-06	P09125	SWISSPROT	PROTEIN MOV-10
1527	14560	27531	1.67	1.0E-06	AL163278.2	NT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1576	14609	27582	1.22	1.0E-06	AA034141.1	EST_HUMAN	Mus musculus D6MM5E protein (D6MM5e) mRNA, complete cds
1576	14609	27583	1.22	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
							Homo sapiens chromosome 21 segment HS21C078
							Z06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982.3' similar to contains Alu repetitive element;
							Z06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982.3' similar to contains Alu repetitive element;

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1587	14620		1.36	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2010	15031	28040	5.53	1.0E-06	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2010	15031	28041	5.53	1.0E-06	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4397	17425	30309	13.21	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5148	18155	31034	1.23	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5148	18155	31035	1.23	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5363	18468	31339	4.93	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c08 BT0800 Homo sapiens cDNA
5388	18491	31387	1.01	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5388	18491	31368	1.01	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5552	18649	31592	1.24	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
5892	18980		0.64	1.0E-06	BE063527.1	EST_HUMAN	CMO-BT0281-031199-087-H04 BT0281 Homo sapiens cDNA
7056	20078	33387	6.4	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
8018	20095		0.56	1.0E-06	BE165330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8334	21303		0.75	1.0E-06	AA912623.1	EST_HUMAN	cl2sc08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8616	21584	35000	1.05	1.0E-06	A1347010.1	EST_HUMAN	qp54s02.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926842 3'
8833	21800	35219	1.26	1.0E-06	A1287678.1	EST_HUMAN	qy23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9659	22816	36270	1.15	1.0E-06	N74635.1	EST_HUMAN	MIR repetitive element;
9734	22762	36217	0.55	1.0E-06	Q39576	SWISSPROT	z555e01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286472 3'
10041	22968	36434	3.97	1.0E-06	U82668.1	NT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
10041	22968	36435	3.97	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
10085	23012	36485	4.9	1.0E-06	AA132611.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
10147	23073		3.89	1.0E-06	AA449257.1	EST_HUMAN	zo17c08.r1 Stratiagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
10854	23774		2.02	1.0E-06	AL163203.2	NT	z04d11.s1 Soares_t04a_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:765493 3' similar to
11960	24839		3.14	1.0E-06	AV890941.1	EST_HUMAN	gb/D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
12672	15031	28040	1.71	1.0E-06	AF184614.1	NT	Homo sapiens chromosome 21 segment HS21C003
12672	15031	28041	1.71	1.0E-06	AF184614.1	NT	Homo sapiens chromosome 21 segment HS21C003
360	13447	26374	1.95	9.0E-07	AF003529.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
360	13447	26375	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8750	21718		0.69	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8898	21864		0.43	9.0E-07	AA448276.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
11577	24515	38070	4.11	9.0E-07	AL163281.2	NT	z063h01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:762833 3'
						EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4804	17821	30716	3.87	8.0E-07	AI288598.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4804	17821	30716	3.87	8.0E-07	AI288598.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5888	19073		8.55	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE: ENDONUCLEASE]
8335	21304		11.24	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11943	24823		5.78	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Strelagene (cat#336206) Homo sapiens cDNA clone HFBEN89
12183	25031		8.17	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5597	18593	31663	0.73	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5597	18593	31664	0.73	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1928	14952	27948	4.86	6.0E-07	AW85558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
2500	15503	28530	5.38	6.0E-07	AF019413.1	NT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
3998	17036		2.25	6.0E-07	P41479	SWISSPROT	7g94f07.x1 NCI_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 45L.
9487	22461	35902	2.17	6.0E-07	BF001887.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
12442	25880		3.45	6.0E-07	AW903222.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
326	13417		0.99	5.0E-07	AI831893.1	EST_HUMAN	EST83815 Supt cells Homo sapiens cDNA 5' end
1060	14106		2.45	5.0E-07	AA380630.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
3044	16101		0.66	5.0E-07	AI831893.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
4876	17697	30584	1.16	5.0E-07	AF149774.1	NT	Mus musculus DG-2 homeodomain protein (DG-2) gene, partial cds
6242	19315	32545	1.23	5.0E-07	U66067.1	NT	Ig06b05.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element:
7266	20001	33300	1.68	5.0E-07	AI393881.1	EST_HUMAN	Ig06b05.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element:
7266	20001	33301	1.68	5.0E-07	AI393881.1	EST_HUMAN	Ig06b05.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element:
7571	20534	33892	15.74	5.0E-07	AW070885.1	EST_HUMAN	xx31a02.x1 NCI_CGAP_Bt18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8618	21586	35002	0.87	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8835	21802		1.86	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10732	23654	37147	5.39	5.0E-07	AI908587.1	EST_HUMAN	CM4-BT178-220499-014 BT178 Homo sapiens cDNA
11845	24728	38314	3.52	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11806	24787		2.12	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12842	25780		4.14	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4024	17082	20964	1.81	4.0E-07	AW009602.1	EST_HUMAN	w984h05.x1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
7394	20354		0.81	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7482	20448	33804	1.3	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7482	20448	33805	1.3	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8255	21224	34634	0.53	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9406	22371	35806	5.52	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCL CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2866548 3'
10486	23408	36904	0.46	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10486	23408	36905	0.46	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10688	23610	37103	0.47	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11284	24234	37760	2.6	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11284	24234	37761	2.6	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11555	24495		2.72	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0093-030300-003-012 BN0093 Homo sapiens cDNA
							Human microtubule-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
441	13515	26448	4.77	3.0E-07	U19719.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
595	13663	26567	3.11	3.0E-07	AJ271735.1	NT	Homo polymorphic microsatellite DNA
1375	14409	27379	2.82	3.0E-07	M99149.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
1630	14663		2.45	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2062	15080		1.01	3.0E-07	AA526763.1	EST_HUMAN	element; contains L1, L3 L1 repetitive element
2296	15308	28330	2.56	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2477	15481	28505	6.03	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2477	15481	28506	6.03	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3047	16104	28018	0.8	3.0E-07	T84704.1	EST_HUMAN	y450f12.r1 Soares fetal liver spleen 1NF5 Homo sapiens cDNA clone IMAGE:111695 5'
3173	16228	29144	1.71	3.0E-07	P38739	SWISSPROT	HYPOPHYSICAL 63.8 KD PROTEIN IN GUT-1 RIM1 INTERGENIC REGION PRECURSOR
4706	17727		0.74	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVOMACROGLOBULIN)
4758	17778	30673	8.86	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLOCCD01 3'
4796	17813	30706	0.81	3.0E-07	A1797236.1	EST_HUMAN	w86b12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
							yc14h09.g1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5103	18113	30985	2.02	3.0E-07	T57850.1	EST_HUMAN	gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
							yc14h09.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5103	18113	30986	2.02	3.0E-07	T57850.1	EST_HUMAN	gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5749	18943	32026	9.02	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6085	19165	32377	0.73	3.0E-07	O42280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							WNT-14 PROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6861	19914		5.12	3.0E-07	AA815175.1	EST_HUMAN	cc04c10.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339880 3'
7752	20705	34074	3.26	3.0E-07	AW787168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
7925	20868		1.09	3.0E-07	AI591065.1	EST_HUMAN	hw28f11.x1 NCL_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
13083	25614		7.27	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
31	13161	26051	4.19	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomere RAP1 protein (RAP1) mRNA, complete cds
155	13258	26185	6.84	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
155	13258	26186	6.84	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
183	13283	26209	152.51	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vesicular) actin gene, complete cds
749	13810	26751	1.29	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
749	13810	26752	1.29	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
760	13820		0.87	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
942	13995	26947	3.12	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 987230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gbl.31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
943	13996	26948	7.18	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1167	14208	27162	1.16	2.0E-07	Q29768	SWISSPROT	I/6 AUTOANTIGEN
1604	14838	27613	2.35	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3633	16376		0.86	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3700	16743	28656	17.94	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
4195	17228	30115	1.42	2.0E-07	AI873583.1	EST_HUMAN	wk20h04.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412919 3'
5417	18520	31397	1.71	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6702	25865	33037	0.9	2.0E-07	AW448968.1	EST_HUMAN	U1H-B13-ake-b-01-q-UJ.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2734008 3'
6820	19874	33163	1.63	2.0E-07	AI208715.1	EST_HUMAN	qg56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
6832	19885	33178	0.81	2.0E-07	AA572953.1	EST_HUMAN	nm33a06.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061938 similar to contains Alu repetitive element;
8813	21780		4.23	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAE002 5'
9043	22009	35430	0.99	2.0E-07	AA035198.1	EST_HUMAN	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10119	23045		1.8	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10630	23552	37052	6.11	2.0E-07	AW692507.1	EST_HUMAN	CM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA
10855	23775	37272	0.92	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10855	23775	37273	0.92	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12138	25503		2.86	2.0E-07	BE153717.1	EST_HUMAN	GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12224	25781		1.86	2.0E-07	AI732482.1	EST_HUMAN	PMO-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA zn85h11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element ;
1104	14148		1.46	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2838	14558	27629	2.95	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3767	14148		1.25	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4321	17350	30234	3.01	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens cDNA clone GLCNF04 5'
4321	17350	30235	3.01	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCNF04 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6652	19708	32986	0.82	1.0E-07	U82674.2	NT	
7050	20072	33378	4.44	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7050	20072	33379	4.44	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7735	20690	34054	9.42	1.0E-07	N55081.1	EST_HUMAN	yy43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7910	20853	34240	0.89	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-505 TN0024 Homo sapiens cDNA
7910	20853	34241	0.89	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-505 TN0024 Homo sapiens cDNA
7940	20882	34272	1.27	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8558	21526	34944	2.28	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8558	21526	34945	2.28	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9306	22271	35702	2.83	1.0E-07	AA693576.1	EST_HUMAN	z51e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:434346 3'
9625	22569	36018	0.96	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9975	22902	36366	0.53	1.0E-07	BE327843.1	EST_HUMAN	hu28h06.x1 NCI_CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13 MER18 repetitive element ;
10296	23221	36705	2.5	1.0E-07	BF674524.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10304	23229	36712	1.26	1.0E-07	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
10831	23752		2.53	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12500	25756	31517	4.03	1.0E-07	BE048770.1	EST_HUMAN	hr53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722 DJ1163J1.1 ;
12634	25320		1.59	1.0E-07	X64467.1	NT	H.sapiens ALAD gene for porphobilinogen synthase
12793	25423		1.89	1.0E-07	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
7498	20463	33823	0.84	9.0E-08	AI539362.1	EST_HUMAN	ts51b06.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23172	36561	2.18	9.0E-08	AV734819.1	EST_HUMAN	AV734819 cDNA Homo sapiens cDNA clone cdABFB08 5'
11515	24456	38008	1.46	9.0E-08	AI891052.1	EST_HUMAN	wn30a07.x1 NCL_OGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
11977	24854	38452	2.32	9.0E-08	AL163301.2	EST_HUMAN	OFR repetitive element;
12463	25212		3.51	9.0E-08	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C101
609	15945		2.97	8.0E-08	AI911352.1	EST_HUMAN	Homo sapiens partial steerin-1 gene
1052	14098		0.77	8.0E-08	BE796469.1	EST_HUMAN	wd18b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
3555	16601		2.07	8.0E-08	BE785469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
							601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
9091	22057	35482	3.38	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9091	22057	35483	3.38	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9985	22912	36377	2.8	8.0E-08	AW970693.1	EST_HUMAN	EST382776 IMAGE resequences, MAGK Homo sapiens cDNA
10928	23848	37363	0.46	8.0E-08	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11576	24513		2.63	8.0E-08	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
81	13197	28121	4.07	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1363	14397	27368	17.17	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3589	16634	29553	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3589	16634	29554	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3949	16989	28904	0.9	7.0E-08	P01606	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3949	16989	28905	0.9	7.0E-08	P01606	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11165	24123		2.33	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 conorm Homo sapiens cDNA 3'
11982	24959	38434	4.32	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12899	16634	29553	1.55	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12899	16634	29554	1.56	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12976	25941		1.9	7.0E-08	AJ131016.1	NT	Homo sapiens SCL gene locus
818	13876	28824	4.23	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
818	13876	28825	4.23	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2371	15379	28403	2.72	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0166-191169-004-g09 HT0166 Homo sapiens cDNA
4276	17305	30184	1.28	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
							Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
8162	21100	34489	0.49	6.0E-08	L44140.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8283	21262		0.74	6.0E-08	P08547	SWISSPROT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9683	22636		0.54	6.0E-08	AA827075.1	EST_HUMAN	ob56c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element ;
11744	24629	38208	1.91	6.0E-08	P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
85	13201	26125	3.22	5.0E-08	AL163303.2	NT	ENDONUCLEASE]
2245	15259	28286	1.95	5.0E-08	AA498851.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
12185	25032		10.16	5.0E-08	P06681	SWISSPROT	element;
12382	25162	31814	1.63	5.0E-08	AW851878.1	EST_HUMAN	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
1775	14804	27789	1.07	4.0E-08	P25723	SWISSPROT	QV0-CT0225-131099-034-412 CT0225 Homo sapiens cDNA
1775	14804	27790	1.07	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
3077	16134		0.95	4.0E-08	A1078417.1	EST_HUMAN	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
3934	16974	29888	0.76	4.0E-08	U82668.1	NT	oz05602.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
6545	19606	32868	0.91	4.0E-08	P62824	SWISSPROT	Homo sapiens shox gene, alternatively spliced products, complete cds
9150	22116	35542	0.8	4.0E-08	O15393	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9494	22458	35898	1.32	4.0E-08	L42571.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
10003	22930		0.82	4.0E-08	P08547	SWISSPROT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
10693	23615		0.65	4.0E-08	A1016342.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10762	23874	37171	3.67	4.0E-08	A1050027.1	EST_HUMAN	q78d12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3'
11411	24355	37889	1.51	4.0E-08	AA393627.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
11411	24355	37890	1.61	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11426	24370	37807	3.11	4.0E-08	BF682493.1	EST_HUMAN	G505579 NA/CA,K-EXCHANGER. ;
11426	24370	37908	3.11	4.0E-08	BF682493.1	EST_HUMAN	G505579 NA/CA,K-EXCHANGER. ;
12190	25907		4.96	4.0E-08	W76159.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12830	25449		1.84	4.0E-08	A1349353.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
3438	16485	29404	0.94	3.0E-08	M83242.1	NT	z465g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.t1 L1 repetitive element ;
5692	18787	31858	3.06	3.0E-08	BE018348.1	EST_HUMAN	ib95a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
						EST_HUMAN	MER18 MER18 repetitive element ;
						NT	Macaca fascicularis apolipoprotein A-1 gene, complete cds
						EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
						EST_HUMAN	SYNTAXIN 17. ;

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7168	18399	31245	4.23	3.0E-08	AI792737.1	EST_HUMAN	qs76f1.y5 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:194045 5'
7787	20740	34113	1.41	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8025	20962		3.85	3.0E-08	AI436352.1	EST_HUMAN	th93h09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
10258	23183		0.57	3.0E-08	AF065066.1	NT	Homo sapiens MHC class 1 region
12157	25013		2.76	3.0E-08	R18420.1	EST_HUMAN	y92f04.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
207	13308		10.64	2.0E-08	AW302986.1	EST_HUMAN	xr87f06.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2767139 3'
230	13330		8.83	2.0E-08	AA425598.1	EST_HUMAN	zw48f07.r1 Soares fetal_fetus_Nb2HF8_9W Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element;
497	13569	26492	1.3	2.0E-08	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
661	13727	28651	9.73	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
661	13727	26652	9.73	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
992	14044		17	2.0E-08	BE280477.1	EST_HUMAN	601156321.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1346	14381	27350	1.93	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1755	14784		1.87	2.0E-08	BE734871.1	EST_HUMAN	G01570463.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1872	14897		3.57	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2550	15552		1.7	2.0E-08	K00216.1	NT	Sheep Hic-IRNA-GUG
3221	16276	28200	8.15	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3221	16276	29201	8.15	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3873	18912		1.62	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-503 ST0197 Homo sapiens cDNA
4104	17138	30033	0.68	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds aa26c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
4434	17461		1.2	2.0E-08	AA469040.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
4994	18009		2.97	2.0E-08	AW572881.1	EST_HUMAN	al60h11.s1 Soares testis_NHT Homo sapiens cDNA clone 1377189 3'
5719	18813	31692	1.26	2.0E-08	AA813204.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3 MER18 MER18 repetitive element;
5932	19018	32213	0.99	2.0E-08	AW088924.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE: ENDONUCLEASE]
8337	21306	34721	1.89	2.0E-08	P10272	SWISSPROT	eb02g06.s1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
8447	21416	34829	1.47	2.0E-08	AA490121.1	EST_HUMAN	AU139978 PLACET Homo sapiens cDNA clone PLACE1011719 5'
9440	22404		0.77	2.0E-08	AU139978.1	EST_HUMAN	

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10886	23806	37310	0.8	2.0E-08	N78097.1	EST_HUMAN	w72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
10888	23806	37311	0.8	2.0E-08	N78097.1	EST_HUMAN	w72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12472	25221		1.88	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12882	25953		1.4	2.0E-08	11431676	NT	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA
1510	15870	27513	1.42	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1780	14819	27804	2.12	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2067	15084		2.49	1.0E-08	BE141859.1	EST_HUMAN	PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA
3208	16281	29181	1.19	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3206	16261	29182	1.19	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5680	18775	31947	4.5	1.0E-08	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
8046	20883	34380	0.98	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8369	21338	34749	0.47	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
8468	21435	34852	0.56	1.0E-08	AF224659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8466	21435	34853	0.56	1.0E-08	AF224659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8892	21858	35280	1.89	1.0E-08	AJ015304.1	EST_HUMAN	c635a05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9559	22521		0.48	1.0E-08	P05593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9560	22522	35970	0.68	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-402 BT0546 Homo sapiens cDNA
10325	23249	36728	0.81	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT-PROTEIN) (CTP)
10921	23841	37357	0.67	1.0E-08	P98063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11844	24581	38149	3.4	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12129	24998	38602	1.5	1.0E-08	P28315	SWISSPROT	Homo sapiens major histocompatibility locus class III region
12129	24998	38603	1.5	1.0E-08	P28315	SWISSPROT	RIBONUCLEASE INHIBITOR
12569	25281		3.12	1.0E-08	X51755.1	NT	RIBONUCLEASE INHIBITOR
12940	25320		1.68	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4271	17300	30179	4.15	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C076
4271	17300	30180	4.15	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C076
10422	23344		0.53	9.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6628	19686		1.59	8.0E-09	AI270615.1	EST_HUMAN	qu86c11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978964 3' similar to contains L1.13 L1 repetitive element;
7479	20445	33801	7.91	8.0E-09	AI183500.1	EST_HUMAN	qq42e07.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.t1 MSR1 repetitive element;
8333	21302	34719	3.04	8.0E-09	AW900159.1	EST_HUMAN	CM10-NN1004-100300-273-e08 NN1004 Homo sapiens cDNA
9340	22305		2.64	8.0E-09	AA938892.1	EST_HUMAN	op74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1682575 3'
3621	16664		1.91	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4034	17072		1.22	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
8234	21203		0.56	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
8382	21351		0.91	7.0E-09	AA256200.1	EST_HUMAN	zr80c05.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element;
9615	22559	36008	3.06	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10543	23465	36960	1.17	7.0E-09	BE254850.1	EST_HUMAN	80111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10711	23633		0.59	7.0E-09	AA058626.1	EST_HUMAN	z568e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element;
11032	23998		3.65	7.0E-09	T07850.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:121918 3'
2162	15178		0.98	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'
4059	17095	29990	0.96	6.0E-09	AA557940.1	EST_HUMAN	nh7a11.s1 NCL_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element;
5017	18031	30917	5.44	6.0E-09	BE169421.1	EST_HUMAN	PMT-H170527-160200-001-h05 HT0527 Homo sapiens cDNA
5454	18556	31467	9.55	6.0E-09	AW195784.1	EST_HUMAN	xn85f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8922	21888	35315	0.88	6.0E-09	BE161653.1	EST_HUMAN	MR3-H10446-260300-201-h12 HT0446 Homo sapiens cDNA
8631	22494	35942	2.12	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10639	23561		4.42	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
1413	14446	27418	4.43	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1870	14895	27894	1.02	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6550	19611	32872	2.31	5.0E-09	AA359454.1	EST_HUMAN	EST68746 Fetal lung II Homo sapiens cDNA 5' end
7025	18357	31277	0.59	5.0E-09	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8932	21898	35326	0.5	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10455	23377	36870	2.63	6.0E-09	AW799967.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
522	13593		1.81	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
966	14018		2.79	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1465	14498	27472	2.79	4.0E-09	9558718	NT	Homo sapiens hypophyseal protein (AF038169), mRNA
2038	15057	28075	1.63	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2038	15057	28076	1.63	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2436	15443	28461	2.87	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to heat shock protein, 90 kDa
8179	21149	34556	0.66	4.0E-09	AA495747.1	EST_HUMAN	zw04c06.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8867	21834	35255	0.66	4.0E-09	IT64942.1	EST_HUMAN	yd11a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66804 3'
							hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
							hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2359	15367	28389	4.28	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2560	15561	28579	1.39	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2659	15656	28674	1.03	3.0E-09	P23249	SWISSPROT	MER18 repetitive element;
							PROTEIN MOV-10
3340	16391	29312	1.15	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3388	16437		0.79	3.0E-09	AA442272.1	EST_HUMAN	MER18 repetitive element;
4124	17157		0.69	3.0E-09	X16874.1	NT	z64a04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4457	17483	30371	3.77	3.0E-09	AF176325.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4540	17563	30450	3.44	3.0E-09	Q973R5	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
							258.1 KDA PROTEIN C21ORF5 (KIAA0933)
5225	18233		0.99	3.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketoadyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
							hx80a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
8232	21201	34607	1.08	3.0E-09	BE465780.1	EST_HUMAN	O55091 IMPACT PROTEIN.;
10509	23531	37026	1.84	3.0E-09	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11361	24310	37836	3.06	3.0E-09	BF109843.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
11361	24310	37837	3.06	3.0E-09	BF109843.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
813	13871		10.64	2.0E-09	X16874.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1263	14298	27261	5.84	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1667	14699		9.53	2.0E-09	AL118873.1	EST_HUMAN	DKFZp761B1710.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2334	15345	28366	2.58	2.0E-09	Q973R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
3958	16998	29913	3.67	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
4039	17077	29977	1.65	2.0E-09	AI263476.1	EST_HUMAN	ql07d09.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5198	18207	31081	0.68	2.0E-09	M23161.1	NT	Human transposon-like element mRNA
5908	18898	32081	0.69	2.0E-09	A1004062.1	EST_HUMAN	047b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6273	19346		0.65	2.0E-09	AL163249.2	NT	Homo sapiens chromosome 21 segment HS27C049
6947	20171		0.8	2.0E-09	AA357407.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7684	20642	34006	7.6	2.0E-09	AA461430.1	EST_HUMAN	z663h06.r1 Soares_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element
7766	20719	34092	0.63	2.0E-09	W28834.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8129	21083	34451	0.82	2.0E-09	AW862126.1	EST_HUMAN	MR1-CT0352-240200-105-b06 CT0352 Homo sapiens cDNA
8062	22028	35452	2.25	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12705	13871		22.38	2.0E-09	X166874.1	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
12772	25975		1.67	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element
12778	25829		1.47	2.0E-09	AW301637.1	EST_HUMAN	x99802.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768234 3'
12913	25492		1.98	2.0E-09	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
1111	14155	27105	1.1	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1111	14155	27106	1.1	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1638	14670		0.91	1.0E-09	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2510	15513		1.16	1.0E-09	A1356088.1	EST_HUMAN	qy64e11.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12
2900	15959	28878	1.83	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2937	15995	28915	4.07	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2937	15995	28916	4.07	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3051	16108	29022	0.89	1.0E-09	BE535440.1	EST_HUMAN	601058802F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4838	17853		5.63	1.0E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5162	18171	31050	0.84	1.0E-09	T60216.1	EST_HUMAN	yc22c09.r1 Stratiagene lung (#937210) Homo sapiens cDNA clone IMAGE:81424 5' similar to contains Alu repetitive element; contains MER28 repetitive element;
5581	18677	31640	0.82	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5930	19016	32211	1.35	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6267	19340	32572	3.11	1.0E-09	P28694	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8113	21050	34449	0.63	1.0E-09	AV728045.1	EST_HUMAN	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8733	21701	35127	0.87	1.0E-09	AI688474.1	EST_HUMAN	AV728645 HTC Homo sapiens cDNA clone HTCBIG07 5'
							wd39b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2930481 3' similar to contains MER25.11 MER25 repetitive element;

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10677	23599		2.87	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12081	24853		1.53	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12618	25918	31425	2.01	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12781	25416		1.6	1.0E-09	T93176.1	EST_HUMAN	ye24e05.11 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:118688 5'
1312	14348	27314	2.49	9.0E-10	AW867740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2845	15905	28630	6.84	9.0E-10	AB70071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraebe_coban_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29, contains element PTR5 repetitive element;
7008	20134	33449	4.22	9.0E-10	AI452982.1	EST_HUMAN	TR:000372 O00372 PUTATIVE P150.;
148	13251	26180	12.13	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3353	16404	29326	0.76	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
4229	17258	30142	3.69	8.0E-10	AA376832.1	EST_HUMAN	EST89564 Small intestine I Homo sapiens cDNA 5' end
10324	23248		2.46	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
702	13764	26688	32.88	7.0E-10	7708225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
702	13764	26689	32.88	7.0E-10	7708225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1626	14659	27636	2.48	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2666	16567		21.84	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3104	18161	28072	2.86	7.0E-10	X00855.1	NT	H. sapiens DHFR gene, exon 3
6309	19380	32619	3.72	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
7647	20607	33973	1.2	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7818	20861		1.46	7.0E-10	P35094	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8308	21277	34688	1.29	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8308	21277	34689	1.29	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
10673	23595	37092	0.68	7.0E-10	L08895.1	NT	Homo sapiens MAD5/MEF2-family transcription factor (MEF2C) mRNA, complete cds
914	13959	26922	2.67	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene and C11orf17 gene
2686	15892	28700	1.37	6.0E-10	AI424405.1	EST_HUMAN	R02407.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2095021 3'
4768	17788		2.72	6.0E-10	AW833719.1	EST_HUMAN	RC3-CT0254-031088-012-g12 CT0254 Homo sapiens cDNA
9135	22101	35527	0.89	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9135	22101	35528	0.89	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E)
9992	22919	36388	0.43	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12221	25058		1.64	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
761	13821		5.01	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_11 434 (synonym: lites3) Homo sapiens cDNA clone DKFZp434N219 5'
3489	16335	29460	1.63	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
5026	18040	30923	1.1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7544	20507		1.74	5.0E-10	BF105159.1	EST_HUMAN	801822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9994	22847	36303	1.95	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9894	22847	36304	1.95	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
111	13222		1.27	4.0E-10	A1221083.1	EST_HUMAN	qq09f09.s1 Soares placenta 8to9weeks_2NbhP809W Homo sapiens cDNA clone IMAGE:1759049 3'
583	13851	26565	0.75	4.0E-10	AA515260.1	EST_HUMAN	similar to contains LTR8.b2 LTR8 repetitive element
2012	15033	28043	1.4	4.0E-10	AW594709.1	EST_HUMAN	tf64a01.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:B24648 3'
2580	15581	28500	5.49	4.0E-10	AL163303.2	NT	hg58g03.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element
7382	20352	33703	17.71	4.0E-10	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C103
10555	23477	36971	0.53	4.0E-10	AW283243.1	EST_HUMAN	(UBE2D3) genes, complete cds
10812	23733	37235	0.87	4.0E-10	A1267342.1	EST_HUMAN	UI-H-B12-ah1-a-07-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10933	23853	37388	0.45	4.0E-10	BE169208.1	EST_HUMAN	aq63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
10933	23853	37369	0.45	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-f08 HT0521 Homo sapiens cDNA
916	13970	26924	1.8	3.0E-10	N36113.1	EST_HUMAN	PM1-HT0521-120200-001-f08 HT0521 Homo sapiens cDNA
1363	14388		4.8	3.0E-10	AY005150.1	NT	yy3206.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1 L1 repetitive element
4568	17589	30480	1.04	3.0E-10	AL163203.2	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
4568	17589	30481	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5530	18528	31594	1.06	3.0E-10	N50109.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
6327	19397	32639	4.03	3.0E-10	P20350	SWISSPROT	yz11g08.s1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:282782 3'
6486	19551	32801	3.08	3.0E-10	BE302970.1	EST_HUMAN	RHOMBOLD PROTEIN (VEINLET PROTEIN)
8036	20973	34357	1.42	3.0E-10	AV743302.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
8036	20973	34358	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
9082	22048	35471	1.04	3.0E-10	H87208.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
9404	22369	35803	1.8	3.0E-10	AW850731.1	EST_HUMAN	ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element
9404	22369	35804	1.8	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
							IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9698	22649		0.73	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10828	23749		2.05	3.0E-10	T65891.1	EST_HUMAN	yc11e12.r1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:30398 5'
10957	23877		1.76	3.0E-10	AA769294.1	EST_HUMAN	nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12865	25468	31728	1.95	3.0E-10	BE179517.1	EST_HUMAN	IL3-H70618-110500-136-E07 HT0618 Homo sapiens cDNA
37	13157	26058	1.55	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
37	13157	26059	1.55	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1913	14937		1.88	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
2899	16057		0.68	2.0E-10	BF675047.1	EST_HUMAN	602138640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5901	18988		3.12	2.0E-10	Q28640	SWISSPROT	(HPRC)
6378	19447	32688	1.55	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7605	20566	33926	6.24	2.0E-10	BE781082.1	EST_HUMAN	601666208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8347	21316	34730	0.54	2.0E-10	P26809	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8347	21316	34731	0.54	2.0E-10	P26809	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9657	22600		0.85	2.0E-10	BF434565.1	EST_HUMAN	7c78d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
1509	14542		2.94	1.0E-10	AW867767.1	EST_HUMAN	MRO-SN0038-290300-001-f01 SN0038 Homo sapiens cDNA
1611	14543	27619	3.27	1.0E-10	AV652723.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2586	15587		1.92	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3511	16557	29481	0.64	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3550	16596		0.81	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3558	16596		0.94	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
4043	17081		6.46	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4154	17185	30072	5.55	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4154	17185	30073	5.55	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4160	17191	30080	2.48	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4189	17230		2.63	1.0E-10	M30829.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5212	18221		0.92	1.0E-10	A1797745.1	EST_HUMAN	we8204.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains
6875	19928	33226	0.61	1.0E-10	AA631233.1	EST_HUMAN	MER31.11 MER31 repetitive element;
6991	20214	33543	0.49	1.0E-10	AF003528.1	NT	nq81a05.s1 NCI_CGAP_Oc9 Homo sapiens cDNA clone IMAGE:1158704 3'
7716	20673		0.56	1.0E-10	P08548	SWISSPROT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7947	20888	34279	0.63	1.0E-10	AU128584.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8582	21550	34968	1.11	1.0E-10	AW408990.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
9002	21968		1.1	1.0E-10	AJ268340.1	EST_HUMAN	fb_6A4 Fetal brain library Homo sapiens cDNA
10562	23484		3.95	1.0E-10	AA081888.1	EST_HUMAN	qtm04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;
11259	24211	37734	3.25	1.0E-10	AJ038280.1	EST_HUMAN	zn23g06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:648314 5'
12166	18354		2.46	1.0E-10	X87344.1	NT	ov65h03.x1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
261	13357	26282	0.98	9.0E-11	BE145600.1	EST_HUMAN	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2114	16131	28151	6.21	9.0E-11	AL134395.1	EST_HUMAN	IL2-HT0203-291099-019-c08 HT0203 Homo sapiens cDNA
2114	15131	28152	6.21	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
3394	16443	29370	2.6	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
3394	16443	29371	2.6	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
4528	17552	30440	0.72	9.0E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5654	18750		3.89	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10514	23436	36934	1.22	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10514	23436	36935	1.22	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12546	25269	31809	4.59	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506B08 5'
3133	16190		8.85	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares_adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4073	17109	30003	4.35	8.0E-11	N23712.1	EST_HUMAN	yn46a06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5890	18978	32170	0.65	8.0E-11	AW674316.1	EST_HUMAN	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982 3'
6829	19883		0.65	8.0E-11	AW166158.1	EST_HUMAN	xf45h11.x1 NCI_CGAP_Brm50 Homo sapiens cDNA clone IMAGE:2821061 3' similar to contains MER10.11
1442	14475	27452	1.87	7.0E-11	AA330942.1	EST_HUMAN	MER10 repetitive element;
							EST34392 Embryo, 6 week Homo sapiens cDNA 5' end

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3885	16925	29834	1.11	7.0E-11	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8843	21810	35228	2.78	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10590	23512		1.19	7.0E-11	P11399	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
412	13485	26421	6.97	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
412	13485	26422	6.97	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6884	19938	33232	0.88	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
7957	20898	34281	3.22	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8707	21675	35100	7.37	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC08 5'
8668	22621	36072	0.42	6.0E-11	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-e03 BT0281 Homo sapiens cDNA
12	13132	26030	0.75	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3377	13132	26030	1.31	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4258	17285	30167	1.51	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5655	19722	32987	1.91	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7774	20727	34099	11.91	5.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1401	14434		1.88	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2802	15794	28812	7.83	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
2981	16039	28962	0.92	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4849	17870	30557	1.24	4.0E-11	D44686.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
5621	19879	32957	3.27	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
7197	20221	33552	0.54	4.0E-11	AA442530.1	EST_HUMAN	zv59f10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757063 5' similar to TR:G1055250 G1055250 PHEROMONE RECEPTOR VN4. ;
7600	20551		3.97	4.0E-11	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
9750	22891		1.68	4.0E-11	BE149425.1	EST_HUMAN	(UBE2D3) genes, complete cds
10020	22947	36415	0.86	4.0E-11	AI608753.1	EST_HUMAN	RC1-HT0256-210100-013-f03 HT0256 Homo sapiens cDNA
12736	25388	31752	1.56	4.0E-11	11545732	NT	tf52g12.x1 NC1_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1 CE00385 ;
1488	14521	27494	2.65	3.0E-11	6678077	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
4305	17334		1.37	3.0E-11	AA309248.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
981	14014	26887	1.48	2.0E-11	AI150502.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 MER10 repetitive element ;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1189	14229	27186	4.46	2.0E-11	R24807.1	EST_HUMAN	y943e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1189	14229	27187	4.46	2.0E-11	R24807.1	EST_HUMAN	y943e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1617	14649	27624	5.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds
1617	14649	27626	5.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds
1620	14653	27629	1.25	2.0E-11	AI126371.1	EST_HUMAN	qc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02982 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.11 L1 repetitive element
2775	15767	28767	1.04	2.0E-11	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
3211	16266	29189	8.7	2.0E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3337	16388	28309	1	2.0E-11	AI478617.1	EST_HUMAN	tm54d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
3375	16425	29350	0.71	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE)(UDP-GALNAc:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE)(GALNAc-T1)
3508	16554		1.09	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4472	17498		1.24	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
4636	17657		0.96	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4973	17988		2.38	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
6258	18331	32562	1	2.0E-11	AW877806.1	EST_HUMAN	QV2-PT0073-280300-109-h08 PT0073 Homo sapiens cDNA
6443	19508	32758	1.71	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:787433 5' similar to SW:PR16_YEAST
7401	20369	33722	0.82	2.0E-11	BF592945.1	EST_HUMAN	P16938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
8214	21183		0.51	2.0E-11	P37072	SWISSPROT	7197c03.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3'
8578	22540		1.31	2.0E-11	AF029308.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
10847	23569	37085	4.42	2.0E-11	Q13606	SWISSPROT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10862	23802	37305	0.85	2.0E-11	AW885874.1	EST_HUMAN	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10882	23802	37306	0.85	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11448	24391	37935	1.54	2.0E-11	AA035369.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11448	24391	37936	1.54	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11477	24420	37969	2.14	2.0E-11	AA261956.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
12326	25128		4.12	2.0E-11	AW842143.1	EST_HUMAN	zs18b04.r1 NCL_CGAP_GC51 Homo sapiens cDNA clone IMAGE:685519 5'
							RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12354	25148	31854	2.14	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12617	25313		1.49	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12754	25399		1.68	2.0E-11	P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13070	25604		3.68	2.0E-11	11417868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
677	13740	26667	0.83	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
784	13944	26769	1.89	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1221	14259	27216	4.66	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1498	14531		2.95	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2053	15072	28091	1.41	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2136	15153	28168	3.18	1.0E-11	AF000573.1	NT	Homo sapiens homogenitae 1,2-dioxygenase gene, complete cds
2170	16186	28207	1.15	1.0E-11	AA309318.1	EST_HUMAN	EST180186 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3510	16558	29480	0.8	1.0E-11	BE004315.1	EST_HUMAN	CMO-BN0106-170300-292-412 BND105 Homo sapiens cDNA
4860	17975	30866	1.01	1.0E-11	A1168625.1	EST_HUMAN	cx68h06.s1 Soares NIHMFu_S1 Homo sapiens cDNA clone IMAGE:1661243 3'
5405	18508	31385	14.43	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5931	19017	32212	0.77	1.0E-11	BF222646.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3648945 3' similar to contains MER10.b3
8112	21049		0.51	1.0E-11	AB042297.1	NT	MER10 repetitive element ;
8543	21511	34928	3.38	1.0E-11	4885546	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
8928	21894	35322	4.18	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9403	22368	35801	1.18	1.0E-11	BF365119.1	EST_HUMAN	y73d08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28166 5'
9403	22368	35802	1.18	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-803 NN1149 Homo sapiens cDNA
11619	24557	38120	1.48	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-803 NN1149 Homo sapiens cDNA
2963	16021	28946	0.82	9.0E-12	P20742	SWISSPROT	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296977 5'
10157	23082	36558	1.02	9.0E-12	AL163300.2	NT	PREGNANCY ZONE PROTEIN PRECURSOR
10157	23082	36559	1.02	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12075	24847	38542	2.85	9.0E-12	AL046939.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
9993	22646		0.92	8.0E-12	BE074720.1	EST_HUMAN	DKFZp58610417_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp58610417 5'
12407	25180		3.22	8.0E-12	AJ271738.1	NT	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
4890	17711	30605	1.46	7.0E-12	Q09504	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2
11677	24643	38220	7.41	7.0E-12	AA704736.1	EST_HUMAN	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
3558	16804		0.95	8.0E-12	AV730554.1	EST_HUMAN	223g01.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
4375	17403	30283	9.29	8.0E-12	AA732516.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW06 5'
							nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6528	19591	32851	0.65	6.0E-12	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8347	22312	35736	0.98	6.0E-12	AF003249.1	NT	Macaca saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9829	22678		1.68	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367888 similar to contains MER29.12
1044	14090	27043	3.57	5.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element ;
3401	18460	29376	1.17	5.0E-12	BE047779.1	EST_HUMAN	EST04482 Fetal brain, Sirelagene (cat#36206) Homo sapiens cDNA clone HFBDV33
3740	18782	29694	6.8	5.0E-12	AJ271736.1	NT	tz2b05.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291217 5'
6137	19214	32441	4.89	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6137	19214	32442	4.99	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6639	19697	32973	9.52	5.0E-12	AW974780.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
7232	19977	33274	1	5.0E-12	AL040739.1	EST_HUMAN	EST336850 MAGE resequences, MAGN Homo sapiens cDNA
7242	19977	33274	1.03	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8571	21539	34960	1.14	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
9015	21981		0.7	5.0E-12	AW887037.1	EST_HUMAN	z01g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.3 L1 repetitive element ;
9346	22311		0.54	5.0E-12	AL079581.1	EST_HUMAN	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA
9464	22428	35887	2.78	5.0E-12	AJ271735.1	NT	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9778	22719	36173	1.38	5.0E-12	P34982	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 1/2
10638	23560		4.14	5.0E-12	AL163303.2	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10729	23651	37144	0.81	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
244	13342	26287	4.17	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
245	13342	26287	5.51	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4650	17671	30558	0.74	4.0E-12	A1689984.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
7891	20825		0.72	4.0E-12	BF445140.1	EST_HUMAN	b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
8585	21553		2.92	4.0E-12	AF109907.1	NT	nad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2
9035	22001	35422	0.75	4.0E-12	AB042815.1	NT	MER7 repetitive element ;
11419	24363	37898	3.26	4.0E-12	AJ226043.1	NT	Homo sapiens S164 gene, partial cds, PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
12658	25338		2.82	4.0E-12	U78027.1	NT	Bos taurus Mth2 mRNA for mitochondrial carrier homolog 2, complete cds
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
618	13683	26600	3.08	3.0E-12	AW341883.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR:O14517 O14517 SMRP.;
618	13683	26601	3.06	3.0E-12	AW341883.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR:O14517 O14517 SMRP.;
5211	18220	31096	0.73	3.0E-12	AL163269.2	NT	Homo sapiens chromosome 21 segment HS21C068
5527	18526	31562	0.96	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7559	20619		0.64	3.0E-12	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
8030	20967		0.55	3.0E-12	AW854328.1	EST_HUMAN	RC3-CT0255-031099-011-r02 CT0255 Homo sapiens cDNA
8718	21686	35114	0.48	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
9462	22426	36864	0.54	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
11016	23981	37507	2.71	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
11016	23981	37508	2.71	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1661	14993	27688	2.41	2.0E-12	AW802131.1	EST_HUMAN	IL5-UM0071-120400-065-a05 UM0071 Homo sapiens cDNA
3480	16526	29451	0.85	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4141	17172	30060	1.09	2.0E-12	J01894.1	NT	Rat USA small nuclear RNA
4141	17172	30081	1.09	2.0E-12	J01894.1	NT	Rat USA small nuclear RNA
4451	17477		1.97	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
5321	18427	31177	0.71	2.0E-12	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6022	19680		1.83	2.0E-12	AW971857.1	EST_HUMAN	EST3393946 MAGI2 resequencing, MAGL Homo sapiens cDNA
7381	20351	33702	3.22	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Berto Soares Homo sapiens cDNA clone HIBBA13 5' end
7667	20930	33869	1.18	2.0E-12	BE173035.1	EST_HUMAN	MR0-HT0559-200400-016-e08 HT0559 Homo sapiens cDNA
7778	20731		0.57	2.0E-12	AW842798.1	EST_HUMAN	MR2-CN0037-210200-101-b02 CN0037 Homo sapiens cDNA
7922	20965	34253	2.1	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9077	22043	35466	0.43	2.0E-12	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
9653	22820		1.55	2.0E-12	AF198864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10345	23269		14.41	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10881	23801	37304	0.8	2.0E-12	AI334130.1	EST_HUMAN	qq0702.x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.;
12308	25116		3.11	2.0E-12	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C083
12511	25245		1.69	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
123	13231	28159	2.83	1.0E-12	AW627674.1	EST_HUMAN	hh90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element;
2004	15025		1.46	1.0E-12	AI871726.1	EST_HUMAN	wn51f07.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element;
3085	16142	29053	0.78	1.0E-12	AF000091.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3086	16142	29054	0.78	1.0E-12	AF000091.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3888	16928	29836	31.6	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3888	16928	29837	31.6	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6078	18158		2.05	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6169	19234		1.65	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0981
6277	19349	32582	0.57	1.0E-12	BF642800.1	EST_HUMAN	EST00008 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6277	19349	32583	0.57	1.0E-12	BF642800.1	EST_HUMAN	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6882	19739	33014	0.78	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7323	20294	33637	1.9	1.0E-12	AF190864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7357	20327	33675	11.35	1.0E-12	AI248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7357	20327	33676	11.35	1.0E-12	AI248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
8834	21801	35220	0.48	1.0E-12	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P1, TCRBV7S2A1N4T, TCRBV13S9/13S>
9053	22019	35444	1.16	1.0E-12	AA782323.1	EST_HUMAN	ac28a05.s1 Stralagene ovary (f937217) Homo sapiens cDNA clone IMAGE:857577 3'
12213	25052	39828	2.92	1.0E-12	AW962164.1	EST_HUMAN	EST374237 IMAGE resequences, MAGG Homo sapiens cDNA
12434	25200		2.54	1.0E-12	AI736592.1	EST_HUMAN	w33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392085 3'
12582	26881		2.51	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1054	14100	27050	0.7	9.0E-13	AW082714.1	EST_HUMAN	xb61f07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580805 3' similar to contains MER28.13 MER28 repetitive element;
3643	16686		1.01	9.0E-13	AJ271735.1	NT	Homo sapiens Xa pseudautosomal region; segment 1/2
3997	17007	29623	0.96	9.0E-13	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9960	22887		2.59	9.0E-13	N69653.1	EST_HUMAN	za26b08.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:293651 3'
718	13780	28714	6.78	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
718	13780	28715	6.78	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1855	14881	27877	3.1	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
8449	21418	34831	0.75	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8449	21418	34832	0.75	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10505	23427		4	8.0E-13	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8127	21064	34462	0.58	7.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8127	21064	34463	0.58	7.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8578	21544		0.49	7.0E-13	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12682	25330		5.56	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
2111	15128	28148	3.56	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3333	16384		0.74	5.0E-13	R78338.1	EST_HUMAN	y82f04.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145759 5'
3408	16457		1.35	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
7060	20082	33390	0.7	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11209	24163	37693	2.07	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1883	14908		6.02	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221098-001-e11 HT0224 Homo sapiens cDNA
2487	16471		2.44	4.0E-13	AF003529.1	NT	Homo sapiens glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene, partial cds and flanking repeat regions
4778	17798		0.89	4.0E-13	AA454054.1	EST_HUMAN	z148c07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
5667	18762	31831	4.36	4.0E-13	BE169131.1	EST_HUMAN	PM8-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7413	20380	33731	1.05	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7870	20814	34192	0.98	4.0E-13	AA431528.1	EST_HUMAN	G452763 COR1 MRNA ;
7999	20928		1.47	4.0E-13	N44291.1	EST_HUMAN	y63g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995
9193	22159	35587	1.2	4.0E-13	AL043810.1	EST_HUMAN	A32995 t complex sterility protein - mouse ;
9860	22796	36249	0.59	4.0E-13	AA076907.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434A0128 5'
10380	23303	36779	5.28	4.0E-13	A1288831.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
11502	24444	37695	1.9	4.0E-13	AA435819.1	EST_HUMAN	q132d05.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu repetitive element;
11502	24444	37696	1.9	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11502	24444	37696	1.9	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
181	13281		5.91	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
866	13922		3.35	3.0E-13	AA430310.1	EST_HUMAN	zw68g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2378	15386	28410	1.65	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2487	15491		2.11	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2873	15870	28688	2.5	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-H08 FT0100 Homo sapiens cDNA
3201	16256		2.19	3.0E-13	AA745844.1	EST_HUMAN	ob18002.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
3514	16560	29484	0.9	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3514	16560	29485	0.9	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5618	18714	31872	0.64	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element ;
5618	18714	31873	0.64	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element ;
6106	19185	32404	0.71	3.0E-13	AW005639.1	EST_HUMAN	w288c02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:075139 075139 KIAA0844 PROTEIN. ;
8215	21184	34594	8.24	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8412	21381	34787	0.51	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re-reactive factor
8412	21381	34788	0.51	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re-reactive factor
10558	23480	36975	0.46	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
11036	24000		2.68	3.0E-13	AID64768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
11386	24332	37861	3.32	3.0E-13	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11924	24805	38398	1.54	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
151	13254	26183	3.93	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
1275	14310	27271	7.14	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3294	16347	29267	1.08	2.0E-13	BF431899.1	EST_HUMAN	nab79f05.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3518	16564	29489	1.25	2.0E-13	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4135	17167		1.61	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6245	19318	32548	4.71	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6987	20210	33538	6.49	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7255	19990	33287	0.59	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7255	19990	33288	0.59	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10824	23745	37246	4.53	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12387	25165		5.43	2.0E-13	AW892155.1	EST_HUMAN	CMO-NN001-100300-274-e11 NN001 Homo sapiens cDNA
291	13385	26312	1.49	1.0E-13	S74129.1	NT	FGF-1 fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
889	13944	26902	4.85	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1339	14373	27343	1.38	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
2037	15056	28074	2.43	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4623	17644	30532	2.2	1.0E-13	BF340987.1	EST_HUMAN	THR repetitive element ;
6586	19646	32915	0.61	1.0E-13	AA090732.1	EST_HUMAN	602038009F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185866 5'
8242	21211	34616	0.78	1.0E-13	AA577812.1	EST_HUMAN	Y1635.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8242	21211	34617	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
10450	23372		0.82	1.0E-13	O15481	EST_HUMAN	nm24d01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
10684	23586	37084	0.49	1.0E-13	AF300701.1	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
11707	24872	38249	10.13	1.0E-13	BF108765.1	EST_HUMAN	Mus musculus osteotesticular protein tyrosine phosphatase mRNA, complete cds
12206	25048		2.34	1.0E-13	AV716377.1	EST_HUMAN	745610.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
12844	25454		3.21	1.0E-13	AJ271735.1	NT	AV716377 DCB Homo sapiens cDNA clone DCBAIE03 5'
333	13422	26345	3.14	9.0E-14	AA781159.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
334	13423	26345	2.37	9.0E-14	AA781159.1	EST_HUMAN	aj24cd1.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element ;
2508	15511		4.8	9.0E-14	AW861577.1	EST_HUMAN	aj24cd1.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element ;
2597	15598	28617	1.03	9.0E-14	AJ133127.1	NT	RC4-CT0322-080100-013-c09 CT0322 Homo sapiens cDNA
2597	15598	28618	1.03	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2764	15756	28777	6.94	9.0E-14	AB038182.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
							Homo sapiens TFF gene cluster for trefoil factor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3128	16185	28094	5.43	9.0E-14	AW513286.1	EST_HUMAN	xc54h05.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707833 3'
3252	13422	26345	0.67	9.0E-14	AA781169.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
3811	16951	29759	7.16	9.0E-14	D14547.1	NT	repetitive element;
4789	17807	30699	1.68	9.0E-14	AJ002153.1	NT	Human DNA, SINE repetitive element
3509	16555		1.44	8.0E-14	BE468263.1	EST_HUMAN	Saguijpus oedipus gene for seminal vesicle secreted protein semenogelin I
3978	17018		3.46	8.0E-14	R76269.1	EST_HUMAN	hz77c09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
9803	21126	34530	21.45	8.0E-14	X89211.1	NT	yf72603.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9918	22739	36192	3.1	8.0E-14	AA216916.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
11762	24690		1.52	8.0E-14	BE062558.1	EST_HUMAN	zq17c10.s1 Stratigene fetal retina 937202 Homo sapiens cDNA clone IMAGE:628970 3'
12590	25294	31783	2.89	8.0E-14	AI688118.1	EST_HUMAN	QV2-BT0258-281099-014-a01 BT0258 Homo sapiens cDNA
1633	15873		3.99	7.0E-14	AW151673.1	EST_HUMAN	wc92h08.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
9272	22238		0.51	7.0E-14	AL163285.2	NT	x87e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.12
							MER10 repetitive element;
							Homo sapiens chromosome 21 segment HS21C086
367	13453	28381	16.94	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10181	23106	36587	2.54	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10181	23106	36588	2.54	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
620	13665	26603	5.23	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
3683	16726		0.95	5.0E-14	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5093	18103	30979	1.39	5.0E-14	AW073791.1	EST_HUMAN	repetitive element;
5811	18707	31864	4.84	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1125	15859		1.95	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1895	14920	27916	7	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3785	16807		1	4.0E-14	AA046502.1	EST_HUMAN	z667d06.r1 Soares_pregnant_uterus_Nb1-IPU Homo sapiens cDNA clone IMAGE:487858 5'
4320	17349	30233	0.96	4.0E-14	N46328.1	EST_HUMAN	y773c12.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element;
							H. sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING6, 9, 13 and 14 genes
8291	21260		0.6	4.0E-14	X87344.1	NT	

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12905	25988		6.38	4.0E-14	A188224.1	EST_HUMAN	wnt08c03.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element
950	14003	25955	4.69	3.0E-14	X95466.1	NT	R. norvegicus mRNA for CPG2 protein
4963	17978	30898	1.16	3.0E-14	7656964	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA
6898	19950	33246	0.96	3.0E-14	A1420786.1	EST_HUMAN	ta91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
6898	19950	33247	0.96	3.0E-14	A1420786.1	EST_HUMAN	ta91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
7021	25876		0.51	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7229	20251	33585	0.57	3.0E-14	AA386311.1	EST_HUMAN	EST186054 Brain IV Homo sapiens cDNA
9139	22105	35531	0.83	3.0E-14	N42165.1	EST_HUMAN	Y07b10.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270523 5'
11337	24287	37811	2.83	3.0E-14	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11568	18347	31293	6.06	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCL CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
12824	25864		1.98	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
390	13465	26395	2.76	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
390	13465	26396	2.76	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
691	15847	26882	9.98	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2397	15404		1.89	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2472	15476		1.4	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2531	15534	28554	2.2	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2547	15548		1.03	2.0E-14	BE222432.1	EST_HUMAN	hvd0g10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.11 OFR repetitive element;
2683	15679		1.48	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5602	18698	31669	0.91	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5702	18797	31972	0.81	2.0E-14	A1312351.1	EST_HUMAN	ta78h01.x2 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5909	18899	32082	3.16	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7067	20089		0.92	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-e06 BN0072 Homo sapiens cDNA
7290	20262	33596	0.57	2.0E-14		NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7502	20467	33828	0.87	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7751	20704	34072	21.51	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7751	20704	34073	21.51	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10277	23202	36687	0.52	2.0E-14	AI978795.1	EST_HUMAN	w59g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element
10783	23704	37203	0.53	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBFB04 5'
11133	24093	37622	3.94	2.0E-14	AW139800.1	EST_HUMAN	UIH-BI-activ-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12822	25857		1.71	2.0E-14	AF008191.1	NT	(Homo sapiens putative G6 protein (GR6) gene, complete cds)
1068	14113	27063	2.09	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1405	14438	27406	8.18	1.0E-14	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
1405	14438	27407	8.18	1.0E-14	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
2017	15038	28049	15.42	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2195	15210	28228	5.77	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2419	15426	28449	5.29	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2955	16013	28940	1.05	1.0E-14	P08227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3182	16237	29154	6.2	1.0E-14	BF33527.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3182	16237	29155	6.2	1.0E-14	BF33527.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3901	16941	29852	1.75	1.0E-14	AA682994.1	EST_HUMAN	aa89c12.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4500	17525	30410	2.07	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5907	18993	32184	2.1	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6831	25669	33176	11.02	1.0E-14	11437160	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6831	25669	33177	11.02	1.0E-14	11437160	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1579	14612	27584	1.78	9.0E-15	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR-T), mRNA
2163	15198						Homo sapiens transcription factor IGHM enhancer 3, JM111 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
7738	20983	34056	1.37	9.0E-15	AF196779.1	NT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8350	21319	34733	1.17	9.0E-15	BE903559.1	EST_HUMAN	60167750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960159 5'
2822	13553		1.42	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7387	20358	33708	1.55	7.0E-15	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
10801	23722						xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element
998	14047	27001	2.45	7.0E-15	AW241958.1	EST_HUMAN	THR12 THR repetitive element
6027	19110	32311	6.55	6.0E-15	AL271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6027	19110	32311	1.11	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6027	19110	32312	1.11	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
410	13483	26418	5.24	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2771	15763	28784	2.05	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3482	18528		1.08	5.0E-15	AW298817.1	EST_HUMAN	UHLBW0-qjb-g-10-Q.U1.s1 NCL_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2731219.3
11035	23999		2.27	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06.5
427	13122	26020	3.54	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6822	19876	33165	0.98	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11401	21088	34487	1.79	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11401	21089	34488	1.79	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4246	17274		6.54	3.0E-15	N89452.1	EST_HUMAN	LY142F Human fetal heart; Lambda ZAP Express Homo sapiens cDNA clone LY142.5' similar to ANF(CARDIODILATIN)
5067	18077	30958	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5067	18077	30959	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6988	20209		1.27	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7495	20460	33819	3.66	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7495	20460	33820	3.66	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
10285	23210		2.66	3.0E-15	AA807128.1	EST_HUMAN	cc38a07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764.3' similar to contains MER19.t1 MER19 repetitive element;
11148	24108	37633	3.42	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
250	13347	28273	4.45	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
368	13464	26382	4.01	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
368	13454	26383	4.01	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2381	15389	28413	1.02	2.0E-15	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to contains MER29.b3 MER29 repetitive element;
2381	15389	28414	1.02	2.0E-15	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256.3' similar to contains MER29.b3 MER29 repetitive element;
4095	17129	30023	1.21	2.0E-15	AW238499.1	EST_HUMAN	xp26h01.x1 NCL_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521.3' similar to contains L1.13 L1 repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4853	17674		2.73	2.0E-15	AI806336.1	EST_HUMAN	wf0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN. ;
6306	19377	32616	1.02	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6306	19377	32617	1.02	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7321	20292		1.42	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7486	20451	33810	2.64	2.0E-15	AA704195.1	EST_HUMAN	z1776c3.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7825	20585	33948	4.75	2.0E-15	W05064.1	EST_HUMAN	za78d10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ;
8117	21054	34451	0.67	2.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9257	22223	35653	2.73	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9427	22391	35829	0.74	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9427	22391	35830	0.74	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9759	22700	36157	1.18	2.0E-15	AW379465.1	EST_HUMAN	CMO-HT0244-201099-078-at12 HT0244 Homo sapiens cDNA
9759	22700	36158	1.19	2.0E-15	AW379465.1	EST_HUMAN	CMO-HT0244-201099-078-at12 HT0244 Homo sapiens cDNA
11187	24143		4.15	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12834	18339	31288	3.19	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
12834	18339	31289	3.19	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2785	15777		2.95	1.0E-15	AI688984.1	EST_HUMAN	b26r05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
3025	16082	20005	1.53	1.0E-15	BE043594.1	EST_HUMAN	hk40a02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
3158	16214	29129	1.2	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5189	18198	31071	1.11	1.0E-15	AI984928.1	EST_HUMAN	wr86a04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494590 3'
6508	19572	32825	1.63	1.0E-15	T06763.1	EST_HUMAN	y40a010.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ;
7205	20229		1.83	1.0E-15	BE074217.1	EST_HUMAN	QV3-B70569-270100-074-g05 B70569 Homo sapiens cDNA
7239	19974	33272	0.76	1.0E-15	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8574	21542	34962	1.04	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8763	21730	35152	4.51	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8763	21730	35153	4.51	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9394	22359	35789	0.49	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9397	22362	35793	1.5	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9802	22806	36055	0.79	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9880	22817	36383	0.95	1.0E-15	AA864653.1	EST_HUMAN	oh37d03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1
11169	24127	37657	4.18	1.0E-15	AF044083.1	NT	repetitive element;
13008	25720	31612	9.25	1.0E-15	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4532	17555	30443	1.15	9.0E-16	4503168	NT	element;
11338	24288	37812	1.94	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
5786	18878	32060	0.79	7.0E-16	4885120	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
7564	20527	33885	1.45	7.0E-16	O88807	SWISSPROT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7564	20527	33885	1.45	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7564	20527	33885	1.45	7.0E-16	O88807	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
12957	25809		1.88	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2151	15167		7.77	6.0E-16	AW972611.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:118052 5'
1489	14522	27495	1.28	5.0E-16	AJ251154.1	NT	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
2689	15885	28702	2.52	5.0E-16	AA992176.1	EST_HUMAN	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
10414	23336	36821	0.48	5.0E-16	AL163246.2	NT	oh80c04.s1 Soares total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1623078 3' similar to
11849	24732	38319	2.54	5.0E-16	BF217368.1	EST_HUMAN	contains element L1 repetitive element;
13044	25585		10.68	5.0E-16	11418127	NT	Homo sapiens chromosome 21 segment HS21C046
2249	15263		1.64	4.0E-16	AB001923.1	NT	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2388	15396	28421	2.21	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2398	15396	28422	2.21	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3471	16517	29438	3.94	4.0E-16	Q16653	SWISSPROT	QV1-JUN0036-200300-115-g02 UM0036 Homo sapiens cDNA
4166	17197	30083	4.74	4.0E-16	BE083876.1	EST_HUMAN	QV1-JUN0036-200300-115-g02 UM0036 Homo sapiens cDNA
4166	17197	30084	4.74	4.0E-16	BE083876.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
7980	20919	34310	37.37	4.0E-16	AL163284.2	NT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
9650	22594	36042	0.97	4.0E-16	11423191	NT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
12280	26106		2.41	4.0E-16	P08548	SWISSPROT	Homo sapiens chromosome 21 segment HS21C084
12362	25169	31816	2.11	4.0E-16	6812459	NT	Homo sapiens hypofunctional protein FLJ10024 (FLJ10024), mRNA
12656	25336		1.36	4.0E-16	R18591.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
133	13238	26169	1.24	3.0E-16	AW022862.1	EST_HUMAN	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
							yf9b11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30489 5'
							df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
133	13238	26170	1.24	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
466	13539		1.91	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
476	13548		3.08	3.0E-16	AF135446.1	NT	Homo sapiens TSX(TSX) pseudogene, exon 5
1446	14479	27435	1.53	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2988	16046	28966	3.94	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3953	16993	28909	0.86	3.0E-16	T08169.1	EST_HUMAN	EST006060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
3980	17020		0.77	3.0E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3981	17021		1.06	3.0E-16	U03887.1	NT	Human BXP20 gene
5350	18455		1.11	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5698	18793	31966	1.2	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9005	21971	35392	4.92	3.0E-16	A1002836.1	EST_HUMAN	an98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684165 3' similar to contains THR.b2 THR repetitive element ;
10250	23175		0.9	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10478	23400	36897	5.77	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13079	25951	31317	1.4	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L1623 5'
973	14025		1.04	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2395	15402		1.32	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2699	15695		1.28	2.0E-16	J03081.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4207	17236	30123	1.14	2.0E-16	X88211.1	NT	H. sapiens DNA for endogenous retroviral like element
6905	19957	33254	0.83	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7984	20923	34316	1.4	2.0E-16	A1470723.1	EST_HUMAN	ij16e11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element ;
8300	21269	34681	1.86	2.0E-16	A1732837.1	EST_HUMAN	nz4706.x5 NCI_CGAP_P112 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849 HYPOPHOSPHATASE 2 4.9 KD PROTEIN. [2] TR:O08905, contains MER7.11 MER7 repetitive element ;
8498	21466	34892	0.73	2.0E-16	BE858026.1	EST_HUMAN	782h09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8498	21466	34893	0.73	2.0E-16	BE858026.1	EST_HUMAN	782h09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8872	21839	35281	0.75	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-401 PT0034 Homo sapiens cDNA
8872	21839	35282	0.75	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-401 PT0034 Homo sapiens cDNA
11274	24226	37752	1.58	2.0E-16	5902145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
186	13286	26210	2.57	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
382	13495		37.96	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares_t0tal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
1988	15009	28014	2.22	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5810	18900	32083	0.68	1.0E-16	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6574	19834		25.8	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6726	19782	33061	3.06	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7802	19634		6.75	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9638	22582	36031	1.06	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
3751	18793	29704	2.77	9.0E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6886	19938		2.35	9.0E-17	A1392864.1	EST_HUMAN	tg22c11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12 MER28 repetitive element;
8445	21414		5.47	9.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element;
10584	23508		2.3	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1020	14068		2.01	8.0E-17	AW680701.1	EST_HUMAN	QV0-O70032-080300-155-d01 OT0032 Homo sapiens cDNA
3907	16947		0.88	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5863	25842	31927	3.24	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7490	20455		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFACB07 5'
8019	20956	34349	0.54	8.0E-17	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahe11), mRNA
1452	14485		2.63	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5396	18489		3.14	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6846	19898	33193	7.34	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
204	13305	26234	6.62	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
8446	19511	32761	1.8	6.0E-17	AW662772.1	EST_HUMAN	h181d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 L1 repetitive element;
10655	23577	37074	0.54	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
10926	23846		0.46	6.0E-17	W92331.1	EST_HUMAN	ze15f03.s1 Soares_fetal_heart_NbH-H19W Homo sapiens cDNA clone IMAGE:359093 3'
421	13116	26014	3.22	5.0E-17	T84110.1	EST_HUMAN	yc05f08.r1 Stragene lung (4937210) Homo sapiens cDNA clone IMAGE:79839 5'
7840	20787	34182	1.76	5.0E-17	T81043.1	EST_HUMAN	yd28f04.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
9717	22745	38186	1.24	4.0E-17	AW129165.1	EST_HUMAN	x20e04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11821	24704	38286	1.96	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12303	25114		2.02	4.0E-17	A1073546.1	EST_HUMAN	ov45604.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
1490	14523		1.72	3.0E-17	D14547.1	NT	Q16530 PMS3 mRNA ;contains MER10.12 MER10 repetitive element ;
2108	15125	28144	1.22	3.0E-17	AW119123.1	EST_HUMAN	Human DNA, SINE repetitive element
3208	16263		1.68	3.0E-17	P35410	SWISSPROT	xd86c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3656	16689	29614	1.33	3.0E-17	BE326522.1	EST_HUMAN	IMAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3656	16699	29615	1.33	3.0E-17	BE326622.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
5068	18078		1.17	3.0E-17	BF51266.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181989 3'
8911	21579	34995	1.16	3.0E-17	N68461.1	EST_HUMAN	UI-H-B14-adj-c-06-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
10060	22987	36455	4.94	3.0E-17	AB026898.1	NT	za14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains
10746	23668	37164	0.73	3.0E-17	BF327012.1	EST_HUMAN	PT5.13 PTR5 repetitive element ;
10746	23668	37165	0.73	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12266	25089		3.31	3.0E-17	11417968	NT	QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA
353	13442	26367	3.4	2.0E-17	A1270080.1	EST_HUMAN	QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA
354	13442	26367	3.97	2.0E-17	A1270080.1	EST_HUMAN	QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA
990	14042		2.04	2.0E-17	AA722932.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
2453	15458	28479	2.3	2.0E-17	Q28983	SWISSPROT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu
2453	15458	28480	2.3	2.0E-17	Q28983	SWISSPROT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu
2941	15999	28922	6.23	2.0E-17	P12036	SWISSPROT	repetitive element
5440	18542	31452	1.8	2.0E-17	M27685.1	NT	q163a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu
5440	18542	31453	1.8	2.0E-17	M27685.1	NT	repetitive element
6395	19483		1.99	2.0E-17	AF05006.1	NT	zq81d04.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:399751 3'
6638	19696		1.66	2.0E-17	AL134881.1	EST_HUMAN	ZONADHESIN PRECURSOR
8133	21070	34469	0.85	2.0E-17	AB037839.1	NT	ZONADHESIN PRECURSOR
8420	21389	34799	1.47	2.0E-17	Q95156	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
8900	21767	35191	1.29	2.0E-17	AA300840.1	EST_HUMAN	Mus musculus ultra high sulfur keratin gene, complete cds
10228	23153	38643	2.95	2.0E-17	BE299888.1	EST_HUMAN	Mus musculus ultra high sulfur keratin gene, complete cds
10264	23189	38673	2.83	2.0E-17	AL163247.2	NT	Homo sapiens MHC class 1 region
							Homo sapiens cDNA clone DKFZp762J0610 5'
							Homo sapiens mRNA for KIAA1418 protein, partial cds
							OLFATORY RECEPTOR-LIKE PROTEIN OLF3
							EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin
							600944690FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2908015 5'
							Homo sapiens chromosome 21 segment HS21C047

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10264	23189	36874	2.83	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10822	23544	37044	5.23	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10745	23667	37162	0.66	2.0E-17	P98083	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10745	23667	37163	0.68	2.0E-17	P98083	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10772	23693	37190	0.57	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10772	23693	37191	0.57	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
12366	25153		1.31	2.0E-17	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
761	13812	26755	3.24	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1721	14751		1.35	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
1782	14811	27797	4.54	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2124	15141	28168	1.95	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2343	15353	28374	2.43	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3581	16826		1.05	1.0E-17	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4162	17193		8.5	1.0E-17	R09942.1	EST_HUMAN	y630e07.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
6600	19660		0.68	1.0E-17	AW468498.1	EST_HUMAN	he38e05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element; contains LTR8.1 LTR8 repetitive element;
6809	18863	33151	1.73	1.0E-17	A1185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6809	18863	33152	1.73	1.0E-17	A1185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7296	20268	33603	0.96	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8939	21905	35329	1.7	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101 299-072-d07 B70263 Homo sapiens cDNA
10366	23289	36768	0.87	1.0E-17	AW066538.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11747	24632	38212	1.64	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
13104	25825		1.63	1.0E-17	BE221470.1	EST_HUMAN	hu25e05.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1 MER13 repetitive element;
9856	22792		2.86	9.0E-18	A1472167.1	EST_HUMAN	ij66d03.x1 Soares_NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3800	16840	28747	1.87	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3899	16939	28850	3.75	8.0E-18	Q07537	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
349	13498	26361	23.15	7.0E-18	AW316676.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb.L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
349	13438	26362	23.15	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
7677	20835	33897	0.95	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0091-170300-011-c03 OT0091 Homo sapiens cDNA
12769	13438	26361	2.67	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12769	13438	26362	2.67	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3306	16359	29278	1.29	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nexin/protease nexin I, enhancer region
4777	17797		4.3	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGA5 C) (TGC)
8593	21561		2.64	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8691	21859	35092	0.57	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11469	24412	37661	1.54	6.0E-18	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
11657	24593	38166	2.06	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12627	25256	31805	2.95	6.0E-18	U87929.1	NT	Human aconitase hydratase (ACO2) gene, exon 4
1150	14192	27144	17.6	5.0E-18	AI280214.1	EST_HUMAN	qnr65g11.x1 Soares_placenta_8tc5weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;
5345	18450	31321	0.99	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
9070	22036	35469	5.53	5.0E-18	BE143312.1	EST_HUMAN	MRO-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
11323	24273	37800	3.26	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11323	24273	37801	3.26	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12849	25332		6.29	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
12980	25544		3.2	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
125	13232	26160	1.04	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
125	13232	26161	1.04	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
1729	14759	27744	1.61	4.0E-18	AA621814.1	EST_HUMAN	h024f11.g1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26328
1906	14930		0.95	4.0E-18	AI738592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); w133h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
2211	15226	28247	1.1	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2211	15226	28248	1.1	4.0E-18	Q06430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
3806	16846	29753	0.76	4.0E-18	A1581586.1	EST_HUMAN	ar33b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5437	18539	31447	2.29	4.0E-18	A1017565.1	EST_HUMAN	ou23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5437	18539	31448	2.29	4.0E-18	A1017565.1	EST_HUMAN	ou23a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8178	21148		0.67	4.0E-18	AA746811.1	EST_HUMAN	nx84a08.s1 NCL_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1266098 similar to contains L1.12 L1 repetitive element;
11348	24298	37826	4.22	4.0E-18	AA371807.1	EST_HUMAN	EST183633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
850	13908	26865	24.96	3.0E-18	AA814196.1	EST_HUMAN	ob23h11.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS6_HUMAN
930	13883	26836	3.54	3.0E-18	BE068634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S5. ;
3972	17012	28926	1.31	3.0E-18	AL163247.2	NT	CMO-BT0690-210300-288-g07 BT0690 Homo sapiens cDNA
7003	20129	33444	6.43	3.0E-18	BE001871.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11271	24223	37748	1.76	3.0E-18	BF218650.1	EST_HUMAN	PMO-BN0081-100300-001-808 BN0081 Homo sapiens cDNA
12774	25412		5.15	3.0E-18	AW022015.1	EST_HUMAN	601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
251	13348	26274	5.97	2.0E-18	AW836820.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
1155	14197		67.85	2.0E-18	BE266097.1	EST_HUMAN	QV1-LT0038-150200-070-e07 LT0038 Homo sapiens cDNA
3140	16197	29107	1.27	2.0E-18	Q39575	SWISSPROT	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5485	18585		3.85	2.0E-18	AA868610.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5584	18880	31844	3.38	2.0E-18	D14547.1	NT	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577 O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ;
5584	18880	31845	3.38	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5978	19063		1.67	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6289	19361	32598	1	2.0E-18	X60459.1	NT	602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
6289	19361	32599	1	2.0E-18	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
6408	19477	32724	0.76	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for Interferon alpha/beta receptor
6451	19516	32767	4.42	2.0E-18	AW565853.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
7670	20629	33983	0.72	2.0E-18	AA457619.1	EST_HUMAN	h194g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.12 MER19 repetitive element ;
8487	21455	34872	0.52	2.0E-18	BE439524.1	EST_HUMAN	aa89d11.1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77 ;
							HTM1-160F1 HTM1 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10407	23328	36813	1.31	2.0E-18	AW151673.1	EST_HUMAN	x167e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element ;
10407	23328	36814	1.31	2.0E-18	AW151673.1	EST_HUMAN	x167e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element ;
11319	24289	37787	3.07	2.0E-18	AW470791.1	EST_HUMAN	ha33d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
12039	24814	38508	2.88	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element ;
12461	14197		3.97	2.0E-18	BE250097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5' ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ;
4445	17471		0.93	1.0E-18	T95406.1	EST_HUMAN	AV653405 GLO Homo sapiens cDNA clone GLCDKE11.3' Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5429	18532	31412	2.71	1.0E-18	AV653405.1	EST_HUMAN	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5650	18746	31914	1.87	1.0E-18	D00039.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5650	18746	31915	1.87	1.0E-18	D00039.1	NT	Homo sapiens chromosome 21 segment HS21C080
6597	19657	32929	1.33	1.0E-18	AL163280.2	NT	oz89d09.x1 Soares, senescent fibroblasts_NBHSF Homo sapiens cDNA clone IMAGE:1680583 3' similar to contains L1.11 L1 repetitive element ;
8785	21752	35174	1.13	1.0E-18	AI148288.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10259	23184	36889	4.28	1.0E-18	U91328.1	NT	Homo sapiens glycylcan 3 (GPC3) gene, partial cds and flanking repeat regions
12412	25184	31821	6.49	1.0E-18	AF003529.1	NT	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element ;
547	13618	26540	5.55	9.0E-19	AA281961.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element ;
548	13618	26540	4.1	9.0E-19	AA281961.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8181	21151		5.71	9.0E-19	F08688.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
8036	22002	35423	2.84	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9038	22002	35424	2.84	9.0E-19	AL163203.2	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11482	24405	37953	3.37	9.0E-19	AB032569.1	NT	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element ;
12172	13618	26540	1.94	9.0E-19	AA281961.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
1050	14096		1.31	8.0E-19	AW874902.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4433	17460		0.98	8.0E-19	P08548	SWISSPROT	MR0-HT0404-210200-001-g06 HTO404 Homo sapiens cDNA
8488	21456	34873	1.04	8.0E-19	BE156936.1	EST_HUMAN	

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2257	15271	28286	1.43	7.0E-19	4758139	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX9) mRNA
6598	19658	32930	1.95	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7519	20484	33845	1.02	7.0E-19	P26444	SWISSPROT	BETA CRYSTALLIN A2
10372	23295	36771	0.43	7.0E-19	A1344951.1	EST_HUMAN	U01c08.x1 NCL_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
12313	25669		3.28	7.0E-19	AA705684.1	EST_HUMAN	z60b01.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3792	16833		1.6	6.0E-19	AW852930.1	EST_HUMAN	PM0-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4490	17516	30403	1.44	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4480	17516	30404	1.44	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4837	17854		1.47	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5064	18074	30854	1.29	6.0E-19	AL120817.1	EST_HUMAN	DKFZp62F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp62F192 5'
5958	19043	32242	4.88	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
6342	19411	32852	0.69	5.0E-19	AW683302.1	EST_HUMAN	h77b06.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
10790	23711	37213	0.78	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11865	24747	38329	4.78	5.0E-19	AW183725.1	EST_HUMAN	X87b02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element :
556	13826	26544	0.89	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2681	15687	28704	1.69	4.0E-19	BF697362.1	EST_HUMAN	602130810F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
5470	18571	31481	1.05	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3866	16905	28812	1.4	3.0E-19	Q28897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3866	16905	28813	1.4	3.0E-19	Q28897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4315	17344	30227	0.69	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4315	17344	30228	0.69	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4475	17501	30385	1.79	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5352	18487		0.63	3.0E-19	AF223467.1	NT	Homo sapiens NP008 protein (NP008) mRNA, complete cds
7612	20572		1.81	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9814	21137	34539	1.11	3.0E-19	X86686.1	NT	M.musculus mRNA for TPCR33 protein
12552	25275		16.28	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PB1) mRNA, complete cds
2587	15688	28588	27.04	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4474	17500		1.23	2.0E-19	A1311783.1	EST_HUMAN	qp91602.x1 NCL_CGAP_Kids Homo sapiens cDNA clone IMAGE:1915698 3' similar to TR:Q69386 Q69386 POL/ENV GENE :

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6172	19247	32480	0.61	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZ008 5'
7561	20524	33982	0.72	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8673	21641	35068	9.35	2.0E-19	AA012854.1	EST_HUMAN	ze34c08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10269	23194	36882	0.66	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
482	13555		2.11	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2174	15180	28211	1.68	1.0E-19	H30795.1	EST_HUMAN	ye79g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2729	15723		2.48	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2860	15920		4.26	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3412	18460	29381	1.18	1.0E-19	AA834987.1	EST_HUMAN	6149b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
5186	18195		0.9	1.0E-19	AW117377.1	EST_HUMAN	xc88h10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604739 3' similar to contains L1.b2 L1 L1 repetitive element;
6193	19287	32502	2.73	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6333	25895		0.63	1.0E-19	AA595527.1	EST_HUMAN	nh22d03.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.t1 L1
7890	20834	34213	0.96	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Naf/glucose cotransporter-related protein mRNA, complete cds
7890	20834	34214	0.89	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Naf/glucose cotransporter-related protein mRNA, complete cds
8085	25894		0.71	1.0E-19	AF200718.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
8793	21760	35182	1.72	1.0E-19	M64657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
9093	22059		0.274	1.0E-19	T98920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFFR repetitive element;
10106	23032		0.97	1.0E-19	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10547	23489	36964	27.33	1.0E-19	AW812259.1	EST_HUMAN	RCO-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
10557	23479	36974	2.1	1.0E-19	N44631.1	EST_HUMAN	y931e09.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:272872 5'
11809	24894		3.69	1.0E-19	AW023137.1	EST_HUMAN	df49h01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487000 5'
6803	19857	33143	2.45	8.0E-20		NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6803	19857	33144	2.45	8.0E-20		NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7761	20714	34084	1.31	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7761	20714	34085	1.31	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3289	16342	29263	0.72	7.0E-20	BF326455.1	EST_HUMAN	PM4-AN0095-050900-003-a04 AN0098 Homo sapiens cDNA
7188	18419	31220	5.58	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D092 5'
8841	21808	35227	9.11	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29 repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	21808	35228	9.11	7.0E-20	AA557657.1	EST_HUMAN	n146c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
12023	24899		8.31	7.0E-20	6912633	NT	MER29 repetitive element ;
3668	16613	29535	3.83	6.0E-20	P38188	SWISSPROT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
4301	17330	30210	2.98	6.0E-20	BE622434.1	EST_HUMAN	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4626	17647		1.05	5.0E-20	AV725123.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
7322	20293	33836	1.19	5.0E-20	AF075301.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HCTBT01 5'
8277	21246	34657	5	5.0E-20	W90525.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8277	21246	34658	5	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
8440	21408	34822	0.79	5.0E-20	BE165980.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
9187	22153	35582	1.24	5.0E-20	AB028174.1	NT	MR3-HT0487-180200-113-g01 HT0487 Homo sapiens cDNA
9187	22153	35583	1.24	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9800	21123		0.93	5.0E-20	O60809	SWISSPROT	Mus musculus MMAN-g mRNA, complete cds
1624	14657	27635	1.73	4.0E-20	AL163247.2	NT	HYPOTHETICAL PROTEIN DJ845O24.1
5732	18926		0.89	4.0E-20	Q99880	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
8258	21227		5.27	4.0E-20	AI874362.1	EST_HUMAN	HISTONE H2B C (H2B/C)
10865	23785	37286	1.9	4.0E-20	AW937469.1	EST_HUMAN	z64g03.x1 NCI_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2263396 3'
2149	15155	28181	0.91	3.0E-20	U03888.1	NT	QV3-DT0043-080200-080-c04 DT0043 Homo sapiens cDNA
4237	17266	30153	1.63	3.0E-20	P23273	SWISSPROT	Human BXP21 gene
4655	17676	30582	1.43	3.0E-20	AA037616.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 14
9287	22253		3.32	3.0E-20	D14547.1	NT	z63b12.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element ;
10684	23606	37099	0.68	3.0E-20	BF185264.1	EST_HUMAN	Human DNA, SINE repetitive element
11024	23989		1.59	3.0E-20	P11369	SWISSPROT	601843661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5'
11840	24723	38308	8.22	3.0E-20	A1284244.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11840	24723	38309	8.22	3.0E-20	A1284244.1	EST_HUMAN	qj70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
12329	25130	31849	4.15	3.0E-20	BE888422.1	EST_HUMAN	qj70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
831	13888		33.91	2.0E-20	AW303868.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3916522 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1113	14157	27107	3.88	2.0E-20	AA516335.1	EST_HUMAN	ng69h08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
1113	14157	27108	3.88	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ; ng69h08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
2828	13888		15.67	2.0E-20	AW303868.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ; x224e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS6_MOUSE
4983	17998	30886	4.76	2.0E-20	Q28983	SWISSPROT	P67461 40S RIBOSOMAL PROTEIN S5. ;
4983	17998	30887	4.78	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
8455	21424	34840	0.9	2.0E-20	AA309457.1	EST_HUMAN	ZONADHESIN PRECURSOR
8545	22508	35957	7.56	2.0E-20	D10083.1	NT	EST180328 Liver III Homo sapiens cDNA 5' end
9545	22508	35958	7.56	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12703	25714	31611	3.88	2.0E-20	H5537.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
2029	15822	28063	4.32	1.0E-20	AA281981.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
4467	17493	30380	1.04	1.0E-20	BF115158.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
7079	20100	33411	1.04	1.0E-20	AF049587.1	EST_HUMAN	MER19 repetitive element ;
9518	22481	35928	2.24	1.0E-20	11418481	NT	h184b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
11879	24761	38346	2.11	1.0E-20	AF223391.1	NT	repetitive element ;
12458	25215		3.08	1.0E-20	AA420453.1	EST_HUMAN	AF049587 Human activated dendritic cell mRNA Homo sapiens cDNA clone GAO5
2923	15981		1	9.0E-21	AJ003314.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
12176	25023		3.77	9.0E-21	AW898189.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9163	22129		1.13	8.0E-21	AW674891.1	EST_HUMAN	nc60g08.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1
11868	24748	38330	4.38	8.0E-21	AA809411.1	EST_HUMAN	repetitive element ;
12342	25140		2.94	8.0E-21	O21330	SWISSPROT	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1p12-BJ21
2082	15099	28115	1.59	7.0E-21	P18800	SWISSPROT	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
2082	15099	28116	1.59	7.0E-21	P15900	SWISSPROT	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
3716	16759	29671	0.63	7.0E-21	AL163300.2	NT	O95189 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
4283	17312		5.22	7.0E-21	AA046502.1	EST_HUMAN	cb71f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
6573	19633	32900	0.81	7.0E-21	AL163218.2	NT	ATP SYNTHASE A CHAIN (PROTEIN 6)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							Homo sapiens chromosome 21 segment HS21C100
							z167a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
							Homo sapiens chromosome 21 segment HS21C018

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8731	21699	35124	1.42	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
9024	21990	35411	11.21	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10472	23394	36891	0.82	7.0E-21	AW866922.1	EST_HUMAN	RCO-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
							zq73d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:396981 3' similar to gb.M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR 13 OFR repetitive element;
11054	24017	37540	1.69	7.0E-21	AA723404.1	EST_HUMAN	Homo sapiens PTD013 protein (PTD013), mRNA
11599	24537	38094	1.67	7.0E-21	7706668	NT	
4130	17163	30052	1.68	6.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
8491	22455		0.59	6.0E-21	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
4390	17418	30302	3.16	5.0E-21	BE968639.1	EST_HUMAN	60194987F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4839	17656	30753	6.18	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
8927	20151		0.92	5.0E-21	AW440864.1	EST_HUMAN	he03e10.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918154 3'
							7683d11.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.t1 OFR repetitive element;
7213	20236	33570	0.96	5.0E-21	BE866505.1	EST_HUMAN	
10939	23859	37374	0.43	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10939	23859	37375	0.43	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
12255	26081		5.38	5.0E-21	AA393574.1	EST_HUMAN	zt72c04.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
							cc86e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA; contains OFR.t1 OFR repetitive element;
1748	14777	27782	1.95	4.0E-21	AA970713.1	EST_HUMAN	Rattus norvegicus mRNA for rTIM, complete cds
7055	20077	33386	3.35	4.0E-21	AB019576.1	NT	
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10139	23065	36541	0.59	4.0E-21	U91328.1	NT	
1854	14880	27876	1.05	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.s1 Stratagene fetal refina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2282	15295	28319	1.48	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3096	16153	28086	4.17	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5577	18673	31636	0.93	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5577	18673	31637	0.93	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5828	18918		0.74	3.0E-21	AV661044.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLCGO10 3'
6303	18374		1.89	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
7271	20006	33306	7.18	3.0E-21	BF361033.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10051	22978	36445	0.77	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-H08 NN0063 Homo sapiens cDNA
147	13260		28.45	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
1219	14257		3.29	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-H06 BT0311 Homo sapiens cDNA
2646	15843	28687	2.26	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2646	15843	28688	2.26	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5561	18658	31604	1.54	2.0E-21	A624582.1	EST_HUMAN	Is30f03.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5556	18752	31918	0.81	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN;
5558	18752	31919	0.81	2.0E-21	AA027211.1	EST_HUMAN	z597a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
6149	18224	32454	0.61	2.0E-21	W44493.1	EST_HUMAN	z597a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8615	21593	34999	0.48	2.0E-21	AJ010770.1	NT	z228h02.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323667 5'
8706	21874	35039	0.64	2.0E-21	BE141785.1	EST_HUMAN	Homo sapiens hyperion gene, exons 1-50
9175	22141	35597	3.96	2.0E-21	AU136779.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
11647	24584	38152	1.72	2.0E-21	BE973828.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11647	24584	38153	1.72	2.0E-21	BE973829.1	EST_HUMAN	60188036F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12560	25278		17.51	2.0E-21	AF176815.1	NT	60188036F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1260	14295	27259	2.06	1.0E-21	AA557657.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1402	14435		7.17	1.0E-21	AI801284.1	EST_HUMAN	n46c04.s1 NCL_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
6634	19892		2.6	1.0E-21	AL079752.1	EST_HUMAN	MER29 repetitive element;
7398	20366	33719	4.83	1.0E-21	A1223104.1	EST_HUMAN	ar88d12.x1 Barstead colon HPLR17 Homo sapiens cDNA clone IMAGE:2152343 3'
10603	23525	37021	0.46	1.0E-21	AL163203.2	NT	DKFZp434I0830_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434I0830 5'
10603	23525	37022	0.46	1.0E-21	AL163203.2	NT	qq47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM
10949	23869		1.67	1.0E-21	5730038	NT	PROTEIN (HUMAN);
12932	25514		1.32	1.0E-21	AF046133.1	NT	Homo sapiens chromosome 21 segment HS21C003
4439	17485	30355	2.03	9.0E-22	A1702438.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8951	21917	35341	1.29	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C003
8951	21917	35342	1.29	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11144	24104	37631	3.13	9.0E-22	AV761874.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
949	14002		7.03	8.0E-22	BE144748.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSGCCG05 5'
8228	21197		3.82	8.0E-22	AA046502.1	EST_HUMAN	CM0-HT0179-281099-076-H05 HT0179 Homo sapiens cDNA
666	13731	26656	6.78	7.0E-22	AL163246.2	NT	z67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487868 5'
							Homo sapiens chromosome 21 segment HS21C046

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4312	17341	30221	2.36	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5076	18086	30966	0.97	7.0E-22	AB009681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
9038	22004		2.46	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9184	22150	35578	3.66	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#936208) Homo sapiens cDNA clone HFBCF07
9961	22888	36349	1.92	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TORBY7S3A2 to TORBY12S2 region
9584	21552		1.88	6.0E-22	AW029123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
5285	18291		0.72	5.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
6666	19723	32988	3.05	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10682	23604	37098	7.82	5.0E-22	U60822.1	NT	Human dyatrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12776	25413		2.76	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3650	16693		0.83	4.0E-22	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8442	21411	34824	0.42	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAUE12 5'
8766	28006		3.36	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11077	24039	37563	2.15	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
12938	25518		2.74	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
960	14013		1.06	3.0E-22	A1469678.1	EST_HUMAN	fm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L18593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.11 L1 repetitive element;
2576	15577	28586	2.15	3.0E-22	A1859038.1	EST_HUMAN	w166b04.x1 NCI_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
3686	16729		1.35	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21;
4838	17655	30752	2.88	3.0E-22	A1090125.1	EST_HUMAN	Human chromosome protein HMG1 related gene
8572	21540		1.21	3.0E-22	BE156813.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_Nb1PU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8577	21545	34964	3.4	3.0E-22	BE089841.1	EST_HUMAN	QV0-HT0368-090200-099-f12 HT0368 Homo sapiens cDNA
8703	21671	35093	0.77	3.0E-22	X60660.1	NT	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8703	21671	35094	0.77	3.0E-22	X60660.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
1970	14891		4.79	2.0E-22	N24942.1	EST_HUMAN	R. rattus RY2G5 mRNA for a potential ligand-binding protein
2528	15531	28552	1.82	2.0E-22	P24916	SWISSPROT	yx73d05.s1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:267369 3'
3431	16478	29398	4.78	2.0E-22	AW817794.1	EST_HUMAN	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
4253	17282	30163	1.26	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
5951	25648	32232	1.34	2.0E-22	W39456.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
6301	19372	32611	3.57	2.0E-22	BF092116.1	EST_HUMAN	zz20f01.f1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
							RCO-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10061	22988	36456	1.61	2.0E-22	A1276522.1	EST_HUMAN	q176h08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains
10156	23081	36558	0.65	2.0E-22	AA715315.1	EST_HUMAN	MER29.13 MER29 repetitive element;
10156	23081	36557	0.65	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
10991	23911	37426	0.55	2.0E-22	R15209.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
12054	24927	38525	1.58	2.0E-22	AW418960.1	EST_HUMAN	yf88c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:29740 5'
12139	25504	31705	1.92	2.0E-22	AL163280.2	NT	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
1896	14921	27917	1.78	1.0E-22	AW865517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2588	15589	28606	1.82	1.0E-22	U50871.1	NT	PM4-SN0020-010400-009-H02 SN0020 Homo sapiens cDNA
3422	16470	29390	1.49	1.0E-22	D14647.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
5295	18300		1.5	1.0E-22	AF003528.1	NT	Human DNA, SINE repetitive element
8016	20953	34347	0.95	1.0E-22	BE084867.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
10918	23838	37354	0.8	1.0E-22	A1365435.1	EST_HUMAN	MRO-BT0859-220200-002-H07 BT0859 Homo sapiens cDNA
10918	23838	37355	0.8	1.0E-22	A1365435.1	EST_HUMAN	q209b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.52
12991	25551		9.05	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element;
3585	16630	29548	0.73	8.0E-23	AF198349.1	NT	MER29 repetitive element;
3322	16373	37852	1.96	7.0E-23	AV647246.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
11376	24323		4.11	7.0E-23	5031952	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3447	16494		1.88	8.0E-23	AF198333.1	NT	AV647246 GLC Homo sapiens cDNA clone GLCAW C07 3'
4297	17326	30206	1.13	6.0E-23	AL163249.2	NT	Homo sapiens Not56 (D. melanogaster)-like protein (NOT56L) mRNA
12281	25099	31834	4.64	6.0E-23	AF224669.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
12281	25099	31835	4.64	6.0E-23	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C049
12480	25228	31795	3.03	6.0E-23	A1209130.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
5519	18618	31552	4	5.0E-23	U82671.2	NT	(UBE2D3) genes, complete cds
6367	25659	32679	3.55	5.0E-23	AF179818.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
7671	25659	32679	3.25	5.0E-23	AF179818.1	NT	qg59c03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to
							SW:MW10_MOUSE_P23249 PROTEIN MOV-10.;
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
							Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
							Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	19840	32908	1.07	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6580	19840	32907	1.07	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8171	21141	34547	4.18	3.0E-23	AA130165.1	EST_HUMAN	z35g08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to
9604	22908	30059	2.74	3.0E-23	Z70684.1	NT	contains MER29.12 MER29 repetitive element ;
9604	22908	30059	2.74	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
10880	23802		1.27	3.0E-23	AW897927.1	EST_HUMAN	Human endogenous retroviral element HC2
667	13732	26657	3.75	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1145	15817		3.02	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2807	15799	28817	2.08	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2807	15799	28818	2.08	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3384	16433		1.5	2.0E-23	AI201458.1	EST_HUMAN	q873f11.x1 NCLCGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TRQ13537 Q13537
3729	16771		2.97	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
4001	17040	29947	2.59	2.0E-23	H59931.1	EST_HUMAN	MR3-H70487-150200-113-g01 HT0487 Homo sapiens cDNA
4001	17040	29948	2.59	2.0E-23	H59931.1	EST_HUMAN	yt16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
5062	18072	30952	8.49	2.0E-23	D14547.1	NT	yt16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
						NT	Human DNA, SINE repetitive element
8205	21175		4.26	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
8195	22161	35589	1.12	2.0E-23	AL163303.2	NT	polypeptide 5 (CYP3A5) gene, partial cds
12262	25086		3.91	2.0E-23	M32658.1	NT	Homo sapiens chromosome 21 segment HS21C103
12787	25419		2.55	2.0E-23	AF006860.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
4558	17581	30472	1.44	1.0E-23	AL163252.2	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
4799	17816		4.76	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C052
6882	19934		3.11	1.0E-23	BE378471.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
8899	21867	35080	4.73	1.0E-23	AA448087.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
						EST_HUMAN	zw82c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782688 5' similar to contains PTR5.12
						EST_HUMAN	PTR5 repetitive element ;
554	13624		3.05	9.0E-24	AA863213.1	EST_HUMAN	ab75a03.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to
4678	17699	30586	1.15	8.0E-24	P23269	SWISSPROT	TR/E19822 E19822 CA PROTEIN. ;
4678	17699	30587	1.15	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
6891	19851	32922	1.34	8.0E-24		NT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
8155	21093	34492	0.77	8.0E-24	1142027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
					1142027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3888	16928		1.36	7.0E-24	AW937854.1	EST_HUMAN	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
707	13769		2.31	6.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
839	13696	26851	15.66	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3994	17034	26942	8.31	5.0E-24	AJ229043.1	NT	Homo sapiens chromosome 21 segment HS21C049
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8034	20971	34385	1.34	5.0E-24	AF223391.1	NT	nm31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085629 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN;
6039	19121	32326	3.63	4.0E-24	AA594178.1	EST_HUMAN	
9029	21995	35415	1.29	4.0E-24	AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-008 ST0197 Homo sapiens cDNA
11514	24455	38005	1.52	4.0E-24	BE544822.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464498 5'
12644	25328	31790	5.58	4.0E-24	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12807	25713	31610	9.62	4.0E-24	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
12876	25509	31708	1.88	4.0E-24	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSET1), mRNA
7285	20062	33368	0.6	3.0E-24	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
							Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
8766	21733		2.89	3.0E-24	AW614871.1	EST_HUMAN	h68c08.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2867960 3' similar to contains MER29.b2 MER29 repetitive element;
8822	21789		1.25	3.0E-24	AW962076.1	EST_HUMAN	EST374149 MAGG resequences, MAGG Homo sapiens cDNA
9820	22869	36126	4.11	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12715	25369	31772	2.16	3.0E-24	BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
2354	15363	28385	2.8	2.0E-24	AA167539.1	EST_HUMAN	zp11f09.r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
3812	16852		0.89	2.0E-24	AW808189.1	EST_HUMAN	RC3-NK0068-090500-021-b03 NK0068 Homo sapiens cDNA
7583	26001		0.61	2.0E-24	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7710	20672	34039	1.12	2.0E-24	AF086824.1	NT	Mus musculus thymocyte-interacting cytochrome kinase (Crik) mRNA, complete cds
7725	20677	34042	0.55	2.0E-24	AL003536.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1p12-5H13
8092	22058	35484	3.09	2.0E-24	AL119158.1	EST_HUMAN	DKFZp761L1712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9130	22096		0.96	2.0E-24	H69214.1	EST_HUMAN	Yr82b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains
10213	23138	36626	0.98	2.0E-24	A1521759.1	EST_HUMAN	MER28 repetitive element ;
10213	23138	36627	0.98	2.0E-24	A1521759.1	EST_HUMAN	U77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12568	25947		10.03	2.0E-24	M28877.1	NT	U77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
1785	14736	27717	2.63	1.0E-24	7706340	NT	Human O family dispersed repeat element
2681	15677		1.52	1.0E-24	AW820194.1	EST_HUMAN	Homo sapiens CGI-127 protein (LOC61646), mRNA
3033	16091	28009	0.78	1.0E-24	D86423.1	NT	QV0-ST0284-100400-185-c10 ST0284 Homo sapiens cDNA
4289	17328		2	1.0E-24	AF143313.1	NT	Mus musculus mRNA for HGT keratin, partial cds
6541	19603	32865	0.68	1.0E-24	7106336	NT	Homo sapiens PTEN (PTEN) gene, exon 2
7796	20748	34123	3.98	1.0E-24	AL163303.2	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
8002	20941	34334	0.68	1.0E-24	BE144526.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
8276	21245	34656	1.81	1.0E-24	AW901184.1	EST_HUMAN	MRO-HT0166-271199-005-d09 HT0166 Homo sapiens cDNA
8625	19883	32981	0.52	9.0E-25	11420402	NT	CMO-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA
12008	24885	38480	1.53	9.0E-25	7706707	NT	Homo sapiens helix-like protein NHL (LOC51750), mRNA
							Homo sapiens putative secreted protein (SIG1), mRNA
5031	18045	30927	2.85	7.0E-25	AA483044.1	EST_HUMAN	ne92a10.s1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8561	21529	34949	6.83	7.0E-25	AA468046.1	EST_HUMAN	MER1 repetitive element ;
12012	24889	38496	3.24	7.0E-25	AA583540.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
7184	18415		4.41	8.0E-25	W87623.1	EST_HUMAN	repetitive element ;
7992	20931	34326	10.26	8.0E-25	7305360	NT	nt25h08.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914943 similar to SW.R14A_YEAST
1659	14591	27687	1.67	5.0E-25	AW850271.1	EST_HUMAN	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
5183	18192		0.92	5.0E-25	AA694228.1	EST_HUMAN	zh65h07.r1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
11645	24892	38150	3.16	5.0E-25	AW979107.1	EST_HUMAN	Mus musculus obogelin (Obog), mRNA
1441	14474	27451	2.3	4.0E-25	T98107.1	EST_HUMAN	IL3-CT0219-161199-031-D04 CT0219 Homo sapiens cDNA
3413	16461		2.68	4.0E-25	AW887671.1	EST_HUMAN	ou48f01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1631161 3' similar to contains Alu repetitive
3923	16983	28876	0.93	4.0E-25	AF000368.1	NT	element ;
4345	17372		3.13	4.0E-25	BE170957.1	EST_HUMAN	ESTT391217 MAGE resequences, MAGP Homo sapiens cDNA
3331	16382	28303	2.77	3.0E-25	8923321	NT	ye55f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3331	16382	28304	2.77	3.0E-25	8923321	NT	PM8-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
5877	16966	32157	0.64	3.0E-25	U53212.1	NT	PM8-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
							Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
							QV3-HT0543-140400-149-g11 HT0543 Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
							Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
							Human degenerate channel MDEG mRNA, partial cds

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6769	19824	33107	0.66	3.0E-25	AA803590.1	EST_HUMAN	np27b02.s1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M81866 ZINC FINGER PROTEIN 85 (HUMAN);
6860	21648	35070	4.08	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1350	14385	27354	2.6	2.0E-25	5032168	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2317	15328	26351	7.52	2.0E-25	BE888016.1	EST_HUMAN	601611530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2842	15551	28572	3.35	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4218	17247	30131	1.98	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4218	17247	30132	1.98	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
10123	23049	36528	2.03	2.0E-25	AL449573.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S16
364	13450	26378	1.4	1.0E-25	AL040229.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
1253	14289		1.34	1.0E-25	9835487	NT	DKFZp434H0313_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
2441	15448	28466	1.04	1.0E-25	Q06055	SWISSPROT	Human endogenous retrovirus, complete genome
4895	17912	30802	2.33	1.0E-25	BE162737.1	EST_HUMAN	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
6719	19775		0.83	1.0E-25	AA189080.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
6965	25676	33516	3.22	1.0E-25	AA582690.1	EST_HUMAN	z44506.e1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
8246	21215	34623	4.36	1.0E-25	AA709079.1	EST_HUMAN	nt54h11.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
9904	22856	36317	0.69	1.0E-25	X60660.1	NT	zf06g04.e1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR6.13 PTR5 repetitive element ;
9904	22856	36318	0.69	1.0E-25	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
11316	24266	37794	2.91	1.0E-25	U93163.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
12278	25097	38180	1.47	1.0E-25	D14547.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12278	25097	38181	1.47	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
13053	26591		1.83	1.0E-25	X51755.1	NT	Human DNA, SINE repetitive element
2491	15494	26519	1.47	9.0E-26	AL163218.2	NT	Human lambda-immunoglobulin constant region complex (germline)
5778	18870		1.56	8.0E-26	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C018
1590	14613	27595	2.88	7.0E-26	AF003528.1	NT	Homo sapiens chromosome 21 segment HS21C018
4005	17044	29852	1.21	7.0E-26	X89211.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4186	17217	30103	1.69	7.0E-26	AW340153.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
5721	18816	31894	0.72	7.0E-26	AL163202.2	NT	h02e12.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2508366 3'
11978	24855		8.08	7.0E-26	AA115895.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
							zr30d08.r1 Stralagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2234	15248	28272	2.28	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3357	16407	29329	1.03	6.0E-26	AA206131.1	EST_HUMAN	zq52h04.r1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:545271 5'
11990	24867	38462	1.91	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1181	14222	27178	1.86	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
1181	14222	27178	1.86	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
1546	14579		0.98	4.0E-26	AA329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' and
9787	22708		3.77	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
11022	23887	37514	2.93	4.0E-26	BE266187.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:548943 5'
1773	14802	27767	2.15	3.0E-26	D14547.1	NT	z130d08.r1 Stralagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5'
2019	15040	28051	1.27	3.0E-26	AL048555.2	EST_HUMAN	similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
2047	15066		3.59	3.0E-26	AA115995.1	EST_HUMAN	z030f10.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3791	16832	29738	1.12	3.0E-26	AA152464.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
3791	16832	29739	1.12	3.0E-26	AA152464.1	EST_HUMAN	z030f10.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
7096	20030	33334	6.22	3.0E-26	BF245458.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11894	24776	38361	2.03	3.0E-26	AW875651.1	EST_HUMAN	601864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
11894	24775	38362	2.03	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11928	24809	38404	4.91	3.0E-26	AA583173.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
13101	25824	31678	1.37	3.0E-26	AF165520.1	NT	nm37d05.s1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:1085057 3' similar to contains OFR.t1
682	13745	26872	10.08	2.0E-26	AL163282.2	NT	OFR repetitive element ;
1884	14909		3.56	2.0E-26	AL038099.2	EST_HUMAN	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
3245	16300	29225	4.92	2.0E-26	X86694.1	NT	Homo sapiens chromosome 21 segment HS21C082
11105	24065		2.38	2.0E-26	D87675.1	NT	Homo sapiens chromosome 21 segment HS21C082
11553	24493	38049	2.55	2.0E-26	AI801412.1	EST_HUMAN	DKFZp566L171_s1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566L171 3'
11748	24633		1.76	2.0E-26	AF055066.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
12097	24968	38565	1.64	2.0E-26	M32788.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12398	25166		1.7	2.0E-26	AB037859.1	NT	to89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element ;
						NT	Human endogenous retroviral element S71
						NT	Homo sapiens MHC class I region
						NT	Homo sapiens mRNA for KIAA1438 protein, partial cds

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137	13242	28172	37.48	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2063	15081	28100	1.33	1.0E-26	AL038363.2	EST_HUMAN	DKFZp434H1910_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H1910 5'
2697	15693		11.4	1.0E-26	AF261085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
7016	20142		2.79	1.0E-26	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
11239	24192		2.12	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146_r1_566 (synonym: hifd2) Homo sapiens cDNA clone DKFZp566C2146 5'
12630	25966		2.65	1.0E-26	H55083.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
7837	20784		1.24	9.0E-27	BF371227.1	EST_HUMAN	RC8-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9658	22815		4.04	9.0E-27	U93183.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12142	25006		5.95	9.0E-27	BF445556.1	EST_HUMAN	nas03c07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.t1 OFR repetitive element;
11	13131	26029	4.71	8.0E-27	AI831482.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
559	13629		4.61	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1414	14447	27419	30.06	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1414	14447	27420	30.06	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2177	15192	28214	1.1	8.0E-27	AW884778.1	EST_HUMAN	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
3199	18254	29174	1.17	8.0E-27	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3364	18414	28339	0.84	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5778	18871	32053	0.97	8.0E-27	AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB08 5'
7170	18401		2.12	8.0E-27	BE926660.1	EST_HUMAN	MR4-BT0398-250800-204-d08 BT0398 Homo sapiens cDNA
7248	19983	33280	2.41	8.0E-27	N84970.1	EST_HUMAN	J1761F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
9564	22528	35975	1.41	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
9564	22526	35976	1.41	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
684	13747		1.65	7.0E-27	Z70664.1	NT	Human endogenous retroviral element HC2
5126	18135		2.05	7.0E-27	AW629172.1	EST_HUMAN	h151h12.x1 Soares NFL.T.GBC.S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN.;
9209	22175		0.98	7.0E-27	D86984.1	NT	Human mRNA for KIAA231 gene, partial cds
11101	24061		3.24	7.0E-27	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12759	25402		1.54	7.0E-27	AV723965.1	EST_HUMAN	AV723965 HTB Homo sapiens cDNA clone HTBAHE02 5'

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11080	24042	37595	10.71	8.0E-27	M26897.1	NT	Human nuclear protein (B23) mRNA, complete cds
8055	20992		0.79	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10597	23519	37010	3.37	5.0E-27	BF666914.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
10597	23519	37011	3.37	5.0E-27	BF666914.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6908	19960	33256	1.72	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
8271	21240		1.22	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8316	21285		1.25	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10101	23027	36504	0.72	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11928	24810	38405	1.98	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2057	16076	28036	4.38	3.0E-27	X60668.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4300	17329	30209	1.08	3.0E-27	BE071924.1	EST_HUMAN	PMO-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5419	18522	31400	5.68	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
8089	21025	34424	0.67	3.0E-27	BE870351.1	EST_HUMAN	7e3f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9660	22817	36271	4.46	3.0E-27	BF035327.1	EST_HUMAN	60148831F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
43	13163	26066	8.25	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1911	14935		24.32	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.a1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3126	16183		10.81	2.0E-27	AW629172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
3238	16293	28215	1.61	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3238	16293	28216	1.61	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6833	19886	33179	0.72	2.0E-27	H02655.1	EST_HUMAN	y96e01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8427	21396	34807	1.44	2.0E-27	A1868347.1	EST_HUMAN	SP:HMGC_MOUSE Q02591 HOMEBOX PROTEIN ;
9624	22558		2.61	2.0E-27	AA551527.1	EST_HUMAN	w128g07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
10151	23076	36552	0.78	2.0E-27	X60658.1	NT	repetitive element ;
10395	23317	36797	1.32	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
10395	23317	36798	1.32	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stragene (cat#836206) Homo sapiens cDNA clone HFBCF07
11302	24252	37778	2.97	2.0E-27	AU121685.1	EST_HUMAN	EST00738 Fetal brain, Stragene (cat#836206) Homo sapiens cDNA clone HFBCF07
11816	14935		19.93	2.0E-27	AA565345.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000745 5'
							nk01b10.a1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
436	13510		2.26	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
998	14049	27002	1.58	1.0E-27	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1707	14738	27720	0.95	1.0E-27	4827059	NT	Homo sapiens xylulokinase (H. Influenzae) homolog (XYLB) mRNA
4108	17142		1.08	1.0E-27	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3
6894	19751	33028	5.21	1.0E-27	6005855	NT	MER29 repetitive element;
7054	20076	33384	2.01	1.0E-27	F30158.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7054	20076	33385	2.01	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8957	21923	35351	0.71	1.0E-27	AB007623.1	NT	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
9337	22302		2.33	1.0E-27	BE079780.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
10080	23007	36478	2.7	1.0E-27	DB7449.1	NT	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
12016	24893	38490	3.73	1.0E-27	AF111093.1	NT	Human mRNA for KIAA0280 gene, partial cds
143	13245		2.16	9.0E-28	BE348399.1	EST_HUMAN	Bos taurus latrophilin 3 splice variant bbaa mRNA, complete cds
311	13403	26329	2.64	9.0E-28	AU128260.1	EST_HUMAN	hw17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
4817	17834	30732	1.08	9.0E-28	P50447	SWISSPROT	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ;
12222	25059		3.71	9.0E-28	BF377859.1	EST_HUMAN	AU128260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
12553	25817		1.9	8.0E-28	AW157571.1	EST_HUMAN	ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1-
1185	14226	27182	8.98	7.0E-28	AU142750.1	EST_HUMAN	ANTIPROTEINASE)
11520	24461	38012	2.43	7.0E-28	11417866	NT	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12181	25029		2.98	7.0E-28	AV735348.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
9271	22237		1.09	6.0E-28	AF016052.1	NT	TR:Q0302 O60302 KIAA0555 PROTEIN. ;contains element MER22 repetitive element ;
12806	25433		3.82	6.0E-28	AA604562.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
318	13410		3.1	5.0E-28	AJ921003.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
4035	17073	29973	1.52	5.0E-28	R78762.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
2633	15632	28657	1.48	4.0E-28	AW195086.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF181 (ZNF181) gene, complete cds
2989	16047	28987	1.18	4.0E-28	4505316	NT	aa60e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
3125	16182	29092	1.93	4.0E-28	BE409100.1	EST_HUMAN	repetitive element;contains element PTR5 repetitive element ;
							wc18c07.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2455592 3' similar to contains THR.b1
							THR repetitive element ;
							y89f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
							kr33c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895504 3' similar to SW:GG95_HUMAN
							Q08379 GOLGIN-95. ;
							Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
							601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7551	20514	33872	2.45	4.0E-28	A1198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
11213	24166		3.51	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
11349	24289		38.65	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
11364	20514	33872	3.87	4.0E-28	A1198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12589	25301		1.86	4.0E-28	AW854244.1	EST_HUMAN	RC3-C10254-240400-210-f12 C10254 Homo sapiens cDNA
1288	14923		2.61	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
9179	22145	35572	1.94	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-f09 HT0713 Homo sapiens cDNA
11282	24232	37758	2.14	3.0E-28	U53598.1	NT	Homo sapiens MHC class 1 region
12628	25315		2.92	3.0E-28	A1831991.1	EST_HUMAN	wj98f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element;
89	13205	26129	11.64	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1047	14093	27045	4.14	2.0E-28	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
1169	14210	27164	12.37	2.0E-28	Y11107.3	NT	Homo sapiens ITG84 gene for integrin beta 4 subunit, exons 3-41
2485	15489	28513	2.27	2.0E-28	A1348634.1	EST_HUMAN	qc35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
3373	16423	29348	0.76	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8440	19505	32756	1.48	2.0E-28	BF224402.1	EST_HUMAN	hr76c03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element;
8464	19520		6.46	2.0E-28	BF12805.1	EST_HUMAN	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8378	21348	34760	0.76	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9943	22870		8.68	2.0E-28	AW972305.1	EST_HUMAN	EST384394 MAGe resequences, MAGL Homo sapiens cDNA
11636	24817	38414	1.92	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12609	26308		2.06	2.0E-28	H06376.1	EST_HUMAN	yf79c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
1474	14507	27481	3.15	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2229	15243	28268	1.84	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-350-503 BT0821 Homo sapiens cDNA
2692	15888	28705	0.92	1.0E-28	AF000905.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
4985	18000	30889	0.64	1.0E-28	AV732194.1	EST_HUMAN	AV732194 HTF Homo sapiens cDNA clone HTFB1H05 5'
8193	21163		8.03	1.0E-28	11429385	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
8352	21321		3.37	1.0E-28	8922703	NT	Homo sapiens hypothetical protein FLJ10988 (FLJ10988), mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9633	22577	36027	4.47	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to
10235	23160	36648	6.47	1.0E-28	4759431	NT	retroviral LTR
10235	23160	36649	6.47	1.0E-28	4759431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
12186	25033		4.36	1.0E-28	AA054182.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
12931	25716		2.58	1.0E-28	AL163247.2	NT	Z51c01.F1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
13037	25918	31302	3.46	9.0E-29	AW663987.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
12713	26367		3.12	8.0E-29	Q00130	EST_HUMAN	h176906.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
1606	14638	27615	1.04	7.0E-29	AW966447.1	EST_HUMAN	HYPOTHETICAL GENE 50 PROTEIN
3564	16610		0.9	7.0E-29	BE254708.1	EST_HUMAN	EST378521 IMAGE resequences, MAGI Homo sapiens cDNA
13086	25616		9.37	7.0E-29	AJ132352.1	NT	601114990F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355367 5'
597	13664	26578	6.67	8.0E-29	A0936748.1	EST_HUMAN	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
12489	25234		8.12	6.0E-29	BE940438.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR.O15475
12574	25284		1.97	6.0E-29	BF668097.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN , contains LTR7 b1 LTR7 repetitive element ;
5033	18047		1.34	5.0E-29	AL163203.2	NT	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
9083	22049		8.5	5.0E-29	AW897541.1	EST_HUMAN	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
3246	16301		1.33	4.0E-29	A1752387.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
6125	19203		5.91	4.0E-29	BE164930.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
8417	21386	34794	0.92	4.0E-29	A1678101.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8417	21386	34795	0.92	4.0E-29	A1678101.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
9097	22063	35488	2.97	4.0E-29	J04998.1	NT	w335g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
2379	15387	28411	0.94	3.0E-29	U67847.1	NT	MER28.12 MER29 repetitive element ;
4444	17470	30359	1.61	3.0E-29	AB042297.1	NT	w335g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
4764	17764	30680	0.94	3.0E-29	BF333236.1	EST_HUMAN	MER28.12 MER29 repetitive element ;
6040	19122	32327	0.77	3.0E-29	BE314018.1	EST_HUMAN	Human 90 kD heat shock protein gene, complete cds
9085	22051	35473	2.19	3.0E-29	D33044.1	NT	Human beta-galactosidase alpha2,6-sialyltransferase (SIAT1) mRNA, exon U
9655	22598	36047	1.97	3.0E-29	AW303317.1	EST_HUMAN	Homo sapiens P.TS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds
9889	22842		2.2	3.0E-29	AL163246.2	NT	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
							601152657F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3508527 5'
							Human gene for Ah-receptor, exon 7-9
							xv17603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
							repetitive element; contains MER19.12 MER19 repetitive element ;
							Homo sapiens chromosome 21 segment HS21C048

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10318	23242		0.73	3.0E-29	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12386	26163		2.34	3.0E-29	D63882.1	NT	MER29 repetitive element;
493	13566	20487	1.68	2.0E-29	AF084869.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
493	13566	26488	1.68	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
1535	14568	27538	7.19	2.0E-29	AI963604.1	EST_HUMAN	wr65d10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546
1535	14568	27539	7.19	2.0E-29	AI963604.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN;
4308	17337	30215	2.4	2.0E-29	AI963604.1	EST_HUMAN	wr65d10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546
5251	18259	31128	0.99	2.0E-29	O54827	SWISSPROT	HERV-E ENVELOPE GLYCOPROTEIN;
5924	19010	32203	1.08	2.0E-29	AI082459.1	EST_HUMAN	POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE VA
6304	19375	32813	1.22	2.0E-29	AI808418.1	EST_HUMAN	os71e04.x1 NCL_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.L2 L1
7808	19375	32613	1.18	2.0E-29	AI808418.1	EST_HUMAN	repetitive element;
8309	21278	34690	1.04	2.0E-29	BE887157.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains
8924	21890	36317	0.63	2.0E-29	10567821	NT	element MER6 repetitive element;
8924	21890	36318	0.63	2.0E-29	10567821	NT	element MER6 repetitive element;
8966	22802	36255	3.5	2.0E-29	AL163248.2	NT	601442206F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5'
8966	22802	36256	3.6	2.0E-29	AL163248.2	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
10599	23521	37013	3.27	2.0E-29	AL163248.2	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
10599	23521	37014	3.27	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11806	24692		4.13	2.0E-29	11425108	NT	Homo sapiens chromosome 21 segment HS21C048
11844	24727		2.03	2.0E-29	AW980701.1	EST_HUMAN	Homo sapiens splicing factor similar to dnuJ (SPF31), mRNA
8144	22110	35536	10.17	1.0E-29	AW983880.1	EST_HUMAN	QV0-O10032-080300-155-d01 OT0032 Homo sapiens cDNA
10986	23906	37420	0.59	1.0E-29	X60658.1	NT	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6734	19790	33070	3.26	9.0E-30	AA761215.1	EST_HUMAN	R.rattus RYA3 mRNA for a potential ligand-binding protein
12263	25087		2.14	9.0E-30	11422745	NT	nz20c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1
6452	19517		9.62	8.0E-30	F09688.1	EST_HUMAN	MER4 repetitive element;
8613	21591	34997	3.18	8.0E-30	AA393873.1	EST_HUMAN	Homo sapiens zincfinger regulated transporter-like (ZIFTL), mRNA
9031	21997	35416	3.9	8.0E-30	AI557072.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1518	14550		1.02	7.0E-30	BE081133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1571	14604		1.4	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
1788	14817	27802	1.8	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3204	16259	29178	2.51	6.0E-30	BE008028.1	EST_HUMAN	QV0-BN0147-230400-214-f12 BN0147 Homo sapiens cDNA
4791	16259	29178	1.02	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-230400-214-f12 BN0147 Homo sapiens cDNA
10905	23826	37337	0.74	6.0E-30	AF177227.1	NT	Homo sapiens CTL tumor antigen se20-10 mRNA, partial cds
13054	14804		4.35	6.0E-30	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4041	17079	29978	32.98	5.0E-30	AI399992.1	EST_HUMAN	ig92g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116278 3' similar to contains Alu repetitive element
5310	25746		4.98	5.0E-30	U87631.1	NT	Human aconitate hydratase (ACO2) gene, exon 7
11233	24186		2.21	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11489	24432	37981	2.03	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11489	24432	37982	2.03	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2153	15169	28185	1.79	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2153	15169	28186	1.79	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
7035	18367	31254	0.55	4.0E-30	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
9256	22222	35652	2.5	4.0E-30	AW812488.1	EST_HUMAN	ENDONUCLEASE
1154	14196		4.51	3.0E-30	AI338561.1	EST_HUMAN	CM1-ST0181-091189-035-f08 ST0181 Homo sapiens cDNA
3770	16812	29721	1.03	3.0E-30	AF128993.1	NT	qq93c05.x1 Soares total Tetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element ;
7470	20436	33793	0.5	3.0E-30	T18862.1	EST_HUMAN	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
8284	21253		0.52	3.0E-30	AF078779.1	NT	b120561 Testis 1 Homo sapiens cDNA clone b12056
8631	21798		0.44	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10900	23721	37224	2.18	3.0E-30	BE350127.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10932	23852	37366	0.52	3.0E-30	AB032969.1	NT	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
10932	23852	37367	0.52	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11541	24482	38034	5.69	3.0E-30	P34056	SWISSPROT	Homo sapiens mRNA for KIAA1143 protein, partial cds
676	13739	26666	1.57	2.0E-30	AW887315.1	EST_HUMAN	TRANSCRIPTION FACTOR AP-2
1086	14130		3.03	2.0E-30	F08688.1	EST_HUMAN	CMO-CT0307-310100-158-H03 CT0307 Homo sapiens cDNA
1475	14508	27482	5.36	2.0E-30	BE175877.1	EST_HUMAN	HS223F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
2727	15721	28738	11.19	2.0E-30	BE765232.1	EST_HUMAN	RC8-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2930	15988	28909	6.11	2.0E-30	AF114158.1	NT	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
							Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3803	16943	29751	2.1	2.0E-30	AW206581.1	EST_HUMAN	UIH-B11-af-c-12-O-JL1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4812	17829	30726	1.76	2.0E-30	BE298945.1	EST_HUMAN	60111860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4812	17829	30727	1.76	2.0E-30	BE298945.1	EST_HUMAN	60111860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6922	18972	33269	0.71	2.0E-30	BF306337.1	EST_HUMAN	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138993 5'
8820	21787	35211	0.69	2.0E-30	AA019103.1	EST_HUMAN	ze58c10.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5'
8882	21849	35270	7.02	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (Tfujiwara) Homo sapiens cDNA clone GEN:570C01 5'
8982	21948	35371	3.99	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8982	21948	35372	3.99	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
10356	23280	36756	3.88	2.0E-30	AW971588.1	EST_HUMAN	EST363657 MAGC resequences, MAGL Homo sapiens cDNA
10442	23364	36854	8.55	2.0E-30	AW470701.1	EST_HUMAN	he33d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3 THR repetitive element ;
288	13381	26309	19.55	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (Tfujiwara) Homo sapiens cDNA clone IMAGE:2910891 3' similar to contains Homo sapiens chromosome 21 segment HS21C003
539	13610	26529	7.04	1.0E-30	AW468897.1	EST_HUMAN	MER1.13 MER1 MER1 repetitive element ;
717	13779	26713	1.23	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2222	15236	28260	3.82	1.0E-30	AA664377.1	EST_HUMAN	ac77b08.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:8685599 3'
2469	15473	28496	2.39	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4157891 5'
3067	16124	28037	1.12	1.0E-30	AA316045.1	EST_HUMAN	EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
7995	20934	34328	2.08	1.0E-30	BF183230.1	EST_HUMAN	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
12862	25841		11.93	1.0E-30	H55593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22.728 5'
8667	21635	35056	0.92	9.0E-31	R18214.1	EST_HUMAN	yf99b08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8667	21635	35057	0.92	9.0E-31	R18214.1	EST_HUMAN	yf99b08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8971	21937		1.79	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
8973	21839	35364	0.49	9.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
1078	14123	27076	1.82	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2423	15430		5.96	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4955	17970	30860	1.12	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
4955	17970	30861	1.12	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
712	13774		1.99	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2676	15672	28691	2.38	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2678	15672	28692	2.38	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8744	21712	35133	0.99	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8744	21712	35134	0.99	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9621	22565		0.92	7.0E-31	BE408911.1	EST_HUMAN	601304726F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12711	25366	31771	5.66	7.0E-31	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3691	18734		3.06	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8493	21461		7.57	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region
8874	21842	35087	0.7	6.0E-31	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146255 3' similar to contains MER29.b3
11080	24050	37573	1.86	6.0E-31	AU119105.1	EST_HUMAN	MER29 repetitive element;
12325	25127	31848	2.27	6.0E-31	AW372868.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12458	25784		2.08	6.0E-31	BE894488.1	EST_HUMAN	RC5-BT0377-091299-031-D12 B10377 Homo sapiens cDNA
194	13295	26222	2.83	5.0E-31	M60694.1	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
194	13295	26223	2.83	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8768	21755		1.46	5.0E-31	BF056540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
598	13665		3.45	4.0E-31	AJ271735.1	NT	7K06104.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT. contains L1.1 L1 repetitive element;
						NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1615	14647	27622	1.01	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
1834	14661		2.09	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2800	15792		1.98	4.0E-31	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10900	23820	37329	0.43	4.0E-31	AF084464.1	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
2603	15603	28625	0.98	3.0E-31	6005871	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
7562	20525	33883	6.73	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8) mRNA
7736	20691	34055	1.28	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8501	21469		2.35	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
9939	22866	36328	4.66	3.0E-31	D14923.1	NT	Horse mRNA for ferritin L-chain, complete cds
10961	23881	37394	0.52	3.0E-31	AA421242.1	EST_HUMAN	zu06a04.r1 Soares_NHT Homo sapiens cDNA clone IMAGE:731047 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10995	23961	37486	3.17	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11487	24430		6.84	3.0E-31	BF035327.1	EST_HUMAN	801458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1932	14956	27853	1.33	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-403 LT0051 Homo sapiens cDNA
2224	15238	28262	0.98	2.0E-31	A1393386.1	EST_HUMAN	ig44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2347	15356	28379	2.53	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2447	15452	28473	5.67	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
5347	18452	31323	0.72	2.0E-31	AW444498.1	EST_HUMAN	THR.L2 THIR repetitive element;
5798	18890	32072	2.86	2.0E-31	BE350127.1	EST_HUMAN	UI-H-B13-akb-f09-0-UI.s1 NCL CGAP_Sub55 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
9431	22395		2.71	2.0E-31	AA877764.1	EST_HUMAN	MER29 repetitive element;
9562	22824	35973	4.13	2.0E-31	7661535	NT	mer37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
10266	23191	36677	1.13	2.0E-31	AV710948.1	EST_HUMAN	homo sapiens B9 protein (B9), mRNA
10268	23191	36678	1.13	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuaALB07 5'
10435	23357	36844	2.57	2.0E-31	BE408611.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuaALB07 5'
10435	23357	36845	2.57	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12427	25195		1.91	2.0E-31	AF148512.1	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12566	25987		3.94	2.0E-31	A1114527.1	EST_HUMAN	Homo sapiens hexokinase II gene, promoter region
17	13137	26036	11.03	1.0E-31	U93163.1	NT	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
1671	14703	27678	3.34	1.0E-31	O95371	SWISSPROT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1671	14703	27679	3.34	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1671	14703	27680	3.34	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4666	17987	30571	1.35	1.0E-31	AL134376.1	EST_HUMAN	OLFACTORY RECEPTOR 2C1
4666	17987	30572	1.35	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
5365	18470	31341	3.75	1.0E-31	AW391679.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
6266	19329	32556	2.31	1.0E-31	AF048727.1	NT	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
7506	20471	33831	1.08	1.0E-31	AF126145.1	NT	Homo sapiens minisatellite ceb1 repeat region
8132	21069	34488	0.76	1.0E-31	BE972818.1	EST_HUMAN	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
10596	23518	37009	0.68	1.0E-31	U93163.1	NT	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
							Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11261	24213	37737	4.86	1.0E-31	A1086434.1	EST_HUMAN	q121h03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRAXIN.
12103	24974	38571	1.5	1.0E-31	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HV8 rellc, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBU1S1, TCRBU1S2.>
6795	19849	33134	2.13	9.0E-32	AV723978.1	EST_HUMAN	AV723978 HTB Homo sapiens cDNA clone HTBAA001 5'
7598	20559	33919	0.53	9.0E-32	L31770.1	NT	Bos taurus vacuolar H+-ATPase subunit mRNA, complete cds
7848	20795		0.85	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2090	15107	28126	3.05	8.0E-32	A1056770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:1676384 3'
5559	18656	31601	0.89	8.0E-32	AW987214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA
4896	17913	30803	1.16	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
12405	25178		7.68	7.0E-32	X17283.1	NT	Human chromosome 22 Immunoglobulin V(K) gene, part. with 5' breakpoint between orphon and neighbouring non-amplified region
2742	15736	28752	1.2	6.0E-32	A1478104.1	EST_HUMAN	hm34e10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994 3' similar to contains MER29.13 MER29 repetitive element.
7691	20552		1.29	6.0E-32	BE898016.1	EST_HUMAN	601511330F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
1035	14081	27032	17.73	5.0E-32	AF116927.1	NT	Homo sapiens PRO1181 mRNA, complete cds
931	13984		1.85	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7861	20805	34181	3.03	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7861	20805	34182	3.03	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8702	21670		1	4.0E-32	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-H08 BT0311 Homo sapiens cDNA
456	13529	28459	3.32	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1448	14481	27458	9.76	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
9749	22690	36147	19.67	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
9749	22690	36148	19.67	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
11270	24222	37747	2.81	3.0E-32	AA77621.1	EST_HUMAN	z195a07.s1 Soares_fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.33 THR repetitive element.
11550	24491		1.46	3.0E-32	BF035327.1	EST_HUMAN	601458631F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
12430	25197		5.4	3.0E-32	BE276086.1	EST_HUMAN	601155285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12786	18336	31283	3.46	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12786	18336	31284	3.46	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (tritorax (Drosophila) homolog); translocated to, 4 (MLL T4) mRNA
12937	25517		4.33	3.0E-32	BE278086.1	EST_HUMAN	601166285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
4918	17935	30827	0.97	2.0E-32	BE296813.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
6381	19449	32690	0.87	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6824	19882	32959	6.86	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6824	19882	32880	6.86	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8621	21589	35006	2.19	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8621	21589	35007	2.19	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
13049	25589	31683	4.17	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFIA08 5'
13049	25589	31684	4.17	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFIA08 5'
3110	16167		1.07	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3634433 5'
7266	19991	33289	6.73	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame B (C11ORF9), mRNA
8943	21809	35334	6.78	1.0E-32	AA720574.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182246 3' similar to TR:O88539 O88539 THR.13
3493	16540		5.7	9.0E-33	BE327112.1	EST_HUMAN	WW DOMAIN BINDING PROTEIN 11.1
6580	19820		3.43	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9140	22106	35532	1.82	9.0E-33	BF347228.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
11150	24110		4.08	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
63	13182	26098	2.4	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
63	13182	26099	2.4	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2169	15185	28206	2.43	7.0E-33	AI690115.1	EST_HUMAN	tot12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element
2657	15654		7.82	7.0E-33	AV730059.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
2841	14737	27719	1.82	7.0E-33	AV730015.1	EST_HUMAN	AV730015 HTF Homo sapiens cDNA clone HTFANF08 5'
3256	16310		16.32	7.0E-33	AW971307.1	EST_HUMAN	EST383398 MAGI ressequences, MAGI Homo sapiens cDNA
9298	22264		1.07	7.0E-33	X54890.1	NT	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphatase) (EC 3.1.3.48)
11178	24134	37664	2.89	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
11578	24518	38071	2.65	7.0E-33	AW971568.1	EST_HUMAN	EST383657 MAGI ressequences, MAGI Homo sapiens cDNA
12409	25182	31819	3.85	7.0E-33	AA601416.1	EST_HUMAN	not16h01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.11 L1 repetitive element

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3749	16791		0.69	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6185	19260	32494	1.09	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
6185	19260	32495	1.09	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8825	21891	35319	7.52	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
9050	22016	35440	3.18	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
10371	23294	36769	1.73	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10371	23294	36770	1.73	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1792	14821		1.83	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA
1898	14923		1.27	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1914	14938	27933	1.31	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1914	14938	27934	1.31	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2280	15293		1.49	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4087	17121	30015	1.28	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
6823	19877	33166	51.92	5.0E-33	AA189080.1	EST_HUMAN	z445b06 s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE 632627 3' similar to contains Alu repetitive element;
10810	23532	37027	0.85	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10810	23532	37028	0.85	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
1130	14173		0.87	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2135	15152	28167	1.53	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2428	15435		2.92	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2552	15554	28574	2.35	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4509	17534	30418	1.65	4.0E-33	AW293349.1	EST_HUMAN	UI-H-BI2-ah1-c-03-O-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5477	18578	31487	21.95	4.0E-33	AA053053.1	EST_HUMAN	z71a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12871.maf1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6532	19595	32857	2.14	4.0E-33	8393394	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6532	19595	32858	2.14	4.0E-33	8393394	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1091	14135		6.18	3.0E-33	BE350127.1	EST_HUMAN	h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
1092	14135		4.81	3.0E-33	BE350127.1	EST_HUMAN	MER29 repetitive element;
2456	15894		0.91	3.0E-33	AV647851.1	EST_HUMAN	h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
10806	23727	37228	1.02	3.0E-33	AA861510.1	EST_HUMAN	h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone GLC8CF09 3'
							ak32b12.s1 Sceres testis_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579
							Q13579 MARINER TRANSPOSASE.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
18	13138		0.63	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
105	13138		2.93	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
4449	17475		4.22	2.0E-33	BE159039.1	EST_HUMAN	MR0-HT0405-160300-202-008 HT0405 Homo sapiens cDNA
5021	18035	30920	9.82	2.0E-33	AA626883.1	EST_HUMAN	ab51g11.1 Stratiagens lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5129	18138	31015	2.58	2.0E-33	11421332	NT	Homo sapiens hypothetical protein S1RP-b2 (S1RP-b2), mRNA
5129	18138	31016	2.58	2.0E-33	11421332	NT	Homo sapiens hypothetical protein S1RP-b2 (S1RP-b2), mRNA
6563	18823	32888	1	2.0E-33	AI277492.1	EST_HUMAN	q196d01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
9456	22420		2.29	2.0E-33	AI052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10979	23999	37411	0.9	2.0E-33	11421332	NT	Homo sapiens hypothetical protein S1RP-b2 (S1RP-b2), mRNA
10979	23999	37412	0.9	2.0E-33	11421332	NT	Homo sapiens hypothetical protein S1RP-b2 (S1RP-b2), mRNA
9	13129		2.05	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5669	18764	31934	0.7	1.0E-33	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
7637	20597	33981	1.18	1.0E-33	MI13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
10381	26010		0.73	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11377	24324	37853	1.72	1.0E-33	AV744220.1	EST_HUMAN	AV744220 OB Homo sapiens cDNA clone CBOAAA11 5'
11650	24587	38157	1.78	1.0E-33	AW998818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
11973	24851	38448	2.59	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12685	26352		1.98	1.0E-33	AI927191.1	EST_HUMAN	wo88c06.x1 NCI CGAP_Ki67 Homo sapiens cDNA clone IMAGE:2482410 3'
12852	13128		3.4	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4644	17665		1.17	9.0E-34	BE155575.1	EST_HUMAN	PM4-HT0352-181199-001-D02 HT0352 Homo sapiens cDNA
13069	25903		3.44	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2181	15196	26216	0.93	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
8077	21014	34414	0.49	8.0E-34	BE069882.1	EST_HUMAN	MR4-BT0399-200100-001-h03 BT0399 Homo sapiens cDNA
1439	14472	27449	2.93	7.0E-34	T70845.1	EST_HUMAN	y416c05.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
10359	14472	27449	0.6	7.0E-34	T70845.1	EST_HUMAN	y416c05.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
12479	26227		1.69	7.0E-34	HI12868.1	EST_HUMAN	y14c10.r1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
471	13543	26471	2.11	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
471	13543	26472	2.11	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12287	25103	31836	1.86	6.0E-34	U03696.1	NT	Mus musculus DAB/2J hair-specific (hac1) gene
1897	14922		2.38	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5101	18111	30983	4.68	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
9218	22184	35617	1.17	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11015	23980	37506	2.03	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11583	24521		1.49	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2014	15035	28046	1.71	4.0E-34	AI804667.1	EST_HUMAN	h94c06.x1 NCI_CQAP_P28 Homo sapiens cDNA clone IMAGE:2249194 3'
5223	18231	31108	0.84	4.0E-34	AW886252.1	EST_HUMAN	RC5-OT0078-280300-022-002 OT0078 Homo sapiens cDNA
9393	22358	35788	1.07	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6359	19428	32671	0.74	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11486	24429		3.18	3.0E-34	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
9303	22268	35698	1.93	2.0E-34	AI678101.1	EST_HUMAN	w335g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element;
9303	22268	35698	1.93	2.0E-34	AI678101.1	EST_HUMAN	w335g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element;
11498	24439	37987	1.57	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
11498	24439	37988	1.57	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1505	14538	27510	8.53	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3687	16730	28841	1.35	1.0E-34	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4098	17132	30025	0.81	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4098	17132	30026	0.81	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4508	17631		6.11	1.0E-34	BE071414.1	EST_HUMAN	RC2-B70506-240400-016-h08 BT0506 Homo sapiens cDNA
6261	19334	32565	1.98	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
6261	19334	32566	1.98	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
9881	22634	36090	0.46	1.0E-34	P23266	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN F5
10055	22982	36450	14.47	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563.1 564 (synonym: nfr2) Homo sapiens cDNA clone DKFZp564A1563 5'
11516	24457	38007	1.71	1.0E-34	BE781790.1	EST_HUMAN	601470692F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11516	24457	38008	1.71	1.0E-34	BE781790.1	EST_HUMAN	601470692F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11530	24471	38022	3.22	1.0E-34	11439569	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12654	25921		1.4	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
12874	25507		4.01	1.0E-34	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	16702	29617	1.25	9.0E-35	AW663302.1	EST_HUMAN	hh77b06.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
227	13328		13.21	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1751	14780	27765	4.47	8.0E-35	BF869837.1	EST_HUMAN	naa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1751	14780	27768	4.47	8.0E-35	BF869837.1	EST_HUMAN	naa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4902	17919	30811	2.91	8.0E-35	BF183196.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
11049	24012	37537	1.84	8.0E-35	BE378480.1	EST_HUMAN	naa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
12402	25175		5.41	8.0E-35	BF669282.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
6831	19889	32988	1.85	7.0E-35	11425417	NT	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
1411	14444	27416	0.93	6.0E-35	AA767115.1	EST_HUMAN	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
1985	15006	28009	2.85	6.0E-35	8005875	NT	602184924T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
4083	17117	30012	0.76	8.0E-35	AW287181.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
8229	21198	34605	3.68	6.0E-35	6005921	NT	alt53h03.s1 Soares_testis_NHT1 Homo sapiens cDNA clone 1309397 3'
9058	22024	35447	0.51	8.0E-35	X94232.1	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
9058	22024	35448	0.51	8.0E-35	X94232.1	NT	UI-H-BWO-gid-d-09-0-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
10025	22952	36420	0.68	6.0E-35	AB002364.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10263	23188	36872	3.04	6.0E-35	AB037786.1	NT	H. sapiens mRNA for novel T-cell activation protein
1722	14752	27737	61.6	5.0E-35	X63392.1	NT	H. sapiens mRNA for novel T-cell activation protein
2765	15787	28805	0.9	5.0E-35	AB007886.2	NT	Human mRNA for KIAA0368 gene, partial cds
3021	18079	29000	1.47	5.0E-35	6912639	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
							Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							Homo sapiens cdk2 kinase (CLK2), prolin1, cote1, glucocerebrosidase (GBA), and melanin genes, complete cds; melanin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
4438	17484	30354	2.05	5.0E-35	AF023268.1	NT	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
4742	17762	30656	0.99	5.0E-35	BE246065.1	EST_HUMAN	sapiens cDNA clone TCBAP3842
8525	21493		4.74	5.0E-35	BE800992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8552	21520	34939	2.2	5.0E-35	A1208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT1 Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
8552	21520	34940	2.2	5.0E-35	A1208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT1 Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
11512	24453		2.39	5.0E-35	AA001786.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1429	14483	27440	19.86	4.0E-35	BE257807.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1835	14862	27859	7.51	4.0E-35	H91193.1	EST_HUMAN	y98a07.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
4844	17861		0.83	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5145	18154		0.93	4.0E-35	BE409102.1	EST_HUMAN	601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'
7416	20383		1.81	4.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3148266 3' similar to contains MER29.b3
8863	21830	35253	8.37	4.0E-35	AL046598.1	EST_HUMAN	MER29 repetitive element ;
1682	14816	27688	21.76	3.0E-35	BE268182.1	EST_HUMAN	DKFZb434L148_r1 434 (synonym: hles3) Homo sapiens cDNA clone IMAGE:3345063 5'
2338	15349		3.36	3.0E-35	AF224492.1	NT	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
5413	18516	31393	27.9	3.0E-35	BF433100.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, complete cds
5413	18516	31394	27.9	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
9844	22780		1.71	3.0E-35	AF223391.1	NT	Q9QZH7 F-BOX PROTEIN FBL2. ;
10535	23457	36954	0.93	3.0E-35	AW003083.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
108	15832	26146	0.83	2.0E-35	N88965.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
1192	14232	27188	1.39	2.0E-35	T11909.1	EST_HUMAN	w03a05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL.1_HUMAN
2227	15241	26260	5.04	2.0E-35	AB018413.1	EST_HUMAN	P102868 RETROVIRUS-RELATED POL POLYPYPTASE [CONTAINS: REVERSE TRANSCRIPTASE ;
2893	15689	28706	1	2.0E-35	AW685005.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
3323	16374	29294	0.93	2.0E-35	6912459	NT	A971F Heart Homo sapiens cDNA clone A971
3323	16374	29295	0.93	2.0E-35	6912459	NT	Homo sapiens mRNA for Gab2, complete cds
3570	16615		1.06	2.0E-35	AB020702.1	NT	h186a12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to SW:TR12_HUMAN Q14689 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
3930	16970	29883	1.42	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3930	16970	29884	1.42	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4697	17718		2.65	2.0E-35	H49239.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
5662	18758	31926	1.8	2.0E-35	BF332417.1	EST_HUMAN	TCBAP2E-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylax-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
							TCBAP2E-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylax-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
							y16a12.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:274079 5'
							QV0-BT0701-210400-199-504 BT0701 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7311	20282	33622	0.65	2.0E-35	BE832638.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7311	20282	33623	0.65	2.0E-35	BE932636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11148	24108	37634	11.23	2.0E-35	X59417.1	NT	H. sapiens PROS-27 mRNA
12158	16374	29284	2.39	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA05571), mRNA
12158	16374	29295	2.39	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA05571), mRNA
12340	25138	31851	1.47	2.0E-35	BE904978.1	EST_HUMAN	601466774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12340	25138	31852	1.47	2.0E-35	BE904978.1	EST_HUMAN	601466774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12854	25462		7.86	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12973	15832	26146	1.72	2.0E-35	N88965.1	EST_HUMAN	K932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K8932 5' similar to REPETITIVE ELEMENT
48	13188	26073	5.26	1.0E-35	AA631949.1	EST_HUMAN	frnc18 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13188	26074	5.26	1.0E-35	AA631949.1	EST_HUMAN	frnc18 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
753	13814	26756	95.25	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
753	13814	26757	95.25	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
910	13965		0.99	1.0E-35	T87947.1	EST_HUMAN	y463a01.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2549	15550	26571	3.02	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2778	15770	28790	1.85	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
2778	15770	28781	1.85	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
3177	16232	29148	3.44	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
3177	16232	29149	3.44	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
4452	17478	30365	4.04	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4452	17478	30366	4.04	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5683	18684	31953	1.54	1.0E-35	11526236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7189	18420	31221	0.59	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA
7189	18420	31222	0.59	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA
7725	20681	34045	0.83	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7903	20846	34231	0.94	1.0E-35	11418002	NT	Homo sapiens KIAA0845 gene product (KIAA0845), mRNA
9800	25699	36312	3.17	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
9800	25699	36313	3.17	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10942	23862	37377	0.63	1.0E-35	BF569594.1	EST_HUMAN	naa05d06.x1 NCL_CGAP_Pir28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:031341 O31341 BETA-GALACTOSIDASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10942	23862	37378	0.63	1.0E-35	BF589594.1	EST_HUMAN	naa06d06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:Q31341
12052	24925	38522	1.72	1.0E-35	AB028980.1	NT	Q31341 BETA-GALACTOSIDASE ;
12052	24925	38523	1.72	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12057	24930		1.59	1.0E-35	AI525119.1	EST_HUMAN	Homo sapiens mRNA for KIAA1057 protein, partial cds
12188	25887		1.71	1.0E-35	11418274	NT	promtne-7.D01.1 b1 tumor Homo sapiens cDNA 5'
12320	15580	28571	1.42	1.0E-35	7705994	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12404	25177		1.77	1.0E-35	11418110	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
12747	25398		1.97	1.0E-35	BE792832.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
4011	17050	29958	2.35	9.0E-36	AW821707.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
6123	19201	32425	0.75	8.0E-36	X78479.1	NT	RC9-ST0315-180200-013-f12 ST0315 Homo sapiens cDNA
							B bovis BBSc mRNA for scinderin
9585	22647	35998	0.61	8.0E-36	AA348480.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
10516	23438		0.45	8.0E-36	7706259	NT	Homo sapiens CGI-09 protein (LOC51605), mRNA
2942	16000	28923	1.68	7.0E-36	AW857579.1	EST_HUMAN	GM1-CT0315-091299-063-407 CT0315 Homo sapiens cDNA
3135	16192		4.05	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7916	20859	34247	6.21	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
7916	20859	34248	6.21	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
12558	25278	31778	2.01	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
2021	15042	28053	4.16	6.0E-36	7706622	NT	Homo sapiens rhinjurin 2 (NINJ2), mRNA
2427	15434		5.3	6.0E-36	AB035346.1	NT	Homo sapiens TOL6 gene, exon 12
3653	16698	29611	1.88	6.0E-36	BF515101.1	EST_HUMAN	U1-HBW1-amp-c-12-Q1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5404	18507	31384	5.66	8.0E-36	AI435169.1	EST_HUMAN	th93b05.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126185 3' similar to
							gb:MI1949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
							h006h02.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IM22_HUMAN
							P52292 IMPORTIN ALPHA-2 SUBUNIT ;
7316	20287	33629	3.48	6.0E-36	AW780143.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
8999	21965	35390	2.51	6.0E-36	AF208181.1	NT	C16827 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-535C11 5'
10585	23507		0.6	6.0E-36	C16927.1	EST_HUMAN	tf95c09.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
							MER9 repetitive element ;
11874	24756	38339	3.51	6.0E-36	AI380499.1	EST_HUMAN	601305084F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
12963	25804	31526	1.9	6.0E-36	BE737154.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
138	13243	26173	12.86	5.0E-36	A1271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2761	15753	28773	12.8	5.0E-36	BE388436.1	EST_HUMAN	601285557F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3626	16669	29681	1.32	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4827	17844	30743	1.21	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4827	17844	30744	1.21	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
8070	21007	34405	0.77	5.0E-36	11079227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12186	13243	28173	2.97	6.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12455	25214	31832	3.03	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1228	14266	27223	1.24	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1436	14469	27447	0.99	4.0E-36	P10266	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1652	14684	27658	1.63	4.0E-36	BE382574.1	EST_HUMAN	601288574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2231	15245	28340	1.64	4.0E-36	AW247772.1	EST_HUMAN	2820020 Spriime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3365	16415	28340	0.65	4.0E-36	BE389299.1	EST_HUMAN	601282286F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3366	16415	28341	0.65	4.0E-36	BE389299.1	EST_HUMAN	601282286F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4766	17804	30696	0.71	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment H521C004
5804	18895		0.96	4.0E-36	R64023.1	EST_HUMAN	y1905.r1 Soares placenta Nb21P Homo sapiens cDNA clone IMAGE:139713 5'
6173	19248	32481	2.48	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7915	20858	34246	1.74	4.0E-36	M33320.1	NT	Human platelet Glycoprotein IIb (GP1Ib) gene, exons 2-29
8901	21867	35290	1.2	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8901	21867	35291	1.2	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11332	24282	37806	1.8	4.0E-36	AA400370.1	EST_HUMAN	zu69c10.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
12471	25220		1.86	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
12515	25768		8.26	4.0E-36	AV753629.1	EST_HUMAN	AV753629 TP Homo sapiens cDNA clone TFGABH01 5'
697	13759	26691	3.9	3.0E-36	AF098810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
1497	14530	27502	0.97	3.0E-36	AF110238.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1497	14530	27503	0.97	3.0E-36	AF110238.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
4530	17564	30442	6.81	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3184	16239	29167	2.17	2.0E-36	BE256287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
4998	18011	30898	8.63	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5563	18660	31606	2.52	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5948	19034	32227	3.89	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBB128 5' end
6728	19784	33063	12.4	2.0E-36	T69829.1	EST_HUMAN	yc44807.r1 Stratiagene liver (#837224) Homo sapiens cDNA clone IMAGE:83508 5'
9743	22684	38138	0.82	2.0E-36	BF512794.1	EST_HUMAN	UI-H-BW 1-armu-e-11-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9907	22728	36184	0.57	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA

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Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9907	22728	36185	0.57	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
888	13941	28899	2.74	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2155	15171	28189	1.08	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2155	15171	28190	1.06	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2212	15227	28249	1.35	1.0E-36	BF873761.1	EST_HUMAN	602135493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3355	16406		1.34	1.0E-36	AF16862.1	NT	Homo sapiens human endogenous retrovirus W proC6-19 protease (pro) gene, partial cds
5818	18908	32092	0.82	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G022 5'
6003	19088	32288	1.3	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6307	19378		3.88	1.0E-36	AI867714.1	EST_HUMAN	wb37c12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6529	19592	32852	1.34	1.0E-36	R25012.1	EST_HUMAN	y93g10.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6529	19592	32853	1.34	1.0E-36	R25012.1	EST_HUMAN	y93g10.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6838	19892	33187	0.7	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
8293	21282	34671	2.77	1.0E-36	AA148034.1	EST_HUMAN	z551a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8293	21282	34672	2.77	1.0E-36	AA148034.1	EST_HUMAN	z551a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8388	21357	34784	1.15	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745870
8388	21357	34765	1.15	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745870
8520	21488	34902	0.48	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8520	21488	34903	0.48	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
9394	22349	35781	2.72	1.0E-36	AW103658.1	EST_HUMAN	xe82b07.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10473	23395	36892	3.95	1.0E-36	BF304169.1	EST_HUMAN	QV3-NN1023-010500-199-h01 NN1023 Homo sapiens cDNA
10691	23613	37107	0.65	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
10691	23613	37108	0.65	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
11294	24244	37771	2.84	1.0E-36	AW897638.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11709	24674	38251	2.88	1.0E-36	AW504143.1	EST_HUMAN	UHF-BNO-ale-c-03-Q-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12338	25136		5.51	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12777	25414		4.97	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13034	25579		4.02	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7607	20568	33929	2.3	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7607	20568	33930	2.3	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
3366	16416	29342	1.17	8.0E-37	4757979	NT	Homo sapiens chimerin (chimaerin) 2 (CHN2) mRNA
5320	18426		1.6	8.0E-37	BE686077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5927	19013	32205	3.73	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
5927	19013	32206	3.73	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
5977	19062	32263	6.05	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA H. sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, DOB, DQB2 and RING8, 9, 13 and 14 genes
8216	21185	34595	6.98	8.0E-37	X87344.1	NT	
1289	14324		2.33	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0422 5'
1759	14788	27773	0.92	7.0E-37	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1759	14788	27774	0.92	7.0E-37	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5181	18170	31049	1.96	7.0E-37	AW968823.1	EST_HUMAN	EST380898 MAGC resequences, MAGJ Homo sapiens cDNA w425611.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.k2 PTR5 repetitive element;
11109	24069	37591	8.45	7.0E-37	A1817700.1	EST_HUMAN	h087g03.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2105140 3' similar to contains L1.b3 L1 repetitive element;
11241	24194	37712	1.83	7.0E-37	A1538702.1	EST_HUMAN	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
8782	21749	35171	0.59	6.0E-37	AF169899.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
12903	25487		3.58	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6212	19286	32518	4.33	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6212	19286	32519	4.33	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9109	22075	35501	0.88	5.0E-37	AV750211.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPOCBGH09 5'
11285	24217		3.87	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
12333	25103		6.43	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2431	15438	28455	2.41	4.0E-37	AA702784.1	EST_HUMAN	z60604.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4814	17831	30729	1.05	4.0E-37	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5268	18275		0.93	4.0E-37	N62051.1	EST_HUMAN	EST52g10 WATM1 Homo sapiens cDNA clone 52g10 similar to human STS G04101
6419	19486	32735	0.59	4.0E-37	AW794502.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9711	22684	36121	0.57	4.0E-37	AA843808.1	EST_HUMAN	ak08c02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2033	15052	28068	3.07	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2033	15052	28069	3.07	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2519	15522		1.74	3.0E-37	AW981150.1	EST_HUMAN	EST379222 MAGC resequences, MAGF Homo sapiens cDNA
2976	16034		3.71	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGC resequences, MAGF Homo sapiens cDNA
5964	19049	32250	0.73	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547G067 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7804	20754	34130	0.75	3.0E-37	A1749952.1	EST_HUMAN	at3c405.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373898 3' similar to TR:Q13337
381	13494	26426	3.06	2.0E-37	D89780.1	NT	Q13537 SIMILAR TO POGO ELEMENT; ;
381	13494	26427	3.06	2.0E-37	D89780.1	NT	Homo sapiens mRNA for AML1, complete cds
1082	14126	27079	2.49	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
1082	14126	27080	2.49	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1981	15002	28005	2.43	2.0E-37	AL163247.2	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
3908	16948	29859	5.24	2.0E-37	4503210	NT	Homo sapiens chromosome 21 segment HS21C047
5482	18584		0.74	2.0E-37	BF035327.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrolendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
6696	19753	33030	0.55	2.0E-37	11990617	NT	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
6816	19870	33159	3.92	2.0E-37	AA346720.1	EST_HUMAN	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
8329	21298	34713	0.51	2.0E-37	BE537784.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
8329	21298	34714	0.51	2.0E-37	BE537784.1	EST_HUMAN	601087634F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8372	21341	34752	3.33	2.0E-37	BF204032.1	EST_HUMAN	601087634F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
11885	24766	38353	8.89	2.0E-37	AF176013.1	NT	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5'
12738	25607		1.81	2.0E-37	11417972	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
13074	25607		4.68	2.0E-37	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2099	15116	28138	5.41	1.0E-37	AL163281.2	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
3985	17025	29938	4.56	1.0E-37	AF168011.1	NT	Homo sapiens chromosome 21 segment HS21C081
4191	17222	30111	1.09	1.0E-37	BE872365.1	EST_HUMAN	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4978	17893	30882	2.21	1.0E-37	BF371719.1	EST_HUMAN	601448619F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852652 5'
6119	19197		1.01	1.0E-37	7305360	NT	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
8557	21525	34943	0.7	1.0E-37	BE546032.1	EST_HUMAN	Mus musculus otogelin (Olog), mRNA
9087	22053	35476	3.45	1.0E-37	AA171406.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
10971	23891	37405	0.44	1.0E-37	AV730743.1	EST_HUMAN	7p21B02.11 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1 t2 L1 repetitive element ;
11056	24019	37542	2.07	1.0E-37	M22878.1	NT	AV730743 HTF Homo sapiens cDNA clone HTFAHG10 5'
12648	25329		4.28	1.0E-37	BE771614.1	EST_HUMAN	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
5872	18961	32150	1.67	8.0E-38	10048482	NT	CM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA
1228	14264	27221	1.85	8.0E-38	11436955	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
2508	15509	28536	2.16	8.0E-38	BF346221.1	EST_HUMAN	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
12698	14264	27221	1.44	8.0E-38	11436955	NT	602018401F1 NC1 CGAP_Bri67 Homo sapiens cDNA clone IMAGE:4153992 5'
3055	16112	29027	1.88	6.0E-38	BF030303.1	EST_HUMAN	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
							601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5670	18765	31935	1.48	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5670	18765	31936	1.48	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7550	20513	33871	0.51	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7613	20573	33936	0.74	6.0E-38	AJ010969.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
7613	20573	33937	0.74	6.0E-38	AJ010969.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
12189	25035		3.19	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12677	25347	31765	18.01	6.0E-38	AB020269.1	NT	Homo sapiens DNA for Human P2X ₁ , complete cds
13052	25733	31616	1.66	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
728	13788	26724	1.28	5.0E-38	AW971819.1	EST_HUMAN	EST383908 MAGC resequences, MAGL Homo sapiens cDNA
2460	15484	28487	1.24	6.0E-38	AJ237740.1	NT	Homo sapiens RIBIIR gene (partial), exon 8
7228	20250	33584	1.8	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
119	13228	26154	3.65	4.0E-38	Z25466.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
119	13228	26155	3.65	4.0E-38	Z25466.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2110	15127		3.98	3.0E-38	AF003550.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3710	16763		1.24	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dhaJ-like) (HIRIP4), mRNA
3869	16808	29817	1.98	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3869	16808	29818	1.98	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
6917	25571	33264	7.83	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7455	20421	33776	0.6	3.0E-38	AW302461.1	EST_HUMAN	XW04401.X1 NCI_OGAP_Brm63 Homo sapiens cDNA clone IMAGE:2827009 3'
7832	20780		0.57	3.0E-38	AA376327.1	EST_HUMAN	EST91188 Synovial sarcoma Homo sapiens cDNA 5' end
7844	20781	34167	6.28	3.0E-38	BF373694.1	EST_HUMAN	CM3-F10181-140700-241-407 F10181 Homo sapiens cDNA
8997	21863	35388	1.97	3.0E-38	H85494.1	EST_HUMAN	yw88b04.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:249776 5'
8997	21863	35389	1.97	3.0E-38	H85494.1	EST_HUMAN	yw88b04.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:249775 5'
10331	23255		2.06	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12809	18333	31171	1.46	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
52	13172	26081	2.54	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1380	14414	27384	2.28	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1653	14885	27659	2.07	2.0E-38	AA437353.1	EST_HUMAN	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1653	14885	27660	2.07	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
2418	15425	28448	1.11	2.0E-38	W79571.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
6271	18160	31040	0.79	2.0E-38	AA437181.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
							SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
							zw66g09.r1 Soares testis NBHT Homo sapiens cDNA clone IMAGE:345664 5'
							zw61409.r1 Soares testis NBHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR:G817957
							G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5807	18897	32079	0.61	2.0E-38	Z28634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
5807	18897	32080	0.61	2.0E-38	Z28634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7988	20927	34322	1.27	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8828	21795		5.59	2.0E-38	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9246	22212	35642	0.55	2.0E-38	FO6450.1	EST_HUMAN	HSC18F031 normalized Infant brain cDNA Homo sapiens cDNA clone c-18f03
9316	22281	35711	1.21	2.0E-38	AF069756.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9576	22538		1.04	2.0E-38	BE222256.1	EST_HUMAN	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:002710 002710
10815	23736	37239	1.74	2.0E-38	D63479.2	NT	GAG POLYPROTEIN.
11819	24702	38284	4.62	2.0E-38	BE712790.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11965	24834	38429	3.66	2.0E-38	AF190501.1	NT	QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA
11955	24834						Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12240	26071	38430	3.66	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12242	25072		3.39	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAHX07 5'
12538	25262		2.13	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12548	25271	31810	2.91	2.0E-38	M55630.1	NT	Human topoisomerase I pseudogene 2
13065	25599		6.8	2.0E-38	H55641.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
1095	14139		3	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
2015	15036	28047	2.38	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
2035	15094	28071	1.92	1.0E-38	4885288	NT	MER19 repetitive element ;
2502	15505	28532	1.17	1.0E-38	7681909	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
4182	17213	30101	2.01	1.0E-38	AF270831.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4352	17379	30259	0.99	1.0E-38	AB037863.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4352	17379	30260	10.48	1.0E-38	AL163203.2	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4627	17648	30536	10.48	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5143	18152	31032	0.93	1.0E-38	8922543	NT	Homo sapiens chromosome 21 segment HS21C003
6143	19218	32447	0.77	1.0E-38	AA077528.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
6143	19218	32448	6.58	1.0E-38	7305360	NT	7B44-H06 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44-H06
7634	20594	33957	6.58	1.0E-38	7305360	NT	Mus musculus obogelin (Obog), mRNA
9508	22471	35915	3.03	1.0E-38	AB014512.1	NT	Mus musculus obogelin (Obog), mRNA
			0.55	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9765	22706	36162	6.34	1.0E-38	BE350127.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3
12401	25712		2.08	1.0E-38	AL163284.2	NT	MER29 repetitive element;
58	13178	26087	5.73	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C084
1395	14429	27368	0.94	8.0E-39	4758229	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1846	14872		1.54	8.0E-39	AI823404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
2105	15122	28142	5.19	7.0E-39	AL163227.2	NT	wh53f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3284491 3' similar to TR:P87890 P87890
11160	24118	37645	1.8	6.0E-39	BF331829.1	EST_HUMAN	POL PROTEIN;
12981	25545		3.12	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1009	14058	27010	1.43	5.0E-39	AF003528.1	NT	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
							7634c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to W.P.R151.6
							CE00828;
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2998	18058	28976	8.13	5.0E-39	AI750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
12689	25358		2.82	5.0E-39	11420289	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7 t1 LTR7 repetitive element;
552	13622	26542	20.77	4.0E-39	AB015610.1	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
3587	16632	29550	0.92	4.0E-39	AL163210.2	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
5928	19014	32207	0.65	4.0E-39	11422113	NT	Homo sapiens chromosome 21 segment HS21C010
5928	19014	32208	0.65	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
							Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
							ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
8411	21380	34786	1.14	4.0E-39	AA882949.1	EST_HUMAN	OFR.b1 OFR repetitive element;
9684	22637	36092	0.61	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
9684	22637	36093	0.61	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12704	25363		3.29	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12819	25441		3.15	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0063-260900-278-c06 FN0063 Homo sapiens cDNA
49	13169	26076	14.8	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	13169	26076	14.8	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	13169	26077	14.8	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							ox63a10.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
12233	25065	38183	6.14	3.0E-39	AI084557.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
12233	25065	38184	6.14	3.0E-39	AI084557.1	EST_HUMAN	ox63a10.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12882	25100		11.16	3.0E-39	H37903.1	EST_HUMAN	yp51c06.s1 Scarsa retina N2b4HR Homo sapiens cDNA clone IMAGE:180954 3'
898	13953		9.79	2.0E-39	BE409203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
913	13968		13.84	2.0E-39	AI525119.1	EST_HUMAN	promina-7.D01.r bytumor Homo sapiens cDNA 5'
1033	14079		4.67	2.0E-39	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1532	14565		24.51	2.0E-39	AW372318.1	EST_HUMAN	PMO-BT034C-211299-003-d02 BT0340 Homo sapiens cDNA
1990	15011	28017	3.62	2.0E-39	AA720574.1	EST_HUMAN	hw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
2638	15635	28659	2.3	2.0E-39	AL163248.2	NT	THR repetitive element;
4431	17458	30348	1.58	2.0E-39	BF370207.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
5568	18665	31824	4.2	2.0E-39	AA508880.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
7694	20555	33915	2.34	2.0E-39	AA080867.1	EST_HUMAN	ng86103.s1 NCL_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941693
7776	20729	34101	0.61	2.0E-39	AL163202.2	NT	zn06102.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
7776	20729	34102	0.61	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8653	21621	35041	0.58	2.0E-39	AF078779.1	NT	Homo sapiens chromosome 21 segment HS21C002
9851	22787		1.32	2.0E-39	AA984531.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9884	22911		0.53	2.0E-39	AI686660.1	EST_HUMAN	am68c11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'
11761	24889	38271	2.58	2.0E-39	D86984.1	NT	tu35e03.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2263052 3'
1516	14548	27520	3.52	1.0E-39	AJ006345.1	NT	Human mRNA for KIAA0209 gene, partial cds
1516	14548	27521	3.52	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQ11 gene
1533	14566	27535	6.96	1.0E-39	7657020	NT	Homo sapiens KVLQ11 gene
4889	17710	30803	6.87	1.0E-39	AW851995.1	EST_HUMAN	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
4889	17710	30804	6.87	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGE Homo sapiens cDNA
4731	17751	30843	8.48	1.0E-39	7657020	NT	EST364085 MAGE resequences, MAGE Homo sapiens cDNA
5432	18534	31442	0.87	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaforin) 5A (SEMA5A), mRNA
5432	18534	31443	0.87	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaforin) 5A (SEMA5A), mRNA
5711	18805	31982	1.2	1.0E-39	T80876.1	EST_HUMAN	yd26g06.r1 Scarsa fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element; contains LTR1 repetitive element;
5747	18841	32023	4.7	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)
5747	18841	32024	4.7	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (NIX1 gene)
7000	20128		1.68	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7589	20550	33911	2.1	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8910	21876	35302	0.96	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
557	13627	26545	1.8	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1239	14275	27234	14.84	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1239	14275	27235	14.84	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1443	14476	27453	0.99	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3789	16839	29746	0.88	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3997	18315	29943	4.05	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4527	17401	30281	0.78	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3054	18111	29026	0.91	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3945	16985		2.39	8.0E-40	BE396541.1	EST_HUMAN	80128898F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
7985	20924	34317	2.22	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7985	20924	34318	2.22	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11243	24198	37715	1.76	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2737	15731	28746	7.6	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2737	15731	28747	7.5	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6049	19730		2.05	6.0E-40	BE504766.1	EST_HUMAN	hz40g01.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3210480 3'
6270	19343		1.32	6.0E-40	7661959	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7121	20055	33359	3.38	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7121	20056	33360	3.38	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10336	23260	36798	9.47	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
10336	23260	36799	9.47	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2812	15811	28635	1.12	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1894	14919	27915	3.21	4.0E-40	A1696005.1	EST_HUMAN	tt91b01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O79505 O79505 POL PROTEIN. ;
2117	15134		2.22	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4415	17442	30333	8.57	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8218	21187	34597	0.44	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8324	21293	34707	4.81	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.r1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
9470	22375	35812	5.53	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9410	22375	36813	5.53	4.0E-40	BE008416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
11071	24033	37557	1.86	4.0E-40	AW841885.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4158	17189	30077	1.02	3.0E-40	AI925949.1	EST_HUMAN	wh12107.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6607	19665	32940	0.66	3.0E-40	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6796	19850	33135	7.89	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMASA), mRNA
8724	21082	35118	3.94	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9320	22285	35715	1.23	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9566	22528	35977	1.34	3.0E-40	AF078776.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11597	24535	38092	9.3	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
325	13418		4.59	2.0E-40	AI223036.1	EST_HUMAN	qg52108.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
795	13854		29.29	2.0E-40	AW303868.1	EST_HUMAN	x224e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS5_MOUSE
1842	14868		1.77	2.0E-40	AV731601.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5 ;
1951	14974	27973	1.94	2.0E-40	4506188	NT	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1951	14974	27974	1.94	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2085	15102	28119	1.01	2.0E-40	AI988562.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2179	15194	28215	1.84	2.0E-40	5453592	NT	w80a11.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929
2700	15698		1.79	2.0E-40	BE275932.1	EST_HUMAN	ZINC FINGER PROTEIN ;
3143	16200	29111	4.44	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4937	17953	30845	1.7	2.0E-40	AL163280.2	NT	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
5237	18245	31117	1.12	2.0E-40	AL163280.2	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
884	13939		1.63	1.0E-40	AA225989.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2629	15628	28653	1.47	1.0E-40	BF036681.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2698	15892		1.54	1.0E-40	BE018348.1	EST_HUMAN	Homo sapiens plasmidogen (PLG) mRNA
2747	15740	28756	1.38	1.0E-40	BF541030.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007608
2747	15740	28757	1.38	1.0E-40	BF541030.1	EST_HUMAN	601460375F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3863803 5'
3309	16362		1.58	1.0E-40	4507142	NT	601460375F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3863803 5'
4640	17661	30549	4.18	1.0E-40	4508012	NT	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
							SYNTAXIN 17 ;
							602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
							602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
							Homo sapiens eukaryotic protein 3 (SNX3) mRNA
							Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products

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6384	19452	32695	0.73	1.0E-40	W92708.1	EST_HUMAN	zh78f11.s1 Soares fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6384	19452	32696	0.73	1.0E-40	W92708.1	EST_HUMAN	zh78f11.s1 Soares fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7283	20265	33599	1.92	1.0E-40	AA573201.1	EST_HUMAN	n42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7283	20265	33600	1.92	1.0E-40	AA573201.1	EST_HUMAN	n42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7443	20409	33761	0.84	1.0E-40	P26808	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
11282	24214	37738	2.42	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
12659	25847		14.2	1.0E-40	BF334112.1	EST_HUMAN	MR2-CT0222-21:1099-002-s10 CT0222 Homo sapiens cDNA
12813	25922		1.64	1.0E-40	Z00015.1	NT	H.sapiens V(k) gene low repetitive L-family member (cos 20)
8254	21223	34633	1.59	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
829	15852	26840	1.81	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
829	15852	26841	1.81	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5337	18442	31195	0.95	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
8124	19202	32426	2.97	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
8488	19553	32803	1.08	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7186	18417	31218	0.88	7.0E-41	U72355.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11763	24691	38272	2.6	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
13072	25844		10.83	7.0E-41	11417872	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
280	13375	26304	0.65	6.0E-41	AE037183.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2120	15137	28167	1.67	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
8304	21273	34684	1.59	6.0E-41	BF513783.1	EST_HUMAN	U1-HBW1-amp-b-03-O-U1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
1819	14846	27838	1.75	5.0E-41	T82828.1	EST_HUMAN	yc03a10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79626 3'
4134	17166		1.03	5.0E-41	4886630	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6998	19755		2.06	5.0E-41	BE067042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
391	13466		1.73	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1100	14144	27094	1.16	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1408	14441	27411	9.16	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:000597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1408	14441	27412	9.16	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:000597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1420	14453	27427	2.75	4.0E-41	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1641	14873	27846	6.9	4.0E-41	AI500408.1	EST_HUMAN	tm86c04.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OPR.b1
2889	15958	28876	3.56	4.0E-41	AJ229041.1	NT	ORF repetitive element ;
2899	15958	28877	3.56	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4168	17199	30085	2.26	4.0E-41	X92885.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6658	17115		1.31	4.0E-41	AV758295.1	EST_HUMAN	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
10052	22979	36446	8.41	4.0E-41	BF304683.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMBHC06 5'
11981	24858		11.66	4.0E-41	AV710480.1	EST_HUMAN	601888086F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
947	14000	26952	2.51	3.0E-41	AB030176.1	NT	AV710480 Cu Homo sapiens cDNA clone CUAAC007 5'
4362	17389	30271	2.6	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5148	18167		1.15	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5659	18666	31625	9.46	3.0E-41	X87689.1	NT	H.sapiens mRNA for putative p64 GLOP protein
6518	19681	32839	1.61	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7473	20439	33787	0.62	3.0E-41	AA356168.1	EST_HUMAN	EST64883 Jurkat T-cells VI Homo sapiens cDNA 5' end
8072	21008	34407	0.52	3.0E-41	R54755.1	EST_HUMAN	y75d08.r1 Soares breast 2NBHbet Homo sapiens cDNA clone IMAGE:154575 5'
12116	24986	38587	3.46	3.0E-41	AW994941.1	EST_HUMAN	QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA
12116	24986	38588	3.46	3.0E-41	AW994941.1	EST_HUMAN	QV0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA
12195	26040		1.49	3.0E-41	AA603768.1	EST_HUMAN	af17f10.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1031947 3'
1841	14595	27570	15.21	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1975	14996	27998	2.16	2.0E-41	AA331940.1	EST_HUMAN	EST135818 Embryo, 8 week I Homo sapiens cDNA 5' end
2228	15242	28267	1.37	2.0E-41	D96982.1	NT	Human mRNA for KIAA0207 gene, complete cds
2278	15289	28314	4.43	2.0E-41	X99631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2839	14595	27670	7.98	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3851	16891	29796	0.9	2.0E-41		NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4852	17673	30580	1.13	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4852	17673	30581	1.13	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
5617	18713	31871	0.61	2.0E-41	AA584575.1	EST_HUMAN	no12d07.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:X52851_mna1
6782	19837	33121	0.85	2.0E-41	4504778	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
7335	20877	34267	6.36	2.0E-41	AF039404.1	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
8148	21085	34484	0.6	2.0E-41	11422047	NT	Homo sapiens homolog of Need5 (Nded5) mRNA, complete cds
8403	21372	34780	1.63	2.0E-41	M96944.1	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L), mRNA
8403	21372	34781	1.63	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8403	21372	34781	1.63	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8433	21402	34815	1.47	2.0E-41	AA328265.1	EST_HUMAN	EST31723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
9326	22291	35721	1.61	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
9772	22713	36167	0.72	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9772	22713	36168	0.72	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11815	24700	38281	2.21	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3219	16274	29197	1.33	1.0E-41	BE869735.1	EST_HUMAN	601445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
3219	16274	29198	1.33	1.0E-41	BE869735.1	EST_HUMAN	601445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4598	17819	30512	7.8	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
7026	18358	31278	0.49	1.0E-41	H99078.1	EST_HUMAN	yc18b03.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:262061 3'
9773	22714	38169	1.73	1.0E-41	AI217868.1	EST_HUMAN	q75c10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
11494	24437	37986	1.55	1.0E-41	AW847812.1	EST_HUMAN	IL3-CT0213-190200-040-F09 CT0213 Homo sapiens cDNA
12332	25132		2.72	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8863	21832		1.06	9.0E-42	BE179191.1	EST_HUMAN	RC0-HT0813-210300-032-g01 HT0613 Homo sapiens cDNA
9529	22492	35939	3.08	9.0E-42	11590151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9529	22492	35940	3.08	9.0E-42	11590151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
463	13536	28462	6.85	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2118	15135	28155	1.18	8.0E-42	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5197	18206	31080	1.06	8.0E-42	6679031	NT	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1), mRNA
12376	26850		28	8.0E-42	AA493896.1	EST_HUMAN	inh07c02.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304
12394	25726		1.55	8.0E-42	AW088062.1	EST_HUMAN	367BP EXPRESSED SEQUENCE TAG MRNA ;
932	13985		1.46	7.0E-42	AL163285.2	NT	xc97a04.x1 NCL CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2582174 3' similar to contains OFR.12
8814	21781		0.6	7.0E-42	R10963.1	EST_HUMAN	OFR repetitive element ;
9598	22603	36052	1.67	7.0E-42	AI204358.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
11508	24450	38000	3.47	7.0E-42	AA569592.1	EST_HUMAN	yc38g04.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:129174 5'
11508	24450	38001	3.47	7.0E-42	AA569592.1	EST_HUMAN	q758g12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1873	14898	27895	3.35	6.0E-42	AF012872.1	NT	nt23g07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1873	14898	27896	3.35	6.0E-42	AF012872.1	NT	nt23g07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
2287	15309		5.49	6.0E-42	AW238656.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
							Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
							xp28f08.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L.1.11 L1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5039	18052		1.48	6.0E-42	A1284770.1	EST_HUMAN	q124h09.x1 NCI_CGAP_Br12 Homo sapiens cDNA clone IMAGE:1965761 similar to contains Alu repetitive element;
5543	18840	31580	1.8	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5805	18840	31580	1.37	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
136	13241		5.99	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
438	13612	28443	1.7	5.0E-42	BE217913.1	EST_HUMAN	h331e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
487	13560		4.65	5.0E-42	5730038	NT	Homo sapiens SET domain and meriner transposase fusion gene (SETMAR) mRNA
488	13561		1.37	5.0E-42	5730038	NT	Homo sapiens SET domain and meriner transposase fusion gene (SETMAR) mRNA
6844	19897	33191	1.07	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6844	19897	33192	1.07	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
8971	20194	33522	2.61	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7409	20376	33727	1.6	5.0E-42	AF071569.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
8110	21047	34447	0.51	5.0E-42	4826977	NT	Homo sapiens reelin (RELN) mRNA
9131	22097	36524	2.98	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10970	23890	37403	0.48	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10970	23890	37404	0.48	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
12087	24959	38555	3.28	5.0E-42	X98411.1	NT	H. sapiens mRNA for myosin-II
12087	24959	38556	3.28	5.0E-42	X98411.1	NT	H. sapiens mRNA for myosin-II
754	13815	26758	23.04	4.0E-42	AF050066.1	NT	Homo sapiens MHC class 1 region
754	13815	26759	23.04	4.0E-42	AF050066.1	NT	Homo sapiens MHC class 1 region
1087	14112	27082	2.03	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4223	17252	30139	1.24	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4255	17284	30186	1.12	4.0E-42	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4277	17306	30185	4.28	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4613	17834	30526	10.89	4.0E-42	4508003	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5290	18295	31155	1	4.0E-42	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5290	18295	31156	1	4.0E-42	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10850	23770	37269	0.54	4.0E-42	AW371201.1	EST_HUMAN	CMO-BT0282-171289-127-b03 BT0282 Homo sapiens cDNA
11010	23975	37499	1.88	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11010	23975	37500	1.88	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11741	24628	38205	2.69	4.0E-42	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1479	14512	27488	4.08	2.0E-42	BF376834.1	EST_HUMAN	RCO-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2402	15409	28433	0.93	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCCBB08 5'
2422	15429		3.65	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-110 NN0070 Homo sapiens cDNA
2432	15439	28456	3.27	2.0E-42	AW250059.1	EST_HUMAN	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283 3'
5850	18940	32124	11.89	2.0E-42	AW955388.1	EST_HUMAN	EST387438 MAGE resequences, MAGE Homo sapiens cDNA
5850	18940	32125	11.89	2.0E-42	AW955388.1	EST_HUMAN	EST387438 MAGE resequences, MAGE Homo sapiens cDNA
6636	19884	32971	0.73	2.0E-42	M29145.1	NT	Human hepatocyte growth factor (hHGF) mRNA, complete cds
6918	19988	33263	0.77	2.0E-42	A1052596.1	EST_HUMAN	ow83d05.x1 Soares_fetal_liver_spleen_1NF1.S1 Homo sapiens cDNA clone IMAGE:1663417 3'
10201	23126	36612	1.17	2.0E-42	BE638819.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10415	23337	36822	0.61	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
10415	23337	36823	0.61	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
10974	23884	37408	0.82	2.0E-42	AW834834.1	EST_HUMAN	RCO-LT0001-150200-032-d11 LT0001 Homo sapiens cDNA
12045	24919	38515	1.48	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
735	13795	28734	2.47	1.0E-42	X57147.1	NT	Human endogenous retrovirus pR1.1 (ERV9)
1043	14089	27042	0.76	1.0E-42	AW265809.1	EST_HUMAN	U1-H-B1-afth-e-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1103	14147	27097	1.27	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1103	14147	27098	1.27	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1247	15862	27248	12.69	1.0E-42	AF087186.1	NT	Homo sapiens NADH-ubiquinol oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1247	15862	27249	12.69	1.0E-42	AF087186.1	NT	Homo sapiens NADH-ubiquinol oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1711	14741	27725	2.08	1.0E-42	11423218	NT	Homo sapiens rec (LOC51201), mRNA
2046	15065	28085	1.05	1.0E-42	AF110298.1	NT	Homo sapiens PDN1 gene, exon 17
2551	15553	28573	1.88	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2975	16033	28956	10.93	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3721	16784	29675	2.43	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3948	16988	29903	1.02	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4274	17303	30183	1.85	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4624	17645	30533	0.77	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161089-012-a03 ST0197 Homo sapiens cDNA
4776	17798	30888	2.44	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4783	17798	30888	2.44	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4813	17830	30728	5.31	1.0E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4897	18012	30899	0.79	1.0E-42	Z46120.1	EST_HUMAN	HS00FF071 normalized infant brain cDNA Homo sapiens cDNA clone c-0ff07

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Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10446	23368	36859	4.15	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
653	13719	26541	14	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
653	13719	26542	14	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
701	13763	26595	4.8	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
701	13763	26596	4.8	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
701	13763	26597	4.8	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
6783	18875	32057	0.78	8.0E-43	H13952.1	EST_HUMAN	y05a11.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3655	16698	28613	7.28	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
9121	22087		3.41	7.0E-43	A1836748.1	EST_HUMAN	wp65b01.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
1347	14382		14.15	6.0E-43	AA491890.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
2598	15599		2.91	6.0E-43	AV708201.1	EST_HUMAN	ne72d06.s1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:309803 similar to gb:L05095 60S
6444	19509	32759	2.16	6.0E-43	8955979	NT	RIBOSOMAL PROTEIN L30 (HUMAN);
7093	20027	33331	1.91	6.0E-43	AW468897.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADCAGC10 5'
10210	23135	36622	2.31	6.0E-43	AA195154.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant
11437	24390		2.08	6.0E-43	AL119158.1	EST_HUMAN	MRP3B, mRNA
144	13247		1.8	5.0E-43	AL163113.2	NT	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910691 3' similar to contains
503	13575	26496	3.96	5.0E-43	AA382780.1	EST_HUMAN	MER1.13 MER1 MER1 repetitive element ;
2859	15919	28840	1.63	5.0E-43	AV732578.1	EST_HUMAN	z35a06.r1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:865410 5' similar to TR:G529641
6438	20021	33323	1.15	5.0E-43	A1613509.1	EST_HUMAN	G529641 DB1, COMPLETE CDS, ; contains element PTR7 repetitive element ;
7087	20021	33323	0.65	5.0E-43	A1613509.1	EST_HUMAN	DKFZp761L1712.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
8528	21496	34910	0.7	5.0E-43	AA442271.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
8528	21496	34911	0.7	5.0E-43	AA442271.1	EST_HUMAN	EST96033 Testis 1 Homo sapiens cDNA 5' end
9231	22197		0.59	5.0E-43	H74277.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'
9719	22747	36198	4.22	5.0E-43	AA45288.1	EST_HUMAN	tw22e07.x1 NCI CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
10763	23684	37180	2.36	5.0E-43	A1733244.1	EST_HUMAN	tw22e07.x1 NCI CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
10802	23723	37225	1.45	5.0E-43	AL049110.1	EST_HUMAN	z35a06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
11115	24075	37598	4.88	5.0E-43	AW863007.1	EST_HUMAN	z35a06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
11768	23941	37463	3.46	5.0E-43	X15804.1	NT	y49g12.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:229510 5'
							aa33d08.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:816055 5'
							oo52c10.x5 NCI CGAP_Lus5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591
							PV14 GENE ;
							DKFZp434D0119.r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D0119
							MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
							Human mRNA for alpha-actinin

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
974	15816	26979	3.95	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5331	18437	31189	1.18	4.0E-43	AI056338.1	EST_HUMAN	oy47n03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1659013 3'
6505	19559	32821	0.78	4.0E-43	6906009	NT	Homo sapiens glycyl-IRNA synthetase (GARS), mRNA
7337	20308		1.94	4.0E-43	11418793	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
8518	21486	34900	5.73	4.0E-43	AI244341.1	EST_HUMAN	q76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
8518	21486	34901	5.73	4.0E-43	AI244341.1	EST_HUMAN	q76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
10678	23600	37095	1.39	4.0E-43	6005967	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
12306	25115		6.35	4.0E-43	R20950.1	EST_HUMAN	yg06b05.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;
1218	14266		3.95	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1704	14734	27716	1.63	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autoantigen
3586	16631	29549	1.32	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4319	17348	30232	1.02	3.0E-43	AA548154.1	EST_HUMAN	nk55d08.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
5003	18017	30904	0.98	3.0E-43	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
5424	18527	31405	0.51	3.0E-43	M69269.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
5424	18527	31406	0.51	3.0E-43	M59259.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
5996	19090	32277	0.9	3.0E-43	D34613.1	NT	Human TBXA31 gene for thromboxane synthase, promoter region and exon 1
6492	19557	32807	1.86	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6492	19557	32808	1.86	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6890	19942	33238	4.38	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8503	21471		8.69	3.0E-43	AA458824.1	EST_HUMAN	aa88f1.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element ;
9172	22136	35584	1.82	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
10223	23148	36637	0.6	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (Ht. sapiens) (LOC63948), mRNA
185	13285		9.29	2.0E-43	AI190764.1	EST_HUMAN	qd81c09.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1733988 3' similar to contains PTR7.13
6820	19878	32955	0.95	2.0E-43	BE222778.1	EST_HUMAN	PTR7 PTR7 repetitive element ; hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6620	10678	32956	0.95	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Bim41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
7491	20486	33814	1.07	2.0E-43	AW207390.1	EST_HUMAN	UI-H-B1-af-a-09-0-UI.st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8651	21619		9.34	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11632	24473		2.86	2.0E-43	T03007.1	EST_HUMAN	FB1G5 Fetal brain, Stralagene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1657	14689	27684	4.13	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1657	14689	27685	4.13	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1717	14747	27733	2.13	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2794	15728	28742	5.67	1.0E-43	BF948283.1	EST_HUMAN	602022313F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4157866 5'
6484	18584	31498	0.77	1.0E-43	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6764	19818	33098	6.3	1.0E-43	4507169	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6764	19818	33099	6.3	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
7159	18391	31235	1.87	1.0E-43	R19751.1	EST_HUMAN	Yg40d01.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP-BD38_MOUSE P28658 BRAIN PROTEIN DN38 ;
8264	21233	34844	0.97	1.0E-43	AF175265.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8401	21370		3.16	1.0E-43	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
9189	22155	35584	30.83	1.0E-43	AW963676.1	EST_HUMAN	EST1375749 IMAGE resequences, MAGH Homo sapiens cDNA
10654	23576	37073	0.62	1.0E-43	AW953229.1	EST_HUMAN	EST1365299 IMAGE resequences, MAGB Homo sapiens cDNA
11311	24261	37767	5.9	1.0E-43	A1984961.1	EST_HUMAN	wr87t01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
11693	24658	38236	3.35	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12244	25074		2.8	1.0E-43	AL137664.1	EST_HUMAN	DKFZp781D1015.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781D1015 5'
12542	25265	31808	2.24	1.0E-43	A1675416.1	EST_HUMAN	wb9b04.x1 NCI_CGAP_P288 Homo sapiens cDNA clone IMAGE:2313775 3'
12745	25394	31757	2.8	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
891	13948	26904	7.09	8.0E-44	A1222985.1	EST_HUMAN	qh23g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
891	13948	26905	7.09	8.0E-44	A1222985.1	EST_HUMAN	qh23g01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8894	21850	35271	2.88	8.0E-44	X94354.1	NT	H sapiens DNA for Cone cGMP-PDE gene
10702	23624	37120	0.47	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
10702	23624	37121	0.47	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11499	24442	37993	3.83	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
11965	24872	38469	2.24	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
12495	25237	31801	2.95	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12536	25577	31698	1.53	8.0E-44	11418088	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12870	25755	31516	2.68	8.0E-44	11418089	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
13029	25577	31698	1.58	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
660	13726		0.87	7.0E-44	R06035.1	EST_HUMAN	ye89e07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2243	15257	28283	0.95	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2877	16035	28957	2.88	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2977	16035	28958	2.68	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3876	16915	29824	2.55	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4270	17289	30177	1.07	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4270	17289	30178	1.07	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5168	18177	31055	1.04	7.0E-44	AF111186.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8526	21494	34308	5.87	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
6223	19287	32531	0.85	6.0E-44	Z20946.1	EST_HUMAN	HSAAADEYU P. Human foetal Brain Whole tissue Homo sapiens cDNA
12070	24943	38538	1.83	6.0E-44	AW954050.1	EST_HUMAN	EST366120 IMAGE resequences, MAGC Homo sapiens cDNA
303	13397		3.9	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
332	13421		2.86	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
8220	21189	34598	3.85	5.0E-44	AI568523.1	EST_HUMAN	In40402.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9739	22767		2.65	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element
3425	16473	29392	3.2	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5050	18062		1.02	4.0E-44	AI435225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7711	20868	34035	0.66	4.0E-44	BE883178.1	EST_HUMAN	it11d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8614	21582	34998	0.64	4.0E-44	L21948.1	NT	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
9230	22796		0.49	4.0E-44	BE176618.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11659	24508	38065	8.23	4.0E-44	U90878.1	NT	RC3-HT0585-010400-023-c08 HT0585 Homo sapiens cDNA
1801	14829		0.95	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
2537	15539	28562	0.95	3.0E-44	BE880628.1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
3114	16171	29081	6.12	3.0E-44	AA169851.1	EST_HUMAN	601491520F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3853839 5'
3905	16945	29858	1.71	3.0E-44	AA337234.1	EST_HUMAN	zp18b05.11 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:609777 5'
8074	21011	34410	0.55	3.0E-44	BE884820.1	EST_HUMAN	EST42299 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
9877	22830	36284	0.58	3.0E-44	AF005273.1	NT	601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
1051	14097	27047	1.04	2.0E-44	4826685	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1051	14097	27048	1.04	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1212	14250	27208	2.52	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1212	14250	27209	2.52	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1316	14350	27318	5.49	2.0E-44	AF133588.1	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1370	14404	27374	1.05	2.0E-44	BE465325.1	EST_HUMAN	hwt4g06.xt NCJ CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2161	15177	28198	2.57	2.0E-44	AF070651.1	NT	P22059 OXYSTEROL-BINDING PROTEIN. ;
2618	15816		2.01	2.0E-44	5901833	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
3484	16530	29455	1.18	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4600	17821	30514	1.8	2.0E-44	AW864379.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6214	19288	32521	1.59	2.0E-44	11448901	NT	PM4-SN0016-120500-003-g04 SN0016 Homo sapiens cDNA
							Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
7037	18369	31256	1.73	2.0E-44	AF038988.1	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds
7646	20605	33970	3.8	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7645	20605	33971	3.8	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8771	21738	35158	0.72	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8771	21738	35159	0.72	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8966	21832	35357	1.83	2.0E-44	BE388058.1	EST_HUMAN	601286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813566 5'
							TCBAP1E2785 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2785
12152	25010		1.44	2.0E-44	BE244902.1	EST_HUMAN	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12695	26898		1.32	2.0E-44	4828863	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
13047	25987		1.58	2.0E-44	11628293	NT	Homo sapiens Mischep/NIK-related kinase (MINIK), mRNA
54	13174	26084	7.76	1.0E-44	7657334	NT	Homo sapiens Mischep/NIK-related kinase (MINIK), mRNA
54	13174	26085	7.76	1.0E-44	7657334	NT	Homo sapiens Mischep/NIK-related kinase (MINIK), mRNA
592	13650	26564	1.85	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0248-030300-028-h12 CT0249 Homo sapiens cDNA
1202	14241		1.85	1.0E-44	AW894803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1577	14610		7.03	1.0E-44	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
							zw53d02.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element ;
2233	15247	28270	4.49	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element ;
2233	15247	28271	4.49	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element ;
2280	15889	28327	0.95	1.0E-44	AA398089.1	EST_HUMAN	z88g11.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
							Homo sapiens transcription factor IG-HM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha
2770	15762	28783	2.5	1.0E-44	AF196779.1	NT	aa01c08.s1 Soares NIH-HMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
3738	16780		3.01	1.0E-44	AA455869.1	EST_HUMAN	Homo sapiens alpha satellite DNA, M1 monomer type
5165	18165	31043	0.64	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5165	18165	31044	0.64	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type

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8608	21576	34991	1.17	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8608	21576	34992	1.17	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAGJ Homo sapiens cDNA
8903	21859	35385	1.23	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9381	22346	35778	0.59	1.0E-44	AI337183.1	EST_HUMAN	q88g07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009628 3'
11354	24304		12.74	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11658	24740	38325	3.23	1.0E-44	10092664	NT	Homo sapiens Sush1 domain (SCR repeat) containing (BK63A6.2), mRNA
11917	24788	38388	2.7	1.0E-44	AW849867.1	EST_HUMAN	RC1-CT0198-160989-011-C08 CT0198 Homo sapiens cDNA
11917	24788	38388	2.7	1.0E-44	AW849867.1	EST_HUMAN	RC1-CT0198-160989-011-C08 CT0198 Homo sapiens cDNA
4609	17630	30522	1.16	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4609	17630	30523	1.16	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6806	19860	33147	1.52	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2529	16532	28663	1.57	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5119	18129	31005	8.66	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8444	21413	34827	0.85	8.0E-45	AA377885.1	EST_HUMAN	EST80893 Synovial sarcoma Homo sapiens cDNA 5' end
2969	16027		0.96	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22
1556	14588		1	9.0E-45	AI075425.1	EST_HUMAN	w596c06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.11 L1 repetitive element;
4003	17042		3.48	9.0E-45	AW157570.1	EST_HUMAN	eu83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2792909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
12836	25948		1.53	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
803	13948		1.56	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2018	15039	28050	4.99	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-101 CN0044 Homo sapiens cDNA
3223	16278	29203	1.49	5.0E-45	AI523766.1	EST_HUMAN	tg94f07.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1 ;
5580	18686	31654	8.41	5.0E-45	AA397781.1	EST_HUMAN	z172d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
6135	19212	32439	1.46	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6136	19212	32440	1.48	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6163	19258	32491	0.84	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6183	19258	32492	0.84	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6313	19384	32625	1.07	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6313	19384	32626	1.07	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8619	21587	35003	0.66	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9388	22361	35792	1.29	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12003	24880	38476	2.3	5.0E-45	8923998	NT	Homo sapiens golgin-like protein (GLP), mRNA
1146	14188	27139	10.78	4.0E-45	X95828.1	NT	H.sapiens ART4 gene
2299	16311	28331	1.91	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
4535	17558	30446	0.72	4.0E-45	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
9308	22273		0.89	4.0E-45	AA226220.1	EST_HUMAN	nc26607.s1 NCL_OGAP_P1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element:
12167	25894	31418	1.4	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
4115	16393		0.99	3.0E-45	T71480.1	EST_HUMAN	y435107.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6364	19433	32678	1.13	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahe11), mRNA
6384	19433	32677	1.13	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahe11), mRNA
8794	21761		1.53	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAA001 5'
8143	22109	35535	3.82	3.0E-45	4768451	NT	Homo sapiens golgi autanigen, golgin subfamily a, 2 (GOLGA2) mRNA
10670	23592	37087	10.86	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10670	23592	37088	10.98	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12954	25888		4.13	3.0E-45	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2511	15514		1.96	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3045	18102	29016	1.9	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6671	19728	33004	5.17	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7868	20812	34189	1.25	2.0E-45	BE782184.1	EST_HUMAN	601487793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870338 5'
8768	21725	35148	1.08	2.0E-45	AW834834.1	EST_HUMAN	RC0-J10001-150200-032-411 LT0001 Homo sapiens cDNA
11154	25704	37639	25.96	2.0E-45	BE834350.1	EST_HUMAN	MR0-HT0923-180800-201-a02 HT0923 Homo sapiens cDNA
11611	24462	38002	3.5	2.0E-45	AA458770.1	EST_HUMAN	aa87112.11 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11832	24715	38268	1.87	2.0E-45	AW270280.1	EST_HUMAN	TR-G1144569 G1144569 R-SLY1.
11832	24715	38268	1.87	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_OGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
12669	25555		3.46	2.0E-45	11418157	NT	xp72a03.x1 NCL_OGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
124	13482		1.84	1.0E-45	BE389855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
409	13482		2.09	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
473	13545	28474	1.93	1.0E-45	4506412	NT	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
1178	14219	27175	1.94	1.0E-45	7657260	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3120	16177	29088	7.12	1.0E-45	U32169.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3503	16550	29477	0.84	1.0E-45	8659558	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
4503	17528	30413	4.06	1.0E-45	BE386633.1	EST_HUMAN	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
							601280116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3819803 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4757	17777		1.01	1.0E-45	H57443.1	EST_HUMAN	yr05b02.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:204363 5'
8365	21334	34746	0.57	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8365	21334	34746	0.57	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8954	21920	35346	0.85	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9476	22440	35880	4.82	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9880	22833	36287	1.03	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0209 gene, partial cds
12369	25155	31856	9.31	1.0E-45	11418098	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12551	25274		9.31	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12556	25277		6.48	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12962	25532	31715	3.88	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8570	21638	34959	1.68	9.0E-46	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
8981	21947		7.02	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10845	23765	37284	9.09	9.0E-46	AW246984.1	EST_HUMAN	2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2448	15453	28474	11.23	8.0E-46	A1493281.1	EST_HUMAN	1132008.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
2448	15453	28476	11.23	8.0E-46	A1433281.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8389	21358		6.79	8.0E-46	BE167244.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
2248	15262	28289	1.17	7.0E-46	U46007.1	NT	RC5-HT0506-280200-012-G12 HT0506 Homo sapiens cDNA
4611	17632		3.58	7.0E-46	BE886165.1	EST_HUMAN	Rattus norvegicus eepin mRNA, complete cds
4845	17862		1.14	7.0E-46	BE064388.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
6150	18235	32466	3.92	7.0E-46	8922708	NT	RC4-BT0310-110300-016-f10 BT0310 Homo sapiens cDNA
6842	19700	32976	1.95	7.0E-46	BF105545.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
2765	15757	28778	5.63	6.0E-46	A1884381.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042738 5'
2765	15757	28779	5.63	6.0E-46	A1884381.1	EST_HUMAN	wm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
6252	18325	32556	10.15	6.0E-46	A1635448.1	EST_HUMAN	wm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
7426	20393	33743	0.76	6.0E-46	AW513244.1	EST_HUMAN	MER19 repetitive element
7609	20570	33933	0.51	6.0E-46	BF509740.1	EST_HUMAN	ts58r10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE.
205	13306		6.47	5.0E-46	AL163210.2	NT	xc42604.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:L08069 DNAJ
3639	16686	29508	1.01	5.0E-46	BE677194.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
							UH-BI4-aps-5-06-0-U1.st NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
							Homo sapiens chromosome 21 segment HS21C010
							7d81g01.x1 LupsK_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3539	16585	29509	1.01	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupskl_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6899	19951	33248	1.84	5.0E-46	BF590442.1	EST_HUMAN	naa3807.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202
7128	20104	33415	3.97	5.0E-46	BF347229.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
7302	20273	33609	0.87	5.0E-46	AW682263.1	EST_HUMAN	602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
7614	20574	33938	0.56	5.0E-46	BE549744.1	EST_HUMAN	QV4-ST0212-120100-075-009 ST0212 Homo sapiens cDNA
							7638b06.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
642	13708		2.88	4.0E-46	AA601143.1	EST_HUMAN	nc034609.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
							FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1715	14745	27729	7.91	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
							LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
1715	14745	27730	7.91	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
2749	15742	28759	3.26	4.0E-46	M18048.1	NT	LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
4447	17473	30361	0.95	4.0E-46	AB014522.1	NT	Human endogenous retrovirus RTVL-H2
4447	17473	30362	0.95	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
5194	18203	31076	0.78	4.0E-46	BE044280.1	EST_HUMAN	Homo sapiens mRNA for KIAA0622 protein, partial cds
5194	18203	31077	0.78	4.0E-46	BE044280.1	EST_HUMAN	ho42a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5511	18611	31542	2.11	4.0E-46	M36852.1	NT	ho42a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5511	18611	31543	2.11	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12792	25422	31737	2.51	4.0E-46	AB002059.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
4421	17448	30339	1.21	3.0E-46	4506376	NT	Homo sapiens DNA for Human P2XM1, complete cds
							Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4809	17826	30722	2.84	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
4809	17828	30723	2.84	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
9102	22068	35494	10	3.0E-46	A1831492.1	EST_HUMAN	wj49c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
9358	22323	35750	0.59	3.0E-46	L08850.1	NT	THR repetitive element;
9358	22323	35751	0.69	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
11898	24779	38365	2.01	3.0E-46	D31765.1	NT	Human AD amyloid mRNA, complete cds
							Human mRNA for KIAA0061 gene, partial cds
838	13895	26850	10.84	2.0E-46	AA468946.1	EST_HUMAN	nc034609.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
							repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1564	14597		2.13	2.0E-46	AA678246.1	EST_HUMAN	z127a11.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431986 3'
1647	14679	27652	4.43	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
5010	18024	30910	1.06	2.0E-46	AA399286.1	EST_HUMAN	z159a02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE
7726	20682	34048	7.69	2.0E-46	9910669	NT	Q01730 RSP-1 PROTEIN ;
8404	21373		1.18	2.0E-46	BE869151.1	EST_HUMAN	Mus musculus sperm tail associated protein (Slap), mRNA
11576	24514		1.82	2.0E-46	7657233	NT	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
12857	25741	31619	3.22	2.0E-46	AW277214.1	EST_HUMAN	Homo sapiens small acidic protein (IMAGE145052), mRNA
1237	14273	27233	6.66	1.0E-46	4502864	NT	xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
2289	15302	28328	3.26	1.0E-46	AW978516.1	EST_HUMAN	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2409	15416	28440	2.9	1.0E-46	H97330.1	EST_HUMAN	EST390625 IMAGE resequences, MAGP Homo sapiens cDNA
3262	16316	29238	1.32	1.0E-46	AA631912.1	EST_HUMAN	EST48b095 WATM1 Homo sapiens cDNA clone 48b095
4908	17925		2.93	1.0E-46	AB023197.1	NT	np78b02.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-II mRNA, (HUMAN);
5784	18876	32058	7.06	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
6089	25653	32382	5.57	1.0E-46	8923762	NT	7c92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6089	25653	32383	5.57	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6766	19820	33102	0.65	1.0E-46	BF198247.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
11211	18876	32058	3.61	1.0E-46	BF194707.1	EST_HUMAN	7n48e07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element MER22 repetitive element ;
12322	25124	31845	1.52	1.0E-46	BF531102.1	EST_HUMAN	7c92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
12322	25124	31846	1.52	1.0E-46	BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
13066	25600		4.54	1.0E-46	AV718377.1	EST_HUMAN	602072264F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
767	13826		3.24	9.0E-47	AJ271735.1	NT	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
4968	17983	30873	3.91	9.0E-47	AW770928.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
6513	19577	32832	1.68	9.0E-47	11425439	NT	h93e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009634 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN ;
12816	25843	31432	2.25	9.0E-47	11417968	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
1825	14852	27846	47.72	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1825	14852	27847	47.72	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2728	15722	28739	1.77	8.0E-47	5453955	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
3036	18094	29012	2.12	8.0E-47	AJ229043.1	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
							Homo sapiens 956 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3640	16683	28598	0.78	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
3640	16683	28598	0.78	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
5254	18262	31131	0.65	8.0E-47	7682421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
2555	15557	28575	2.2	6.0E-47	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C046
9040	22008	35427	0.49	6.0E-47	U77054.1	EST_HUMAN	HSU77054 Human Homo sapiens cDNA clone N7
9631	22575	36025	6.5	6.0E-47	A1695189.1	EST_HUMAN	5288102.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286659 3'
10070	22997	38465	0.86	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
10070	22997	38466	0.88	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6729	19785	33064	6.56	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11147	24107		4.6	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratiogene (cat#36206) Homo sapiens cDNA clone HFBCF07
1400	14433	27403	4.48	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
7006	20132	33447	0.98	4.0E-47	BE938986.1	EST_HUMAN	MR4-TN0108-280800-201-d04 TN0108 Homo sapiens cDNA
8825	21792	35214	2.45	4.0E-47	BE16483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8825	21792	35215	2.45	4.0E-47	BE16483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8965	21931	35356	0.81	4.0E-47	AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-05 BN0034 Homo sapiens cDNA
11954	24833		5.51	4.0E-47	AW515509.1	EST_HUMAN	x66607.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
546	13617	26538	1.73	3.0E-47	BE907634.1	EST_HUMAN	Q64282 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
546	13617	26539	1.73	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
819	13677	26826	6.7	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
944	13697	26949	7.86	3.0E-47	AL163284.2	NT	yy54b04.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:277327 3'
3315	16368	29288	0.7	3.0E-47	4504116	NT	Homo sapiens chromosome 21 segment HS21C084
3990	17030		6.21	3.0E-47	U93181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4389	17417	30301	0.98	3.0E-47	M12959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
6128	19206	32429	4.76	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6128	19208	32430	4.76	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BMO-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6716	19772		1.72	3.0E-47	A1222413.1	EST_HUMAN	UI-HF-BMO-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7608	20569	33931	0.59	3.0E-47	A1819755.1	EST_HUMAN	qh04e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7608	20569	33932	0.59	3.0E-47	A1819755.1	EST_HUMAN	wj11h08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9185	22151	35579	0.59	3.0E-47	AW963796.1	EST_HUMAN	wj11h08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9185	22151	35580	0.59	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGe resequences, MAGH Homo sapiens cDNA
149	13252	26181	1.57	2.0E-47	4505318	NT	EST375869 MAGe resequences, MAGH Homo sapiens cDNA
969	14021	26973	2.24	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
969	14021	26974	2.24	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1570	14603		1.08	2.0E-47	AB99279.1	EST_HUMAN	wq8b02.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2479851 3'
1597	14620	27604	2.2	2.0E-47	7662109	NT	Homo sapiens KIA0426 gene product (KIA0426), mRNA
1687	14718	27698	3.87	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:937607 3'
4374	17402	30282	1.82	2.0E-47	4504866	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4411	17439	30327	1.48	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:914852
4411	17439	30328	1.48	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:914852
4534	17557	30445	1.88	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4850	17867	30760	1.22	2.0E-47	AW965166.1	EST_HUMAN	EST377239 MAGE sequences, MAGI Homo sapiens cDNA
5187	18196		0.7	2.0E-47	AI041126.1	EST_HUMAN	ov61h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
5880	18989	32160	1.22	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6088	19168	32380	1.29	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3887487 5'
6088	19168	32381	1.29	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3887487 5'
7884	25692		1.43	2.0E-47	LO9731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8297	21266	34677	1.76	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8297	21266	34678	1.76	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9088	22034	35457	1.75	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9845	22781	36235	0.76	2.0E-47	11526136	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
11800	23955	37478	2.31	2.0E-47	M76125.1	NT	Human tyrosine kinase receptor (axl) mRNA, complete cds
12358	25886	31415	2.12	2.0E-47	R42423.1	EST_HUMAN	yf92e08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFR repetitive element;
1404	14437	27405	6.91	1.0E-47	AB333429.1	EST_HUMAN	qp59h03.x1 Soares_fetal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3835	16875	29776	1.18	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3835	16875	29777	1.18	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5112	18122	30897	2.55	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
7244	19879	33276	6.6	1.0E-47	AB80888.1	EST_HUMAN	att19e06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995
9220	22186		0.77	1.0E-47	AW664648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10721	23643	37136	2.41	1.0E-47	L30115.1	NT	hi84a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M26326
1618	14648	27823	3.85	9.0E-48	AF223391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3509	16614	29536	0.7	9.0E-48	BF359947.1	EST_HUMAN	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
5763	18855	32035	0.84	9.0E-48	BE888196.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5763	18855	32036	0.84	9.0E-48	BE888196.1	EST_HUMAN	CM2-MT0100-310700-290-f05 MT0100 Homo sapiens cDNA
							601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
							601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6220	19294	32528	0.6	9.0E-48	AB83168.1	EST_HUMAN	at75h09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844
6351	19420	32851	0.73	9.0E-48	AU123240.1	EST_HUMAN	O60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN. ;
11452	24395	37940	2.49	9.0E-48	BE393813.1	EST_HUMAN	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
1255	14291		1.5	8.0E-48	4501900	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
1256	14291		1.54	8.0E-48	4501900	NT	Homo sapiens aminoacylase 1 (ACY1), mRNA
3152	16209	29123	3.31	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminoacylase 1 (ACY1), mRNA
3152	16209	29124	3.31	8.0E-48	AW768477.1	EST_HUMAN	hkb1b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
491	13584		1.54	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
492	13564		22.81	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1496	14529	27501	1.04	7.0E-48	6912719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1643	14675	27648	4.5	7.0E-48	5730038	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
6707	19763	33042	24.74	7.0E-48	11416831	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
3812	16657	29575	1.2	6.0E-48	AI781111.1	EST_HUMAN	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
6176	19251	32484	1.12	6.0E-48	AB006955.1	NT	Homo sapiens SET domain and matrin transferase fusion gene (SETMAR) mRNA
6953	20177	33502	0.89	6.0E-48	11420985	NT	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
7702	25687	34022	0.56	6.0E-48	AB046844.1	NT	wf9h03.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
9479	22443	35885	1.94	6.0E-48	AF026916.1	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
9899	22852	36311	1.78	6.0E-48	11427428	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
10047	22974	36441	3.3	6.0E-48	AA189080.1	EST_HUMAN	Homo sapiens putative oncogene protein mRNA, partial cds
3320	18313	29292	1.58	5.0E-48	4828691	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
8921	21887	35314	1.11	5.0E-48	BE064410.1	EST_HUMAN	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
11306	24256	37782	2.83	4.0E-48	AI620420.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
1385	14419	27388	1.33	3.0E-48	AV690964.1	EST_HUMAN	RC4-BT0311-141199-0711-h06 BT0311 Homo sapiens cDNA
1893	15014	28020	16.21	3.0E-48	4885170	NT	tu47a02.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2254154 3'
1993	15014	28021	16.21	3.0E-48	4885170	NT	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
3429	16477	28396	0.93	3.0E-48	AF172453.1	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3647	16680	28806	0.75	3.0E-48	AW664531.1	EST_HUMAN	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
4275	17304		0.9	3.0E-48	AA009541.1	EST_HUMAN	Homo sapiens opid growth factor receptor mRNA, complete cds
							h114b12.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872255 3' similar to SW:DCRB_HUMAN
							P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
							z104g03.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429844 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5987	19081	32278	2.41	3.0E-48	BE084571.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
7215	20237	33571	1.06	3.0E-48	AF087813.1	NT	Human endogenous retrovirus HERV-P-T47D
8734	21702		4.11	3.0E-48	AA659930.1	EST_HUMAN	nr0310.51 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
11221	24174	37700	6.89	3.0E-48	BF514170.1	EST_HUMAN	PTR5 repetitive element;
5	13126	26025	2.4	2.0E-48	AA465007.1	EST_HUMAN	UI-H-BW1-anti-e-10-OU.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
47	13167	26072	1.23	2.0E-48	AA631840.1	EST_HUMAN	z680c03.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810052 5'
1223	14261		0.65	2.0E-48	H24278.1	EST_HUMAN	frnc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
4562	17585	30477	0.92	2.0E-48	BE246055.1	EST_HUMAN	ym55e10.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:52182 5' similar to
5912	18998	32188	0.63	2.0E-48	AA613171.1	EST_HUMAN	SP.M6B_MOUSE P35803 MEMBRANE GLYCOPROTEIN ;
5912	18998	32189	0.63	2.0E-48	AA613171.1	EST_HUMAN	TCBAP-ID3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
7762	20715	34086	3.9	2.0E-48	AB040934.1	NT	not18g01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1101072 3'
7762	20715	34087	3.9	2.0E-48	AB040934.1	NT	not18g01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1101072 3'
7777	20730	34103	3.52	2.0E-48		NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
8696	21666	35089	1.37	2.0E-48	AV743451.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
12318	13128	26025	3.8	2.0E-48	AA465007.1	EST_HUMAN	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
58	13177	26089	3.37	1.0E-48		NT	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
874	13930	26888	1.61	1.0E-48		NT	z680c03.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810052 5'
1077	14122	27073	1.8	1.0E-48		NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
1077	14122	27074	1.8	1.0E-48		NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1299	14335	27298	5.06	1.0E-48		NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1933	14957	27954	14.5	1.0E-48	AL163302.2	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
3500	16547	29473	0.83	1.0E-48	AL163248.2	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
6420	19487	32736	1.17	1.0E-48	AI889077.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
6420	19487	32737	1.17	1.0E-48	AI889077.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
6648	19706		1.03	1.0E-48	Y18000.1	NT	Id17c01.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588
6748	19802	33082	0.7	1.0E-48	AB028994.1	NT	SIMILARITY TO U73941 ;
6748	19802	33083	0.7	1.0E-48	AB028994.1	NT	SIMILARITY TO U73941 ;
						NT	Homo sapiens NF2 gene
						NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
						NT	Homo sapiens mRNA for KIAA1071 protein, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7471	20437	33784	3.15	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9183	22149	35576	0.49	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9183	22149	35577	0.49	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9568	22530	35980	1.19	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9623	22587	36017	7.13	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9924	22808	36260	0.68	1.0E-48	BE169410.1	EST_HUMAN	QV3-HT0613-060400-147-301 HT0513 Homo sapiens cDNA
9941	22868	36330	4.48	1.0E-48	BF304683.1	EST_HUMAN	601888098F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119.5
10736	23658	37151	3.85	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10736	23658	37152	3.85	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
12280	25830		1.53	1.0E-48	W26785.1	EST_HUMAN	1566 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6171	19246	32478	3	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6171	19246	32479	3	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
7017	20143	33460	0.57	8.0E-49	AA642035.1	EST_HUMAN	ns18h03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184021.5
8638	21606	35029	3.32	8.0E-49	U23860.1	NT	Human insulin 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10348	23272	36748	2.1	8.0E-49	AB009681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
11204	24158	37888	2.32	8.0E-49	A1623722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871.3 similar to contains Alu repetitive element; contains element PTR5 repetitive element
140	13468	26398	2.24	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
140	13468	26399	2.24	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	13468	26398	1.53	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	13468	26399	1.53	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
394	13468	26398	2.06	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
394	13468	26399	2.06	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1225	14263	27220	2.85	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5535	18632	31571	1.57	7.0E-49	A1807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663.3 similar to TR:054923
5945	18642	31582	1.33	7.0E-49	AL120837.1	EST_HUMAN	Q54923 RSEC15.1
5903	18632	31571	0.84	7.0E-49	A1807191.1	EST_HUMAN	DKFZp762C033.1 762 (synonym: hme12) Homo sapiens cDNA clone DKFZp762C033.3
							wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663.3 similar to TR:054923
							Q54923 RSEC15.1
198	13289	26227	86.86	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504.3 similar to gb:X17206.40S
4142	17173	30062	1.14	6.0E-49	AL182091.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN); gp:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
6582	18642	32909	0.65	6.0E-49	AU140742.1	EST_HUMAN	DKFZp761A138.s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138.3
							AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148.5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11609	24547	38107	2	6.0E-49	AW452218.1	EST_HUMAN	UIH-B13-alo-a-05-0-J1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11972	24850	38446	4.09	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
11972	24850	38447	4.09	6.0E-49	AA366556.1	EST_HUMAN	EST77625 Pancreas tumor III Homo sapiens cDNA 5' end
12645	25723		1.7	6.0E-49	AA707587.1	EST_HUMAN	Z129c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
713	13775	26708	8.21	6.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
713	13775	26709	8.21	6.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1809	14837	27828	3.44	5.0E-49	AA172121.1	EST_HUMAN	zp29c07.r1 Stragene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:910860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN ; contains LTR7.13 LTR7 LTR7 repetitive element ;
2760	15752	28772	9.75	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3286	16340	29259	6.07	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metalloprotein 1) (H. sapiens) (LOC633362), mRNA
526	13597	26514	25.9	4.0E-49	AW189533.1	EST_HUMAN	X08b01.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B CE08703 ;
7457	20423	33778	1.06	4.0E-49	Z26834.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7457	20423	33779	1.06	4.0E-49	Z26834.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7487	20452	33811	0.68	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
7487	20452	33812	0.68	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
8109	21046	34446	0.71	4.0E-49	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
9216	22182	35514	0.53	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
9216	22182	35515	0.53	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
12508	25939		8.71	4.0E-49	AA210798.1	EST_HUMAN	Homo sapiens copine III (CPNE3), mRNA
12594	25297		3.19	4.0E-49	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
562	13632	28549	1.27	3.0E-49	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
2858	15853		1.93	3.0E-49	AA016131.1	EST_HUMAN	ze37c05.r1 Soares retina N2b44IR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
5019	18033	30919	2.11	3.0E-49	U46999.1	NT	Human type IV collagen (COL4A6) gene, exon 40
7650	20610	33978	10.82	3.0E-49	H39478.1	EST_HUMAN	EST25612 WATM1 Homo sapiens cDNA clone 25612
11633	24570	38134	1.54	3.0E-49	AA337561.1	EST_HUMAN	EST42672 Endometrial tumor Homo sapiens cDNA 5' end
682	13728		3.89	2.0E-49	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3235	16291	29213	1.6	2.0E-49	N28446.1	EST_HUMAN	yx23d06.r1 Soares melanocytes 2NbHM Homo sapiens cDNA clone IMAGE:262571 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3583	16628	29547	0.78	2.0E-49	AF026664.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
6900	19952	33249	1.14	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DCBALB01 5'
8436	21405		1.62	2.0E-49	M86033.1	EST_HUMAN	EST02668 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY60
12603	25821		2.57	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
900	13955		9.35	1.0E-49	BF035327.1	EST_HUMAN	60145853.1F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662086 5'
1557	14589	27660	1.27	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1818	14845	27837	3.33	1.0E-49	BE255216.1	EST_HUMAN	601115789F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
5433	18535	31444	5.72	1.0E-49	BF131007.1	EST_HUMAN	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
6198	19270	32505	0.87	1.0E-49	H18291.1	EST_HUMAN	Yn48h04.r1 Soares adult brain N256HB55Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP.QBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
6202	19276	32510	1	1.0E-49	AW064640.1	EST_HUMAN	EST1376713 MAGE resequences, MAGH Homo sapiens cDNA
7427	20394	33744	0.58	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCVD11 5'
7427	20394	33745	0.58	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCVD11 5'
7433	20400	33753	3.3	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3620863 5'
7433	20400	33754	3.3	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3620863 5'
7520	20485	33846	2.2	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta, 8tc9weeks, 2N6HP8tc9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7520	20485	33847	2.2	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta, 8tc9weeks, 2N6HP8tc9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
8414	21383	34790	0.69	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8414	21383	34791	0.69	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9023	21989		0.78	1.0E-49	9894184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
9344	22309	35734	1.14	1.0E-49	BE409340.1	EST_HUMAN	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10485	23407	36903	1.22	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434D2423 5'
11399	24344	37877	1.99	1.0E-49	AB020335.1	NT	Homo sapiens Pancreas-specific TSA305 mRNA , complete cds
11640	24577	38143	3.12	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12147	25007		1.7	1.0E-49	BE159343.1	EST_HUMAN	MRO-HT0407-010200-006-002-HT0407 Homo sapiens cDNA
12502	25241		2.78	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6544	25997		1.06	9.0E-50	BE295758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
171	13273	26198	3.9	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C0002
720	13782	26716	2.14	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
720	13782	26717	2.14	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1778	14807	27793	4	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2710	15704	28720	2.18	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
621	13686	26604	0.88	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
6952	20176	33500	1.21	7.0E-50	BF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
6952	20176	33501	1.21	7.0E-50	BF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7526	20490	33852	0.62	7.0E-50	AA627822.1	EST_HUMAN	nc59e12.s1 NCL_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X69391.60S
11108	24068	37560	28.05	7.0E-50	A1872137.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
8556	21524		6.09	6.0E-50	BE044076.1	EST_HUMAN	wm55g11.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439908 3'
11166	24124	37652	7.96	6.0E-50	AA312079.1	EST_HUMAN	hc36h04.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
11166	24124	37653	7.96	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1808	14836	27826	1.18	5.0E-50	BF332838.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1808	14838	27827	1.18	5.0E-50	BF332838.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
9448	22412		5.65	5.0E-50	AA557683.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
918	13972		1.45	4.0E-50	AA601143.1	EST_HUMAN	ni45p10.s1 NCL_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5
6497	19561	32813	0.54	4.0E-50	11440683	NT	nc54e08.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
7443	20411	33763	0.93	4.0E-50	BE087536.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1955	14978		2.86	3.0E-50	M18048.1	NT	Homo sapiens cysteine-RNA synthetase (CARS), mRNA
2525	15528	28549	1.11	3.0E-50	BE259196.1	EST_HUMAN	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
3310	16363	29283	0.88	3.0E-50	AA746142.1	EST_HUMAN	Human endogenous retrovirus RTVL-H2
6834	19887	33180	0.6	3.0E-50	11419317	NT	601103717F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350309 5'
6834	19887	33181	0.6	3.0E-50	11419317	NT	ob03f06.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
6929	20163	33472	1.56	3.0E-50	11421514	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
7806	20849	34234	4.3	3.0E-50	AF233436.2	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
7806	20849	34235	4.3	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8929	21895	35323	0.61	3.0E-50	6601589	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
10177	23102	36582	1.1	3.0E-50	AB046818.1	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10186	23111	36595	0.96	3.0E-50	11418514	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
10885	23805	37309	0.74	3.0E-50	AB002287.1	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA
11438	24381	37920	1.99	3.0E-50	11438955	NT	Human mRNA for KIAA0299 gene, partial cds
							Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11792	23947	37468	8.4	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
778	13837		6.9	2.0E-50	AF055066.1	NT	Homo sapiens MHC class 1 region
1081	14125	27078	6.73	2.0E-50	455752	NT	Homo sapiens midline 1 (Optz/BBB syndrome) (MID1) mRNA
1437	14470	27448	0.95	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
3300	16353	29272	0.83	2.0E-50	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
4289	17318	30197	0.75	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
7051	20073	33380	0.51	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001609 5'
8659	21627	35047	1.09	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8659	21627	35048	1.09	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8799	21766	35189	6.78	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8799	21768	35190	6.78	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10244	23169	36657	1.43	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
10244	23169	36658	1.43	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
11971	24849		1.52	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
462	13535	26461	2.26	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2373	15381		9.27	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7970	20909		0.55	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10553	23475	36970	0.97	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6095	19174	32390	1.01	9.0E-51	AW511226.1	EST_HUMAN	hd44e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
6350	19419	32660	0.71	9.0E-51	AA744837.1	EST_HUMAN	O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
9020	21986	35407	0.55	9.0E-51	AI791154.1	EST_HUMAN	ny67h03.s1 NCL_CGAP_GGB1 Homo sapiens cDNA clone IMAGE:1283381 3'
9879	22632	36088	1.2	9.0E-51	AA043738.1	EST_HUMAN	ab23g04.x5 Stratiene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9858	22794	36245	0.52	9.0E-51	AI791154.1	EST_HUMAN	2k51c09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486362 5'
9858	22794	36246	0.52	9.0E-51	AI791154.1	EST_HUMAN	ab23g04.x5 Stratiene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
11804	23959	37483	1.5	9.0E-51	H8078.1	EST_HUMAN	ab23g04.x5 Stratiene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
11804	23959	37484	1.5	9.0E-51	H8078.1	EST_HUMAN	ab23g04.x5 Stratiene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
4599	17620	30513	6.51	8.0E-51	AA010842.1	EST_HUMAN	ab23g04.x5 Stratiene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
7914	20557	34245	2.04	8.0E-51	11439587	NT	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9819	22968		0.85	8.0E-51	AU138590.1	EST_HUMAN	yw24g08.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5' np98e09.s1 NCL_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:U12871_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
							AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'

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3295	16348	29268	1.68	7.0E-51	AW899219.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3374	16424	29349	0.72	7.0E-51	AW274720.1	EST_HUMAN	xs34e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564.3 similar to TR:Q9Z340
4196	17227	30116	1.4	7.0E-51	AL079828.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
4198	17227	30117	1.4	7.0E-51	AL079828.1	EST_HUMAN	DKFZp434B2229.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229.5
4378	17406	30286	1.64	7.0E-51	AW286803.1	EST_HUMAN	DKFZp434B2229.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229.5
11993	24870	38468	2.13	7.0E-51	AF161449.1	NT	UIH-BW0-alp-B-05-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729817.3
1530	14563	27534	0.91	6.0E-51	6678763	NT	Homo sapiens HSPC331 mRNA, partial cds
							Homo sapiens putative DNA binding protein (M98), mRNA
1996	15017	28024	5.54	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3487	16533	29458	17.23	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4338	17365	30247	0.69	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4338	17365	30248	0.69	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6105	19184	32403	2.8	6.0E-51	X01788.1	NT	Human haptoglobin related (Hpr) gene exon 3
6116	19194	32417	8.29	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6116	19194	32418	8.29	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6925	20149	33469	1.13	6.0E-51	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7076	20088	33408	1.03	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
7157	16389	31233	2.29	6.0E-51	11429665	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
9492	22456	35895	0.62	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9492	22456	35896	0.62	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
10042	22969	36436	2.04	6.0E-51	7661530	NT	Homo sapiens B9 protein (B9), mRNA
10120	23048	36525	1.14	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11585	24523	38078	1.65	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL-17R), mRNA
792	13851	26798	8.57	5.0E-51	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
804	13862	26812	1.6	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
993	16868	26998	1.23	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1612	14644	27620	1.02	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2599	15600	28619	7.72	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoprotein 155
3966	17006	28919	1.85	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3965	17005	28920	1.85	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
11610	24548	38108	4.07	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
135	13240	26171	1.63	3.0E-51	A1587348.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1180	14221	27177	3.31	3.0E-51	A1587348.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1940	14964	27961	1.08	3.0E-51	AA211208.1	EST_HUMAN	zq87g01.s1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:649008 3'
4354	17381	30263	2.23	3.0E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
7831	20779	34157	1.2	3.0E-51	R15914.1	EST_HUMAN	ye47c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cd94 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); contains LTR5 repetitive element ;
9191	22157		4.32	3.0E-51	M29063.1	NT	Human hnRNP C2 protein mRNA
9423	26008		0.48	3.0E-51	AW583777.1	EST_HUMAN	la04d06.y1 Human Pancreatic Islets Homo sapiens cDNA 5'
12810	25435		1.36	3.0E-51	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
366	13452	26380	1.19	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
689	13752	26878	0.66	2.0E-51	BE981063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
689	13752	26879	0.66	2.0E-51	BE981063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1697	14727	27710	4.99	2.0E-51	AA233352.1	EST_HUMAN	z30a05.r1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233228 G233228 RTVL-H PROTEIN ; contains LTR7.13 LTR7 repetitive element ;
3745	16787	29689	2.46	2.0E-51	A1492415.1	EST_HUMAN	tr27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4521	17546	30433	0.69	2.0E-51	AW137826.1	EST_HUMAN	U1H-B11-adj-d-02-o-U.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716951 3'
5513	18613	31545	0.57	2.0E-51	A1732851.1	EST_HUMAN	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325809 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
5513	18613	31546	0.57	2.0E-51	A1732851.1	EST_HUMAN	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325809 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
6131	19208	32433	4.17	2.0E-51	BE782015.1	EST_HUMAN	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7531	20494		0.68	2.0E-51	AF219827.1	NT	Homo sapiens diacylglycerol kinase Iota (DGKI) gene, exon 23
7990	20648	34012	0.91	2.0E-51	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
9046	22012	35434	1.54	2.0E-51	BE901994.1	EST_HUMAN	601678787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9046	22012	35435	1.54	2.0E-51	BE901994.1	EST_HUMAN	601678787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9389	22354	35785	0.97	2.0E-51	11037084	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9870	22823	36278	1.35	2.0E-51	A1917078.1	EST_HUMAN	tr74e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
9962	22869	36350	6.78	2.0E-51	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9977	22904	36368	0.53	2.0E-51	AB007926.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10799	23720	37223	1.54	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
10838	23758	37258	1.14	2.0E-51	AA378559.1	EST_HUMAN	EST91296 Synovial sarcoma Homo sapiens cDNA 5' end
11655	18613	31545	7.03	2.0E-51	AJ732851.1	EST_HUMAN	bb34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW.NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
11655	18613	31546	7.03	2.0E-51	AJ732851.1	EST_HUMAN	bb34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW.NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
12122	24991	38592	2.3	2.0E-51	AA011698.1	EST_HUMAN	z03a01.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429872 5'
12803	25430	31740	2	2.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA
114	13225	26149	8.48	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1491	14524		33.7	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBC12 5'
4437	17463	30352	0.99	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4437	17463	30353	0.99	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
5463	18565	31476	3.94	1.0E-51	T18862.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b12056
7811	20854	34242	0.98	1.0E-51	AJ672632.1	EST_HUMAN	ts39g02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
8235	21204	34809	0.79	1.0E-51	BF434359.1	EST_HUMAN	7c96b02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3844091 3' similar to TR:P87892 P87892 PROTEASE ;
12073	26012		1.67	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSB02 5'
12589	25293		5.29	9.0E-52	AA777621.1	EST_HUMAN	z95a07.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.I3 THR repetitive element ;
153	13256	26184	9.3	8.0E-52	AA720574.1	EST_HUMAN	rw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.I3 THR repetitive element ;
1495	14528	27500	1.77	8.0E-52	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1662	14694	27669	2.98	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1662	14694	27670	2.98	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4019	14694	27669	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4019	14694	27670	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7760	20713	34082	0.69	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7760	20713	34083	0.69	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9367	22332	35762	1.55	7.0E-52	W56471.1	EST_HUMAN	zc69a08.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element;
1191	14231		0.65	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271289-049-d07 BT0537 Homo sapiens cDNA
1703	14733	27715	3.37	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5818	18906	32089	1.06	6.0E-52	AI208794.1	EST_HUMAN	qg44f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11543	24484	38037	1.63	6.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGEM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;
4460	17495	30383	1.6	5.0E-52	Z78898.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
9747	22688	36144	0.47	5.0E-52	11437365	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1670	14702	27677	1.25	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1803	14831	27818	1.15	4.0E-52	4758843	NT	Homo sapiens nucleoporin 156kD (NUP155) mRNA
4769	17789	30882	1	4.0E-52	AI766814.1	EST_HUMAN	wl89b02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
5359	18464	31334	1.41	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5359	18464	31335	1.41	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
7943	20885	34276	0.56	4.0E-52	11525731	NT	Homo sapiens RAD51-interacting protein (PIR51), mRNA
8373	21342	34753	2.33	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3915836 5'
8879	21848	35268	6.18	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12426	26194		3.05	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12906	25488		4.73	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4119	17152		11.15	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
564	13634	26550	1.97	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
564	13634	26551	1.97	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2030	15049	28064	1.43	2.0E-52	AB033075.1	NT	Homo sapiens mRNA for KIAA1249 protein, partial cds
2507	15510	28537	1.95	2.0E-52	BE207575.1	EST_HUMAN	bb56b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2746	15739		10.45	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5013	18027	30912	3.26	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5049	18061	30939	0.98	2.0E-52	AI141802.1	EST_HUMAN	qa36e05.s1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5049	18061	30940	0.98	2.0E-52	AI141802.1	EST_HUMAN	qa36e05.s1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5786	18880	32062	3.71	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA
6503	19567	32819	1.7	2.0E-52	11141868	NT	Homo sapiens Interleukin 21 receptor (IL21R), mRNA
6872	19925	33221	1.04	2.0E-52	AB023004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7129	20105	33416	0.73	2.0E-52	AF192146.1	EST_HUMAN	os45d12.y5 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1608311 5'
8121	21058	34455	0.52	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8121	21058	34458	0.52	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
9000	21986		11.89	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
9288	22254	35684	0.87	2.0E-52	AA778795.1	EST_HUMAN	z44g05.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9834	22683		1.05	2.0E-52	4788789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10474	23398	36893	6.19	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10474	23398	36894	6.19	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11538	24479	38029	3.09	2.0E-52	AB131462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11538	24479	38030	3.09	2.0E-52	AB131462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11551	24492	38048	2.73	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DGBAIE03 5'
11680	24648		12.83	2.0E-52	W70260.1	EST_HUMAN	zd49g12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5'
11939	24819		2.73	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
12231	25982	31300	18.5	2.0E-52	AW236297.1	EST_HUMAN	xt72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element;
12633	26319		7.5	2.0E-52	AB08985.1	EST_HUMAN	wf87d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE
534	13605	26524	1.45	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1373	14407	27377	9.6	1.0E-52	4504026	NT	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA
2542	15544		2.17	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3072	16129	29041	1.99	1.0E-52	S61070.1	NT	pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
5406	18509	31386	4.22	1.0E-52	M26426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6533	19596	32859	2.4	1.0E-52	U38954.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
7664	20623	33987	2.35	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8150	21087	34486	0.55	1.0E-52	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8808	21776		1.13	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9543	22508	35955	0.7	1.0E-52	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10941	23861		1.21	1.0E-52	AW020370.1	EST_HUMAN	df08g05.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10951	23871		1.14	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1117	24077	37601	1.84	1.0E-52	U48286.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
13114	25633	31808	1.3	1.0E-52	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3805	18845	29762	0.9	9.0E-53	4506094	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4418	17445	30338	0.91	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12477	26226		2.56	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4132793 5'
12881	25858		6.21	7.0E-53	A1421782.1	EST_HUMAN	#44497.x1 NCL_CGAP_Brm23 Homo sapiens cDNA clone IMAGE:2089077 3' similar to contains THR.11
5215	18224	31098	0.89	6.0E-53	BE299719.1	EST_HUMAN	601175776F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3530946 5'
4126	17159	30047	3	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
12110	24980	38580	1.54	5.0E-53	BE729270.1	EST_HUMAN	601561627F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831175 5'
12522	28253		1.67	5.0E-53	AW813663.1	EST_HUMAN	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
51	13171	26079	2.37	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
51	13171	26080	2.37	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4859	17876	30764	1.11	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
9771	22712		0.82	4.0E-53	A1613037.1	EST_HUMAN	606104.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2278327 3'
10114	23040		0.71	4.0E-53	F13080.1	EST_HUMAN	HSC3ID041 normalized infant brain cDNA Homo sapiens cDNA clone c-3id04
11548	24489	38044	2.93	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4063977 5'
11548	24489	38045	2.93	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4063977 5'
2689	16888	28885	2.64	3.0E-53	AB028698.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3744	16788	29698	1.01	3.0E-53	AW050836.1	EST_HUMAN	wz22c07.x1 Soares Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2558798 3'
6499	18599	31811	0.92	3.0E-53	AF007212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5707	18802	31979	1.09	3.0E-53	11526297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6318	19389	32829	0.95	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
7305	20276	33813	0.98	3.0E-53	Y10388.3	NT	H. sapiens graf gene
7305	20276	33614	0.98	3.0E-53	Y10388.3	NT	H. sapiens graf gene
8647	21615	35037	12.56	3.0E-53	S72043.1	NT	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
9211	22177	35607	0.69	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9412	22377		9.53	3.0E-53	5901963	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
458	13531		2.53	2.0E-53	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
2335	15346	28367	6.08	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2543	15545		11.44	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD, Vacuolar protein-ATPase, subunit E, V-ATPase, subunit E (ATP6E), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2736	16730	28744	1.17	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2738	15730	28745	1.17	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3232	16287	29209	1.46	2.0E-53	7705687	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3259	16313	28234	0.8	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4088	17122	30016	2.78	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
4520	17545	30432	1.23	2.0E-53	4506982	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5193	18202	31074	0.96	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5193	18202	31075	0.96	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5500	18600	31512	3.33	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
5500	18600	31513	3.33	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
8203	21173	34583	1.13	2.0E-53	AW975988.1	EST_HUMAN	EST387707 MAGE rescues, MAGN Homo sapiens cDNA
8340	21309		0.61	2.0E-53	AA095652.1	EST_HUMAN	IS429.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9763	22704		15.48	2.0E-53	AW245876.1	EST_HUMAN	2822685.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822685 5'
1440	14473	27450	2	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3421	18469	29389	1.29	1.0E-53	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5001	18015	30902	1.32	1.0E-53	BE296388.1	EST_HUMAN	601176728F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631919 5'
6850	19903	33198	1.43	1.0E-53	BF364201.1	EST_HUMAN	CM4-NIN1029-150800-543-e02 NIN1029 Homo sapiens cDNA
7459	20425	33781	0.84	1.0E-53	BE012071.1	EST_HUMAN	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
8267	21236	34847	0.55	1.0E-53	AA249072.1	EST_HUMAN	ll9571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9444	22408	35845	13.12	1.0E-53	X79536.1	NT	H.sapiens mRNA for hnRNPcore protein A1
12105	24976	38574	3.08	1.0E-53	X98411.1	NT	H.sapiens mRNA for myosin-IE
12105	24976	38575	3.08	1.0E-53	X98411.1	NT	H.sapiens mRNA for myosin-IE
5375	25636	31353	5.13	9.0E-54	4506786	EST_HUMAN	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
208	13309	28236	1.73	8.0E-54	BE388785.1	EST_HUMAN	60127283F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1852	14878	27874	2.4	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6045	19127	32333	23.25	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
11982	24841	38434	1.67	8.0E-54	AW592568.1	EST_HUMAN	hfa4e05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934752 3'
11982	24841	38435	1.67	8.0E-54	AW592568.1	EST_HUMAN	hfa4e05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934752 3'
384	13497	28429	1.85	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.s1 Soares_besit_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element
1847	14873	27869	1.51	7.0E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2215	15228	28252	4.54	7.0E-54	N27177.1	EST_HUMAN	yw88d12.s1 Soares_placenta_80sweeks_2NbHP809W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7 b3 LTR7 repetitive element ;
10487	23409	36908	1.91	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
11623	24561		3.26	7.0E-54	AI160189.1	EST_HUMAN	qb87g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 OFR repetitive element ;
25	13145	26045	2.05	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
385	13498	26430	0.87	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
385	13498	26431	0.87	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3296	16349	29269	0.89	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3546	16592	29517	0.86	6.0E-54	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4030	17068	29969	1.48	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLON6) mRNA
4489	17514	30402	0.78	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4819	17836	30734	0.94	6.0E-54	AV724895.1	EST_HUMAN	AV724895 HTB Homo sapiens cDNA clone HTBACE02 5'
4880	17897	30788	1.95	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4903	17926		1.23	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p86 isoform
5035	17926		1.27	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p86 isoform
11771	23926	37446	1.6	6.0E-54	11433623	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
11771	23926	37447	1.6	6.0E-54	11433623	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
2160	16176	28197	3.75	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
184	13284		319.6	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
957	14010	28963	29.88	4.0E-54	AA300764.1	EST_HUMAN	EST117696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1822	14849	27842	2.91	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1822	14849	27843	2.91	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3217	16272		1.03	4.0E-54	AI935096.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:002711
7524	20488		0.68	4.0E-54	BE544889.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN ;
93	19209	26133	13.65	3.0E-54	AA313487.1	EST_HUMAN	601076004F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461017 5'
2632	16631		1.1	3.0E-54	AI908757.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6007	19080	32290	1.52	3.0E-54	4502434	NT	IL-BT189-190399-007 BT189 Homo sapiens cDNA
7619	20579	33942	1.49	3.0E-54	AA844081.1	EST_HUMAN	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7619	20579	33943	1.49	3.0E-54	AA844081.1	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
8081	21018	34418	0.51	3.0E-54	AI742822.1	EST_HUMAN	ei92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11363	24312		4.82	3.0E-54	11434808	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA
11423	24387	37802	3.55	3.0E-54	BF345600.1	EST_HUMAN	602019408F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153121 5'
11696	24661	38239	2.11	3.0E-54	AA393362.1	EST_HUMAN	z170712.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
12334	25134	31850	4.08	3.0E-54	AW954559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN, ;
12380	25942		1.87	3.0E-54	AW748965.1	EST_HUMAN	EST366829 MAGE resequences, MAGC Homo sapiens cDNA
643	13709	28929	6.22	2.0E-54	5031900	NT	RC1-BT0313-131189-011-b09 BT0313 Homo sapiens cDNA
1367	14401	27371	1.48	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1550	14583	27554	1.32	2.0E-54	AA655008.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2546	15547	28570	1.04	2.0E-54	AW163175.1	EST_HUMAN	nt78a09.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;
2608	15607	28631	1.45	2.0E-54	AL163210.2	NT	eu92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2905	15964	28887	1.4	2.0E-54	AW057324.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3559	16608		5.43	2.0E-54	AA532925.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
4232	17261		1.73	2.0E-54	4502642	NT	nt45g08.s1 NCI_CGAP_P19 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
4470	17496		1.18	2.0E-54	AF208161.1	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4914	17831	30822	0.99	2.0E-54	7708446	NT	Homo sapiens syncytin precursor, mRNA, complete cds
5278	18284	31147	1.07	2.0E-54	4506962	NT	Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA
5551	18648	31591	1.8	2.0E-54	4759069	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5684	18779	31952	1.25	2.0E-54	BE047864.1	EST_HUMAN	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5856	18946	32131	3.9	2.0E-54	11426657	NT	tz43c11.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5961	19046	32245	10.03	2.0E-54	AB046811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6814	19868	33157	0.77	2.0E-54	AF003915.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6983	20206	33535	0.73	2.0E-54	AB023212.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
6983	20206	33536	0.73	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
7330	20301	33645	7.88	2.0E-54	11426544	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
9987	22914	36379	4.03	2.0E-54	AB001026.1	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
10369	23292	36768	1.61	2.0E-54	11429127	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
10480	23402	36809	0.88	2.0E-54	11416762	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
							Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10480	23402	36900	0.88	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
12034	24910		4.31	2.0E-54	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
4492	17517		1.6	1.0E-54	BF315418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8081	22047	35470	0.51	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
10615	23537	37035	0.51	1.0E-54	AA412409.1	EST_HUMAN	zu10e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731484 5'
10615	23537	37036	0.51	1.0E-54	AA412409.1	EST_HUMAN	zu10e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731484 5'
12998	25554		4.2	1.0E-54	AU077341	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5' end
10724	23648	37139	0.95	9.0E-55	BE081469.1	EST_HUMAN	QV2-BT0635-160400-143-h12 BT0635 Homo sapiens cDNA
1318	14353		0.98	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1321	14356		2.63	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11628	24469		1.73	8.0E-55	AW408714.1	EST_HUMAN	fn02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'
12390	25167		1.3	8.0E-55	BE327189.1	EST_HUMAN	hw08d06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182315 3' similar to TR:Q9Z1J8
1083	14127	27081	1.52	7.0E-55	R09346.1	EST_HUMAN	Y26e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to SP:C561_BOVIN P10897 CYTOCHROME ;
9156	22122		1.54	7.0E-55	AW103839.1	EST_HUMAN	xd76c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2803522 3' similar to TR:O60365
9536	22499	35947	1.22	7.0E-55	AA895581.1	EST_HUMAN	O60365 FOS39554_1 ;
9570	22532	35982	2.15	7.0E-55	AU139909.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407280 3'
11544	24486	38038	8.31	7.0E-55	AI651056.1	EST_HUMAN	AU139909 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'
11544	24485	38039	8.31	7.0E-55	AI651056.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2210249 3'
12135	25004		1.8	7.0E-55	H48714.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2210249 3'
12986	25876		1.78	7.0E-55	H23398.1	EST_HUMAN	yq78d03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201893 5'
11843	24726	38313	1.85	6.0E-55	AB040934.1	NT	ym57g07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'
1785	14814	27798	1.3	5.0E-55	AA704971.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
6690	19747	33023	1.65	5.0E-55	4502240	NT	z95509.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6690	19747	33024	1.65	5.0E-55	4502240	NT	z95509.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
7237	20258	33592	0.69	5.0E-55	7382477	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
7513	20478	33839	0.68	5.0E-55	11434422	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
8327	21298	34711	0.74	5.0E-55	11528491	NT	Homo sapiens Rho GTPase activating protein 6 (RHGAP6), transcript variant 5, mRNA
9399	22384	35796	2.57	5.0E-55	4506302	NT	Homo sapiens BCL2-associated athanogene (BAG1), mRNA
							Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA

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9674	22627		1.9	5.0E-55	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
10397	23319	36801	1.31	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10397	23319	36802	1.31	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10582	23504	36997	1.2	5.0E-55	5453785	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
12419	25189		3.4	5.0E-55	11417872	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
57	15931	26088	1.49	4.0E-55	AW957994.1	EST_HUMAN	EST370064 MAOE resequences, MAOE Homo sapiens cDNA
673	13737	26864	31.1	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1517	14549		1.97	4.0E-55	BF081411.1	EST_HUMAN	7J52b10.X1 Scars_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.3 L1 repetitive element
2040	15059	28078	1.04	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2040	15059	28079	1.04	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2097	15114	28134	8.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2097	15114	28135	8.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2319	15330	28354	2.05	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
8687	21655		11	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11563	24503		2.89	4.0E-55	W28169.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12335	25135		3.64	4.0E-55	BF303941.1	EST_HUMAN	60188657F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6751	19805	33086	0.78	3.0E-55	AA077156.1	EST_HUMAN	7B09A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B09A09
12271	25093		1.91	3.0E-55	BE176519.1	EST_HUMAN	PM1-H10603-080300-001-g08 HT0603 Homo sapiens cDNA
13007	25560		1.9	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
377	13461	26391	2.24	2.0E-55	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
553	13623		1.59	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
650	13716	26638	3.26	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products
2970	16028	28951	1.02	2.0E-55		NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4808	17825	30721	2.19	2.0E-55	BE179886.1	EST_HUMAN	CM1-HT0878-150800-357-g03 HT0878 Homo sapiens cDNA
7747	25689	34067	0.69	2.0E-55	AW501988.1	EST_HUMAN	UJHF-BNO-aks-7-08-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
9420	22385	35823	0.51	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134483 3'
9420	22385	35824	0.51	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134483 3'
9516	22478		6.16	2.0E-55	A1002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element
9596	22558		0.78	2.0E-55	BE007959.1	EST_HUMAN	QV0-BN0147-28040-213-g06 BN0147 Homo sapiens cDNA
10607	23529	37024	0.43	2.0E-55	A1439401.1	EST_HUMAN	l03h08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:214079 3'
11296	24246	37773	1.84	2.0E-55	AU116344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12113	24983	38584	1.51	2.0E-55	BE886059.1	EST_HUMAN	601507718F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908076 5'
98	13212	28136	2.4	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphatase receptor (calion dependent) (M6PR) mRNA
191	13292	26218	93.01	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefia2) mRNA, complete cds
576	13645	28558	0.75	1.0E-55	A026718.1	EST_HUMAN	ov65g09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644160 3'
1152	14194	27146	4.22	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1967	14988	27990	1.65	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
1967	14988	27991	1.65	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2333	15344		3.95	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2345	15824	28376	1.31	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2524	15527	28548	52.04	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2561	15562	28580	4.62	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2561	15562	28581	4.62	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2619	15617	28641	4.76	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
2801	15793	28811	0.98	1.0E-55	AB033045.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3420	16468	29388	0.96	1.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4015	17054	29955	4.23	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4323	17352	30238	1.08	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4702	17782		1.21	1.0E-55	N77261.1	EST_HUMAN	y44g03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245620 5'
4865	17882	30769	1.79	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4866	17882	30770	1.79	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5177	18188	31063	1.3	1.0E-55	8923125	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
5575	18671	31634	0.56	1.0E-55	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6402	19470	32718	7	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6402	19470	32719	7	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7282	20016		0.66	1.0E-55	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
8321	21280	34704	1.25	1.0E-55	11432694	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8321	21280	34705	1.25	1.0E-55	11432694	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8410	21379	34765	0.49	1.0E-55	11421649	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
8418	21387	34766	1.27	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8418	21387	34767	1.27	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
11776	23931	37452	1.65	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11795	23950	37471	1.58	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA Ccl8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F161 5' similar to similar to Chinese Hamster DHFR-camplified protein mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11902	24783	38371	1.74	1.0E-55	10587821	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
7590	20551	33912	1.89	8.0E-56	BE379074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
2743	15737	28753	6.5	7.0E-56	H19934.1	EST_HUMAN	Yn62g03.r1 Soares adult brain N2b5H856Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains
7802	20845	34228	2.13	7.0E-56	AW361213.1	EST_HUMAN	THR repetitive element;
7802	20845	34230	2.13	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1701	14731	27713	1.99	5.0E-56	AW997712.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
9516	22479	35823	0.61	5.0E-56	AW015507.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
10764	23676		1.7	5.0E-56	W28189.1	EST_HUMAN	UI-H-B10p-aa-u-05-Q-U1.s1 NCI CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
12507	25930	31309	5.41	5.0E-56	H55099.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
30	13150	26049	12.5	4.0E-56	AF141349.1	NT	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
30	13150	26050	12.5	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2719	15713	28730	4.9	4.0E-56	4507728	NT	Homo sapiens beta-tubulin mRNA, complete cds
2719	15713	28731	4.9	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2823	13598	26516	3.69	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2843	15620	28644	1.16	4.0E-56	AF632488.1	EST_HUMAN	wb09f08.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA
2843	15620	28644	1.16	4.0E-56	AF632488.1	EST_HUMAN	P27119 ORNITHINE DECARBOXYLASE;
2843	15620	28645	1.16	4.0E-56	AF632488.1	EST_HUMAN	wb09f08.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA
6387	19455	32700	5.85	4.0E-56	AF217508.1	NT	P27119 ORNITHINE DECARBOXYLASE;
6387	19455	32701	5.85	4.0E-56	AF217508.1	NT	wb09f08.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA
10872	23792	37293	3.94	4.0E-56	AF043349.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
11268	24220	37743	7.82	4.0E-56	AF498066.1	EST_HUMAN	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
11268	24220	37744	7.82	4.0E-56	AF498066.1	EST_HUMAN	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
1345	14380	27349	1.74	3.0E-56	8924029	NT	tm65g12.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163046 3'
1779	14808	27794	0.99	3.0E-56	6912743	NT	tm65g12.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163046 3'
3142	16199	29109	1.83	3.0E-56	AA325826.1	EST_HUMAN	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
3142	16199	29110	1.83	3.0E-56	AA325826.1	EST_HUMAN	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3847	18887		1.73	3.0E-56	AF056066.1	NT	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3938	16978	29893	1.1	3.0E-56	BE393512.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
4454	17480	30368	4.84	3.0E-56	AL163286.2	NT	Homo sapiens MHC class 1 region
4603	17624	30517	2.34	3.0E-56	5602085	NT	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4841	17858		1.81	3.0E-56	BE893572.1	EST_HUMAN	Homo sapiens superkiller viralicide activity 2 (S. ceroviridae homolog)-like (SKIV2L), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5767	18659	32038	1.64	3.0E-56	4759163	NT	Homo sapiens sparco/osteoneclin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5767	18659	32039	1.64	3.0E-56	4759163	NT	Homo sapiens sparco/osteoneclin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
7058	20030	33389	5.05	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
9168	22134	35560	5	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10172	23097	36577	1.12	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10846	23766	37265	1.63	3.0E-56	11434958	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
11643	24580	38147	4.57	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA
11643	24580	38148	4.67	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA
11983	24860	38455	7.15	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
11983	24860	38456	7.15	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
12378	25160	31812	2.99	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12378	25160	31813	2.99	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
525	13596		1.82	2.0E-56	AA199818.1	EST_HUMAN	zq62a08.st Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645206 3'
734	15849	26732	2.02	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
734	15849	26733	2.02	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
2392	15400	28425	1.22	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2392	15400	28426	1.22	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
3001	16059	28978	1.52	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3327	16378		1.71	2.0E-56	AB008691.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3544	16580	28515	1.18	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
7297	20269	33604	1.24	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
981	14032		1.28	1.0E-56	AF190930.1	NT	Maceca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3688	16731	29842	2.08	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
3688	16731	29843	2.08	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
5071	18081	30862	1.22	1.0E-56	AI905162.1	EST_HUMAN	QV-BT077-130195-079 BT077 Homo sapiens cDNA
6995	20121	33435	0.56	1.0E-56	AW609520.1	EST_HUMAN	MIR3-ST0203-180100-208-h02 ST0203 Homo sapiens cDNA
10315	23239		0.61	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10408	23330	36815	1.82	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220989-001-E02 CT0163 Homo sapiens cDNA
626	13691		2.17	9.0E-57	AW880885.1	EST_HUMAN	QV0-O10033-070300-152-h03 OT0033 Homo sapiens cDNA
11554	24494	38050	1.51	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11554	24494	38051	1.51	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11850	24733	38320	2.23	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
14	13134	26032	1.11	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
297	13391	26319	3.14	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
885	13940	26868	0.74	8.0E-57	AW284509.1	EST_HUMAN	xs05d10.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1833	14860	27858	2.19	8.0E-57	AA496109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
4948	17962	30852	1.11	8.0E-57	4557630	NT	z551b12.r1 Soares_NHT Homo sapiens cDNA clone IMAGE:757151 5'
5073	18083	30965	1.32	8.0E-57	BE286916.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4) mRNA
5312	25949	31435	1.69	8.0E-57	11418185	NT	600944440F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960864 5'
6539	19601	32863	0.54	8.0E-57	AB020705.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6608	19666	32941	12.65	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
6608	19666	32942	12.65	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7682	20840	34003	0.71	8.0E-57	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8024	20961	34357	2.69	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8024	20961	34358	2.69	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
10848	23768	37267	0.44	8.0E-57	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
11807	13134	26032	2.8	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12088	24960	38557	1.87	8.0E-57	11431260	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
12733	25386	31751	3.29	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12749	25386	31751	1.39	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
3263	16317	29237	1.09	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3263	16317	29238	1.09	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3284	16338	29258	0.65	7.0E-57	8005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3891	16931	29840	2.63	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230), mRNA, complete cds
3891	16931	29841	2.63	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230), mRNA, complete cds
4816	17833	30731	1.03	7.0E-57	U11058.2	NT	Homo sapiens large conductance calcium- and voltage-dependent potassium channel alpha subunit (Maxik) mRNA, complete cds
13075	25984		3.96	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudocautosomal region; segment 1/2
3766	16808	29718	2.12	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
805	13863	28813	0.93	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1334	14388		59.49	3.0E-57	AA230279.1	EST_HUMAN	nc13f07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2400	15407	28431	0.95	3.0E-57	AA348335.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10 ;
							EST54770 Hippocampus II Homo sapiens cDNA 5' and

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2714	15708	28724	1.19	3.0E-57	BE678622.1	EST_HUMAN	733b10.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP.Y47H9C.2
2714	15708	28725	1.19	3.0E-57	BE678622.1	EST_HUMAN	733b10.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP.Y47H9C.2
3711	16764		26.47	3.0E-57	AW853964.1	EST_HUMAN	733b10.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP.Y47H9C.2
6145	19220	32450	1.37	3.0E-57	11225608	NT	733b10.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP.Y47H9C.2
6246	19319	32549	3.49	3.0E-57	BE796537.1	EST_HUMAN	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
8484	21452	34870	2.61	3.0E-57	W28130.1	EST_HUMAN	601588896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3644302 5'
8510	21478	34891	1.9	3.0E-57	11545798	NT	42f6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8510	21478	34892	1.9	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8624	21592	35011	0.56	3.0E-57	11427757	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8772	21739	35160	0.66	3.0E-57	J05262.1	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
9210	22178	35806	4.95	3.0E-57	AU117659	EST_HUMAN	Human farnesyl pyrophosphate synthetase mRNA, complete cds
9605	22609	36060	0.7	3.0E-57	11545798	NT	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9605	22609	36061	0.7	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
11254	24207	37729	2.96	3.0E-57	AW248374.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
12384	25951	31314	7.53	3.0E-57	W23871.1	EST_HUMAN	2820473-5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
1500	14533	27504	1.05	2.0E-57	AF248219.1	NT	2b45d11.r1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
1500	14533	27505	1.05	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3452	16498		2.19	2.0E-57	AL163204.2	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3562	16608	29529	0.65	2.0E-57	R07702.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
3562	16608	29530	0.65	2.0E-57	R07702.1	EST_HUMAN	yes98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3951	16991	29907	0.86	2.0E-57	BE073264.1	EST_HUMAN	yes98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4538	17561	30448	6.69	2.0E-57	AL163283.2	NT	MFO-BT0561-060300-103-b03 BT0561 Homo sapiens cDNA
5139	18148	31027	1.74	2.0E-57	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C003
5751	19845		1.67	2.0E-57	AA016131.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
6150	19225		32.23	2.0E-57	BF115268.1	EST_HUMAN	z631c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element
6283	19355	32591	0.7	2.0E-57	11431281	NT	7i80704.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.1i
8978	21944	35368	1.02	2.0E-57	AF045452.1	NT	MER22 repetitive element
10205	23130	36617	1.63	2.0E-57	AF057722.1	NT	Homo sapiens small inducible cytokine subfamily A (Oys-Oys), member 22 (SCYA22), mRNA
11601	24539	38097	1.88	2.0E-57	11424084	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
11601	24539	38098	1.88	2.0E-57	11424084	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
11601	24539	38099	1.88	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11601	24539	38098	1.88	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11642	24579	38145	1.74	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
11642	24579	38146	1.74	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
2240	16264	28278	1.49	1.0E-57	AW503208.1	EST_HUMAN	UI-HF-BND-ekt-g-07-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
8041	22007		4.47	1.0E-57	BE043031.1	EST_HUMAN	h32a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246 HYPOTHEICAL 9.3 KD PROTEIN ;
12537	25261		3.65	1.0E-57	AW470791.1	EST_HUMAN	h33d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875469 3' similar to contains THR.b3 THR repetitive element;
5760	18853	32033	1.01	9.0E-58	AA297847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
12795	25424	31738	2.37	9.0E-58	BE395061.1	EST_HUMAN	60130948F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
591	13658		2.43	8.0E-58	BE668715.1	EST_HUMAN	60144504F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
655	13721	26844	2.84	8.0E-58	AI798378.1	EST_HUMAN	tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
655	13721	26845	2.84	8.0E-58	AI798378.1	EST_HUMAN	tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1874	14899	27897	1.08	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1874	14899	27898	1.08	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2987	16045		2.65	8.0E-58	7708132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
7449	20415	33769	0.95	7.0E-58	BE561971.1	EST_HUMAN	601346704F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687577 5'
11203	24157		4.98	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
11275	24227	37753	2.79	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BND-ali-g-10-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079887 5'
11275	24227	37754	2.79	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BND-ali-g-10-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079887 5'
2385	15393	28419	4.05	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2912	15970	28893	1.62	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project= TCAA Homo sapiens cDNA clone TCAAP1219
2912	15970	28894	1.62	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project= TCAA Homo sapiens cDNA clone TCAAP1219
6294	19386	32805	1.16	6.0E-58	AF106911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10672	23594	37091	1.02	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12629	25316		1.41	6.0E-58	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
300	13394	26321	4.35	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
711	13773	26707	7.63	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1199	14239	27195	3.77	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1199	14239	27196	3.77	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1200	14239	27195	3.1	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1200	14239	27196	3.1	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3334	16385	29306	3.85	5.0E-58	AA988183.1	EST_HUMAN	or89e07.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4287	17316	30185	0.95	5.0E-58	AI635745.1	EST_HUMAN	te89e07.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA P16994 PROFILIN II:
5710	18804		2.2	5.0E-58	11496282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6302	19373	32612	5.97	5.0E-58	H23072.1	EST_HUMAN	ym51h07.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:52071 5'
6534	19597	32860	0.94	5.0E-58	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6615	19873	32951	1.16	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6945	20169	33482	0.7	5.0E-58	AF051334.1	NT	Homo sapiens fibrin (NBS) mRNA, complete cds
6945	20169	33483	0.7	5.0E-58	AF051334.1	NT	Homo sapiens fibrin (NBS) mRNA, complete cds
7313	20284	33625	0.8	5.0E-58	4885400	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCOS) mRNA
8302	21271	34683	7.52	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
8696	21664	35088	0.78	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
9695	22648	36103	1.34	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNA5E6PL) mRNA
9695	22648	36104	1.34	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNA5E6PL) mRNA
10216	23141	36629	1.01	5.0E-58	11430847	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10482	23404	36901	1.96	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10768	23687	37183	0.51	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10768	23687	37184	0.51	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
12352	25878		2.17	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12797	25904		1.48	5.0E-58	11428423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
13015	26565		2.08	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
373	13459	26388	1.85	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA
797	13856	26803	1.42	4.0E-58	4504634	NT	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA
1464	14497	27471	1.14	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2639	16638	28661	2.02	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3336	16387	28908	1.11	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3753	16795	29706	1.02	4.0E-58	5031650	NT	Homo sapiens EGF-like repeats and discoidin 1-like domains 3 (EDIL3), mRNA
8120	21057	34454	0.69	4.0E-58	BE469857.1	EST_HUMAN	hy18a02.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197842 3'
11671	24607	38184	7.52	4.0E-58	11424059	NT	Homo sapiens E1B-65kDa-associated protein 5 (E1B-AP5), mRNA
335	13424		0.84	3.0E-58	R17879.1	EST_HUMAN	yq10a02.11 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1390	14424	27993	2.32	3.0E-58	4768981	NT	Homo sapiens peptide YY (PYY) mRNA
3163	16248	28165	2.57	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309843 5'
3193	16248	29166	2.57	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309843 5'
6390	19458	32703	0.61	3.0E-58	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-09 BT0702 Homo sapiens cDNA
6587	19647	32916	0.79	3.0E-58	F07056.1	EST_HUMAN	HSC1TG081 normalized infant brain cDNA Homo sapiens cDNA clone c-1lg08
6787	19851	33136	3.92	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAA2G04 5'
939	13992	26944	8.85	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
1294	14329						ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5409	18512	31390	8.41	2.0E-58	BE208532.1	EST_HUMAN	601499981F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:2567704 3'
5431	25638	31413	3.25	2.0E-58	BE907186.1	EST_HUMAN	601499981F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5431	25638	31441	3.25	2.0E-58	BE907186.1	EST_HUMAN	601499981F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6176	19250	32463	1.09	2.0E-58	BF513488.1	EST_HUMAN	UHH-BW1-arms-g-11-0-JL.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
6244	19317	32547	1.95	2.0E-58	AI124974.1	EST_HUMAN	am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN ;
6278	19350	32584	0.83	2.0E-58	R92567.1	EST_HUMAN	yq08h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196379 5'
7112	20046	33348	0.83	2.0E-58	AI291407.1	EST_HUMAN	qm84c01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896424 3'
7364	20334	33883	2.88	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7364	20334	33684	2.88	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
11093	24053	37576	18.24	2.0E-58	BF307746.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4731891 5'
11312	24262	37788	1.48	2.0E-58	AW872641.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
723	13785	26719	0.88	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3'end
1069	14114	27064	5.86	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1330	14365	27333	2.03	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences; MAGD Homo sapiens cDNA
1330	14365	27334	2.03	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences; MAGD Homo sapiens cDNA
1397	14431	27400	0.98	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1672	14704	27681	0.95	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC06 Homo sapiens cDNA clone IMAGE:3168935 3'
2814	15808	28825	1.21	1.0E-58	4759169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
3548	16594	29520	1.19	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3548	16594	29521	1.19	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3733	16775	29887	0.7	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5008	18020	30908	5.17	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Soares_NHMP_u_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
5941	19027	32221	1.18	1.0E-58	BE061860.1	EST_HUMAN	RC1-BT0254-280100-075-e01 BT0254 Homo sapiens cDNA
7046	20068	33374	0.64	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
8451	21420		0.5	1.0E-58	AW979337.1	EST_HUMAN	EST365637 MAGe resequences, MAGM Homo sapiens cDNA
9221	22187	35619	0.59	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
9333	22298	35727	0.94	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09 5'
9436	22400	35837	0.55	1.0E-58	AA412397.1	EST_HUMAN	z89f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9436	22400	35838	0.55	1.0E-58	AA412397.1	EST_HUMAN	z89f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10546	23468	36963	0.58	1.0E-58	11432894	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
12089	24942		2.61	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2238	15252	28276	21.09	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP), mRNA
7076	20141	33458	0.71	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis I Homo sapiens cDNA 5' end
7015	20141	33459	0.71	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis I Homo sapiens cDNA 5' end
8521	21489	34904	3.74	8.0E-59	AF761963.1	EST_HUMAN	wf50d06.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2384771 3'
179	15834		3.9	8.0E-59	BF035327.1	EST_HUMAN	601458331F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3662088 5'
							cm81a04.e1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1553550 3' similar to TR:Q13732 Q13732
8151	21089	34489	1.94	6.0E-59	AA982431.1	EST_HUMAN	SA GENE PRODUCT PRECURSOR.:
8588	21656	34972	0.56	6.0E-59	AI750970.1	EST_HUMAN	cn06h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 random
1768	14787	27782	1.19	5.0E-59	AW157281.1	EST_HUMAN	au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
1768	14787	27783	1.19	5.0E-59	AW157281.1	EST_HUMAN	au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
3144	16201	29112	7.03	5.0E-59	AI807484.1	EST_HUMAN	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4687	17708	30601	7.38	5.0E-59	X83497.1	NT	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
5796	18889	32070	0.58	5.0E-59	6005698	NT	Homo sapiens aladin 2 related protein (A2LP), mRNA
7182	18413	31215	7.91	5.0E-59	AW162304.1	EST_HUMAN	au66d07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element.
9158	22124	35553	0.95	5.0E-59	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (38kD) (RPC39), mRNA
10063	22990	36459	1.84	5.0E-59	AV762869.1	EST_HUMAN	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
11253	24206	37728	3.1	5.0E-59	11434908	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
794	13853	26801	3.22	4.0E-59	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
1242	14278	27239	0.75	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1242	14278	27240	0.75	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
5615	18711	31869	1.04	4.0E-59	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12107	24977	38576	1.6	4.0E-59	7657426	NT	Homo sapiens origin recognition complex, subunit 6 (yeast homolog)-like (ORC6L), mRNA
12492	25810		2.98	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	13130		6.8	3.0E-59	AW965624.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
228	13327	26250	4.47	3.0E-59	7682247	NT	Homo sapiens KIAA0080 gene product (KIAA0080), mRNA
1723	14753	27738	11.42	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1723	14753	27739	11.42	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2139	15156	28171	6.05	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2139	15156	28172	6.05	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3148	18203	29116	2.91	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3146	18203	29117	2.91	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3838	18878	28781	1.26	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4712	17732	30626	1.4	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4878	17895	30785	1.66	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
5091	18101		1.05	3.0E-59	M95961.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 2
6346	19415	32656	1.98	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7684	20646	33908	2.12	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOB1), mRNA
8263	21232	34642	1.5	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
8263	21232	34643	1.5	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
10404	23326	36809	0.84	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
10404	23326	36810	0.84	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12470	25219		1.37	3.0E-59	11417868	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12612	26311		7.97	3.0E-59	11417868	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
5985	19070	32268	0.82	2.0E-59	BF509383.1	EST_HUMAN	UI-H-B14-ey-b-02-Q-U1.s1 NCI_CGAP SubB Homo sapiens cDNA clone IMAGE:3086522 3'
5985	19070	32269	0.82	2.0E-59	BF509383.1	EST_HUMAN	UI-H-B14-ey-b-02-Q-U1.s1 NCI_CGAP SubB Homo sapiens cDNA clone IMAGE:3086522 3'
6979	20002		0.61	2.0E-59	AA470073.1	EST_HUMAN	z88d05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:790377 3'
7272	20207	33307	0.57	2.0E-59	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
8082	21019		0.52	2.0E-59	BF373329.1	EST_HUMAN	MRO-F70144-2560700-002-e10 F70144 Homo sapiens cDNA
9985	22922		4.9	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10893	23813		1.55	2.0E-59	BF365554.1	EST_HUMAN	RCO-NT0036-100700-032-a07 NT0036 Homo sapiens cDNA

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* Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11180	24136	37687	2.34	2.0E-59	AW410698.1	EST_HUMAN	fln07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
11180	24136	37688	2.34	2.0E-59	AW410698.1	EST_HUMAN	fln07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
12373	26169	31857	8.98	2.0E-59	AI631809.1	EST_HUMAN	wa38c12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12884	25836	31426	4.02	2.0E-59	L11645.1	NT	Q86542 RTVL-H PROTEIN; contains LTR7.b1 LTR7 repetitive element;
164	13267		18.92	1.0E-59	BE296411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2625	15624		3.89	1.0E-59	AA748468.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
7812	20761	34137	1.18	1.0E-59	AJ130984.1	NT	oa56h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1308029 3' similar to TR:Q13537
7986	20925	34319	1.07	1.0E-59	BE266814.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
7986	20925	34320	1.07	1.0E-59	BE266814.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
9740	22768	36222	0.85	1.0E-59	11419630	NT	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9963	22890	36351	0.54	1.0E-59	11428849	NT	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9963	22890	36352	0.54	1.0E-59	11428849	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
11201	20761	34137	9.85	1.0E-59	AJ130984.1	EST_HUMAN	Homo sapiens 3-hydroxyisobutyl-Coenzyme A hydrolase (HIBCH), mRNA
764	13824	26768	2.29	8.0E-60	AW977845.1	NT	Homo sapiens mRNA for transcription factor
1467	14600	27474	2.85	8.0E-60	4759159	NT	EST389849 MAGE resequences, MAGE Homo sapiens cDNA
2182	15197	28217	2.65	8.0E-60	5174656	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2182	15197	28218	2.65	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6094	19173	32389	0.94	8.0E-60	AB029004.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6653	19710	32987	1.01	8.0E-60	S63182.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7962	20903	34295	0.99	8.0E-60	11420841	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8298	21267	34679	2.37	8.0E-60	X17033.1	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
9291	22257	35687	2.88	8.0E-60	11428949	NT	Human mRNA for integrin alpha-2 subunit
9828	22675	36130	1.2	8.0E-60	11417118	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
9826	22675	36131	1.2	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10938	23868	37973	0.86	8.0E-60	5453987	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11182	24138	37670	4.65	8.0E-60	AL163204.2	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11182	24138	37671	4.65	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
755	13816	26760	30.34	7.0E-60	AF055066.1	NT	Homo sapiens chromosome 21 segment HS21C004
756	13816	26760	69.13	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
816	13874	26822	1.17	7.0E-60	4504634	NT	Homo sapiens MHC class 1 region
2138	15155	28170	1.04	7.0E-60	AF077188.1	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
							Homo sapiens cullin 4A (CUL4A) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2786	15788	28066	1.18	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4208	17237	30124	3.1	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4606	17627	30519	0.72	7.0E-60	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
9762	22703	36161	3.89	7.0E-60	H58041.1	EST_HUMAN	Y1204.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
11692	24657	38235	1.57	7.0E-60	H58041.1	EST_HUMAN	Y1204.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
2189	15204	28224	1.01	6.0E-60	BE964974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
8156	21094	34493	0.86	6.0E-60	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
8780	21747		8.33	6.0E-60	H52456.1	EST_HUMAN	Yq78h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201863 5' similar to contains OFR repetitive element ;
84	13200	26123	1.13	5.0E-60	AI807917.1	EST_HUMAN	Wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
84	13200	26124	1.13	5.0E-60	AI807917.1	EST_HUMAN	Wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2244	15258	28284	1.25	4.0E-60	AW603208.1	EST_HUMAN	U1HF-BN0-akt-g-07-0-U1.r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078348 5'
2244	15258	28285	1.25	4.0E-60	AW603208.1	EST_HUMAN	U1HF-BN0-akt-g-07-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2984	18042		1.31	4.0E-60	AA289037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7576	20538	33897	0.91	4.0E-60	BF196088.1	EST_HUMAN	hr81f05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
9482	22446		0.59	4.0E-60	AL183278.2	NT	Q61085 GTP-RHO BINDING PROTEIN 1 ;
11628	24566	38127	1.7	4.0E-60	11433597	NT	Homo sapiens chromosome 21 segment HS21C078
11628	24566	38128	1.7	4.0E-60	11433597	NT	Homo sapiens v-rat-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
1876	14901	27900	4.44	3.0E-60	BE562611.1	EST_HUMAN	Homo sapiens v-rat-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
1876	14901	27901	4.44	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1885	14910		1.88	3.0E-60	6031180	NT	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
4485	17510	30398	2.27	3.0E-60	AJ271735.1	NT	Homo sapiens prohibitin (PHB) mRNA
5452	18554	31465	2.11	3.0E-60	BF365143.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
5724	18818	31997	2.11	3.0E-60	AW836198.1	EST_HUMAN	QV4-NN149-250900-423-101 NN1149 Homo sapiens cDNA
7143	18375	31283	0.95	3.0E-60	AI792814.1	EST_HUMAN	RC3-LT0023-200100-012-e01 LT0023 Homo sapiens cDNA
8745	21713	35135	5.22	3.0E-60	5174844	NT	d60h11.y5 NCL_CGAP_K43 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE
8745	21713	35136	5.22	3.0E-60	5174844	NT	PS2624 URIDINE PHOSPHORYLASE ;
8930	21896	35324	0.58	3.0E-60	AI040235.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9094	22060	35485	4.2	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10017	22944	39411	0.42	3.0E-60	BF102612.1	EST_HUMAN	601646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3930990 5'
12970	25871		1.53	3.0E-60	AA485286.1	EST_HUMAN	ab07h04.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.11 LTR10 repetitive element;
33	13153	28054	1.7	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1421	14454	27428	2.76	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1734	14764	27747	1.34	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
1743	14773	27758	1.01	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2492	15495	28520	1.76	2.0E-60	AW380450.1	EST_HUMAN	RC1-HT0268-031299-012402 HT0268 Homo sapiens cDNA
2614	15612	28637	1.38	2.0E-60	7657228	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
2721	15715	28733	0.94	2.0E-60	AW978005.1	EST_HUMAN	EST1390114 IMAGE resequences, MAGO Homo sapiens cDNA
3592	16637	29557	1.49	2.0E-60	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3935	16975	28889	0.83	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4161	17182		0.65	2.0E-60	BF513458.1	EST_HUMAN	U1-H-BW1-ams-e-05-0-U1.st NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070952 3'
6433	18499	32752	0.9	2.0E-60	AI791952.1	EST_HUMAN	nm0112.y5 NCL CGAP_Cos8 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR repetitive element;
6840	18698	32974	1.49	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6874	19927	33224	0.92	2.0E-60	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
7027	18359	31279	2.05	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7027	18359	31280	2.06	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7317	20288	33630	6.8	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7317	20288	33631	6.8	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7434	20401	33755	0.53	2.0E-60	AI308124.1	EST_HUMAN	tb23409.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055185 3' similar to SW:GALR_RAT
7894	20837		1.06	2.0E-60	BF512808.1	EST_HUMAN	Q62805 GALANIN RECEPTOR ;
8338	21307	34722	1.09	2.0E-60	X85597.1	EST_HUMAN	U1-H-BW1-ams-e-02-0-U1.st NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
9219	22185	36618	4.86	2.0E-60	L36033.1	NT	HS15BEST human adult testis Homo sapiens cDNA clone CAM_test16
10337	23281	36740	2.2	2.0E-60		NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
10337	23281	36741	2.2	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
12094	24965	38561	1.9	2.0E-60	AW751191.1	EST_HUMAN	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
12094	24965	38562	1.9	2.0E-60	AW751191.1	EST_HUMAN	CMO-CT0013-290699-017403 CT0013 Homo sapiens cDNA
12094	24965	38562	1.9	2.0E-60	AW751191.1	EST_HUMAN	CMO-CT0013-290699-017403 CT0013 Homo sapiens cDNA

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12647	25330		1.38	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S.cerevisiae)-like 1 (NHP2L1), mRNA
12771	25800		1.82	2.0E-60	AF088757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12773	25411		5.64	2.0E-60	11418068	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC83504), mRNA
12789	25421		2.36	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
523	13594	26512	0.97	1.0E-60	BE178588.1	EST_HUMAN	PM3-HT0605-270200-001-e08 HT0605 Homo sapiens cDNA
3920	16960	29873	1.46	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4993	18008	30896	1.34	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8280	21249	34661	0.98	1.0E-60	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
9108	22074		3.08	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element
9134	22100	35526	1.38	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGEAD05 5'
1101	14145	27095	1.85	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
9061	22027	35450	0.46	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9061	22027	35451	0.46	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2678	15874	28594	1.17	8.0E-61	AW006478.1	EST_HUMAN	w03b10.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2678	15674	28695	1.17	8.0E-61	AW006478.1	EST_HUMAN	w03b10.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2862	16020		1.66	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
8227	21196	34604	0.73	8.0E-61	AA583988.1	EST_HUMAN	nm59p06.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
11926	24807	38400	1.47	8.0E-61	H71225.1	EST_HUMAN	ys12e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:214600 5' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11926	24807	38401	1.47	8.0E-61	H71225.1	EST_HUMAN	ys12e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:214600 5' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
128	13234	26163	0.87	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
128	13234	26184	0.67	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
265	13361	26285	2.61	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
812	13870	26819	2.17	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1324	14359	27326	13.5	6.0E-61	AF119880.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1634	14666	27642	0.9	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1655	14687	27662	2.32	6.0E-61	AA596033.1	EST_HUMAN	nm66h09.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
2137	15154	28169	0.91	6.0E-61	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3317	16370	29290	6.07	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
6147	19222	32452	3.08	6.0E-61	S79249.1	NT	Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7565	20528	33887	1.53	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7878	20822	34198	1.87	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2) mRNA, complete cds
221	13321	28248	1.14	5.0E-61	8922890	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
221	13321	26247	1.14	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
1688	14719	27699	3.18	5.0E-61	4508008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3049	16106	29020	1.96	5.0E-61	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
4006	17045		1.87	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AVL1 and CBR1 on chromosome 21q22; segment 1/3
1774	14803	27768	1.17	4.0E-61	AU140307.1	EST_HUMAN	AU140307 PLACE2 Homo sapiens cDNA clone PLACE2000302 5'
5813	18899	32190	0.51	4.0E-61	7661637	NT	Homo sapiens DKFZP568B023 protein (DKFZP568B023), mRNA
12348	25143		2.27	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFAR801 5'
8764	21731	35154	0.85	3.0E-61	AF150190.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04
489	13571	26493	1.74	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1217	14255	27213	3.4	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1217	14255	27214	3.4	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1674	14706	27694	1.34	2.0E-61	N53039.1	EST_HUMAN	y53d11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:25444 50S RIBOSOMAL PROTEIN L35A (HUMAN);
2849	15648		1.25	2.0E-61	N39397.1	EST_HUMAN	y03f11.1 Soares melanocyte 2NHHM Homo sapiens cDNA clone IMAGE:270189 5'
6566	19626	32891	0.92	2.0E-61	11426166	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
9369	22334	35785	1.07	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCELG06 5'
9920	22741		1.27	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
10282	23207	36982	1.61	2.0E-61	AW500256.1	EST_HUMAN	UJ-HF-BNO-akd-f-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
10812	23534	37031	2.88	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (RPC39), mRNA
11230	24183		6.91	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
13042	25583	31701	1.39	2.0E-61	AW995326.1	EST_HUMAN	QV0-BN0042-170300-162-f10 BN0042 Homo sapiens cDNA
435	13509		1.85	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
774	13833	28779	0.96	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1784	14813		0.95	1.0E-61	U32657.1	NT	Human polymorphic trinuclotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1875	14900	27899	4.69	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2206	15221	28241	1.52	1.0E-61	AW827281.1	EST_HUMAN	zn11b09.y1 NCI_CGAP_LJ15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element MSR1 repetitive element;
2846	15906	28831	1.58	1.0E-61	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
3387	16436	29363	0.87	1.0E-61	7662319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4288	17317	30196	1	1.0E-61	M69840.1	NT	Human monamine oxidase A (MAOA) mRNA, complete cds
4468	17494	30381	1.02	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4468	17494	30382	1.02	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4893	17910	30799	8.18	1.0E-61	AW298181.1	EST_HUMAN	U1-H-BWO-ajl-b-08-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4893	17910	30800	9.18	1.0E-61	AW298181.1	EST_HUMAN	U1-H-BWO-ajl-b-08-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4971	17988	30876	0.94	1.0E-61	7705898	NT	Homo sapiens flavohemoprotein b5+b5R (LOC51167), mRNA
4971	17988	30877	0.94	1.0E-61	7705898	NT	Homo sapiens flavohemoprotein b5+b5R (LOC51167), mRNA
5467	18569	31479	0.68	1.0E-61	M76423.1	NT	H. sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5773	18865	32046	0.74	1.0E-61	7662303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
5884	19069	32287	1.02	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
7085	20019	33321	7.63	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (HP40) gene, complete cds
7298	20270	33605	0.95	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
7397	20365	33717	1.59	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7397	20365	33718	1.58	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8471	21440	34858	4.16	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8656	21824	35044	3.41	1.0E-61	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9637	22581		2.94	1.0E-61	AW999726.1	EST_HUMAN	MRO-BN0070-040400-010-H01 BN0070 Homo sapiens cDNA
9712	22665	36122	0.99	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
10389	23311	36780	5.56	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10988	23964	37488	3.38	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11681	24697		3.58	1.0E-61	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
12283	25846	31433	4.15	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12283	25846	31434	4.15	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12652	25335	31761	23.14	1.0E-61	M20809.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
12942	25521	31711	10.09	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10722	23644	37137	2.13	9.0E-62	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
4581	17603	30500	1.04	8.0E-62	AA830420.1	EST_HUMAN	cc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK
1109	14153	27103	1.9	7.0E-62	AV714334.1	EST_HUMAN	P31795 POL POLYPROTEIN ;
3517	18563	29488	0.7	7.0E-62	P17480	SWISSPROT	AV714334 DGB Homo sapiens cDNA clone DCBAA08 5'
6023	19106	32309	1.13	7.0E-62	11427965	NT	NUCLEAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
11878	24844	38221	9.39	7.0E-62	A1208681.1	EST_HUMAN	(AUTOANTIGEN NOR-90)
3012	16070		1.49	6.0E-62	U09410.1	NT	Homo sapiens hypothetical protein (FLJ20281), mRNA
							gg56a04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103
							O15103 HYPOTHETICAL 27.3 KD PROTEIN. ;
							Human zinc finger protein ZNF131 mRNA, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3395	16444		4.9	6.0E-62	11418255	NT	Homo sapiens CGI-58 protein (CGI-58), mRNA
7887	20831	34209	3.27	6.0E-62	A1762801.1	EST_HUMAN	wi04d02.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2389251 3'
7887	20831	34210	3.27	6.0E-62	A1762801.1	EST_HUMAN	wi04d02.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8422	21391		0.72	6.0E-62	AW501124.1	EST_HUMAN	UI-HF-BP0p-alt-d-09-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
8600	21568	34984	1.4	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
9709	22662	36118	4.02	6.0E-62	AW814393.1	EST_HUMAN	MR3-ST0203-130100-025-609 ST0203 Homo sapiens cDNA
416	13489	26424	2.28	5.0E-62	A1950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
2416	15423	28446	3.61	5.0E-62	AJ271735.1	NT	Q06379 GOLGIN-95; contains element MER22 repetitive element;
2416	15423	28447	3.61	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2596	15597	28615	1.43	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; complete cds
2596	15597	28616	1.43	5.0E-62	U39487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3430	16478	28397	2.95	5.0E-62	4506758	NT	Human xanthine dehydrogenase/oxidase mRNA
4355	17382	30264	1.91	5.0E-62	AA431093.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4689	17611		1.1	5.0E-62	AW905887.1	EST_HUMAN	zw78e09.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
8894	21860	35283	0.64	5.0E-62	4506758	NT	P47245 NARDILYSIN;
9875	22828	36282	8.13	5.0E-62	AW410687.1	EST_HUMAN	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
11598	24534	38090	2.18	5.0E-62	11425574	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
11598	24534	38091	2.18	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
841	13898	26853	2.29	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens muscle specific gene (M9), mRNA
841	13898	26854	2.29	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
842	13898	26853	1.27	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
842	13898	26854	1.27	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1458	14491		1	4.0E-62	AA311281.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2464	15468	28491	2.85	4.0E-62	A1827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2464	15468	28492	2.85	4.0E-62	A1827900.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
3410	16459		6.48	4.0E-62	4557857	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
							wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
							wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
							Homo sapiens keratin 18 (KRT18) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6032	19115	32318	1.63	4.0E-62	4506978	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
6429	19495	32748	2.53	4.0E-62	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7377	20347	33698	2.08	4.0E-62	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
7896	20839	34219	2.59	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
7896	20839	34220	2.59	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
8511	21479	34893	0.93	4.0E-62	11429973	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
9198	22184	35594	5.95	4.0E-62	AB03089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
11353	24303	37830	3.05	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11353	24303	37831	3.05	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11598	24338	38083	1.57	4.0E-62	AW023559.1	EST_HUMAN	d556p04.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487751 5'
12267	25090	38176	3.39	4.0E-62	11418098	NT	Homo sapiens putative nuclear protein (HRHF2122), mRNA
12491	25803		1.3	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae) like 1 (NHP2L1), mRNA
12871	25805	31706	1.96	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12924	25500	31703	19.77	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12924	25500	31704	19.77	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12977	25542	31717	3.07	4.0E-62	11430490	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
75	13192	26114	0.88	3.0E-62	4557794	NT	Homo sapiens neurofilamin 2 (bilateral acoustic neuroma) (NF2) mRNA
3059	16116	29029	1.02	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3059	16116	29030	1.02	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3712	18755	29689	3.52	3.0E-62	X62858.1	NT	Human cyclophilin-related processed pseudogene
8885	21851	35272	4.85	3.0E-62	A1632733.1	EST_HUMAN	wa33f0.4.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298803 3' similar to contains THR.12
1235	14272	27232	2.78	2.0E-62	AL163284.2	NT	THR repetitive element
8142	21079	34479	0.88	2.0E-62	AA307490.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
9127	22083	35520	4.47	2.0E-62	BF329911.1	EST_HUMAN	EST1178374 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9127	22083	35521	4.47	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10533	23455		4.98	2.0E-62	AF224669.1	NT	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
11896	24873		20.5	2.0E-62	BF330876.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
1045	14091	27044	1.88	1.0E-62	AF248540.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1547	14580	27582	12.74	1.0E-62	L78810.1	NT	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
							Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
							Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1815	14842	27833	1.18	1.0E-02	AA625207.1	EST_HUMAN	af70e11.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453;
2925	15983	28908	1.45	1.0E-02	AL039044.1	EST_HUMAN	DKFZp566F104.r1 586 (synonym: hfk2) Homo sapiens cDNA clone DKFZp566F104 5'
3435	16482		1.15	1.0E-02	AB040911.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4556	17579	30470	1.43	1.0E-02	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
5169	18178	31056	0.88	1.0E-02	AA148822.1	EST_HUMAN	z08b08.r1 Soares_pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:491611 5' similar to SW:C561_BOVIN P10897 CYTOCHROME B561.;
5198	18205	31079	0.94	1.0E-02	L23503.1	NT	Human glucagon-like peptide-1 receptor (GLP-1) mRNA, complete cds
8421	19488	32738	2.84	1.0E-02	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (ORTR), CDM protein (CDM), adrenoleukodystrophy protein >
7341	20312	33655	0.91	1.0E-02	AA490060.1	EST_HUMAN	ab05602.s1 Stratiagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839808 3'
7352	20322	33669	2.48	1.0E-02	AA722878.1	EST_HUMAN	z089f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7352	20322	33670	2.48	1.0E-02	AA722878.1	EST_HUMAN	z089f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
9110	22078	35502	0.66	1.0E-02	AA280050.1	EST_HUMAN	zs93e07.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705060 5'
9413	22378	38816	1.82	1.0E-02	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9413	22378	38817	1.82	1.0E-02	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9457	22421	38858	1.97	1.0E-02	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9457	22421	38859	1.97	1.0E-02	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9915	22736	38189	3.42	1.0E-02	AA465170.1	EST_HUMAN	ea33d08.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
11894	24659	38237	2.41	1.0E-02	Z78698.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SO6pA14D8
12750	25397		2.22	1.0E-02	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12856	25526	31714	3.25	1.0E-02	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
338	13427	26349	2.41	9.0E-03	AW819405.1	EST_HUMAN	QVA-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2353	15362		1.51	9.0E-03	C18159.1	EST_HUMAN	C18159 Homo placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN:558C10 5'
4071	17107	30000	9.29	9.0E-03	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4071	17107	30001	9.29	9.0E-03	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5315	18331	38614	2.17	9.0E-03	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5541	18638	31578	1.3	9.0E-03	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
7388	20357	33709	3.41	9.0E-03	11426985	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
8138	21075	34475	0.73	9.0E-03	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8699	21637	35060	1.58	9.0E-03	11421160	NT	Homo sapiens Ras association (Ra)GDS/AF-6 domain family 2 (RASSF2), mRNA
11246	24199	37719	1.54	9.0E-03	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11246	24199	37720	1.54	9.0E-03	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15360	28382	1.1	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2363	15391	28416	2.49	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3475	16521	29443	3.42	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3475	16521	29444	3.42	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4294	17323	30203	3.75	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
929	13982		1.87	7.0E-63	AB72137.1	EST_HUMAN	hm55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
6412	18515		23.22	6.0E-63	AA420803.1	EST_HUMAN	nc83f02.f1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
9228	22192	35622	0.63	5.0E-63	11528464	NT	RIBOSOMAL PROTEIN (HUMAN);
3332	16383	29305	0.7	4.0E-63	AL163276.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3821	16861	29764	1.16	4.0E-63	AB014807.1	NT	Homo sapiens chromosome 21 segment HS21C078
3821	16861	29765	1.16	4.0E-63	AB014807.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6388	19948	32917	2.92	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6388	19948	32918	2.92	4.0E-63	AW750372.1	EST_HUMAN	HM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11467	24410	37958	2.12	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11467	24410	37959	2.12	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-e-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
13023	25571		1.49	4.0E-63	AA629056.1	EST_HUMAN	UI-H-B11-abq-e-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1952	14975	27975	2.52	3.0E-63	AB018280.1	NT	z184b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744849 3' similar to contains L1.11 L1 repetitive element
2790	15782	28798	1.85	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2832	14280	27243	16.82	3.0E-63	6005963	NT	Human Mel-RNA-1 gene 1
6619	19677	32954	32.29	3.0E-63	11545910	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
10064	22991	36480	0.51	3.0E-63	BE787158.1	EST_HUMAN	Homo sapiens hepatocellular carcinoma antigen gene 620 (LOC63928), mRNA
10064	22991	36481	0.51	3.0E-63	BE787158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
193	13294	28221	1.91	2.0E-63	U07804.1	NT	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
199	13300	26228	1.91	2.0E-63	4885225	NT	Human DNA topoisomerase I mRNA, partial cds
498	13570		3.06	2.0E-63	4557624	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
827	13885	26838	1.7	2.0E-63	7657042	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
1569	14802	27577	4.18	2.0E-63	AB030388.1	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
1569	14802	27578	4.18	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1791	14810	27796	1.33	2.0E-63	BE410739.1	EST_HUMAN	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
3288	16351	29271	2.77	2.0E-63	AF109718.1	NT	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
							Homo sapiens chromosome 3 subtelomeric region

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3925	16995	29878	3.64	2.0E-63	L30891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4901	17918	30810	0.95	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5188	18197	31070	1.19	2.0E-63	BE146828.1	EST_HUMAN	QV4-HT0222-011199-018-q01 HT0222 Homo sapiens cDNA
5232	18240	31112	1.59	2.0E-63	6912617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA
5334	25635	31192	0.57	2.0E-63	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
5986	19071	32270	2.49	2.0E-63	BF373641.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
5988	19071	32271	2.49	2.0E-63	BF373641.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6310	19381	32620	0.83	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6310	19381	32621	0.83	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6860	19913	33209	1.23	2.0E-63	U65059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV2TS1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S2A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6911	19983	33259	0.81	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6911	19983	33260	0.81	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7278	20012	33315	1.46	2.0E-63	8910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7278	20012	33316	1.46	2.0E-63	8910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
8058	20995	34391	0.82	2.0E-63	AB046844.1	NT	Homo sapiens chromosome 21 segment HS21C010
8878	21845	35287	3.8	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9409	22374	35810	1.06	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9409	22374	35811	1.06	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
10289	23224	36707	0.98	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11098	24058	37582	13.74	2.0E-63	N7945.1	EST_HUMAN	zb18b05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN);
11127	24087	37814	2.32	2.0E-63	AF099810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
11127	24087	37615	2.32	2.0E-63	AF098810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
12381	25747	31515	6.02	2.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
1515	14547	27518	0.93	1.0E-63	F09485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
1515	14547	27519	0.93	1.0E-63	F09485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4370	17397	30276	3.4	1.0E-63	F09485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4370	17397	30277	3.4	1.0E-63	F09485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5428	18528	31408	1.66	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5864	18953	32140	97.84	1.0E-63	AW582286.1	EST_HUMAN	QV0-ST0215-080100-083-b09 ST0215 Homo sapiens cDNA
6531	19594	32855	0.72	1.0E-63	AW451950.1	EST_HUMAN	U1-H-B13-alk-h-02-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
6531	19594	32856	0.72	1.0E-63	AW451950.1	EST_HUMAN	U1-H-B13-alk-h-02-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
8816	21783		2.94	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
13020	25859		5.18	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6078	19159	32370	0.56	9.0E-64	AW401433.1	EST_HUMAN	U1-HF-BK0-aad-b-09-Q-U1.T NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053153 5'
8199	21168	34579	4.61	9.0E-64	AI478188.1	EST_HUMAN	hm50507.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1048	14094		2.71	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6263	18338	32569	3.28	8.0E-64	BE885755.1	EST_HUMAN	601508988F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
12187	25034		6.22	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12239	25070		2.63	8.0E-64	T60651.1	EST_HUMAN	y69b02.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:3633204 5'
3540	16588		0.8	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4763	17783	30878	3.2	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4763	17783	30879	3.2	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
8096	21032	34430	0.64	7.0E-64	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
10393	23315	36794	4.76	7.0E-64	Y07848.1	NT	Homo sapiens EW'S, gar22, rrp22 and bam22 genes
1735	14765	27748	3.86	6.0E-64	AI651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1735	14765	27749	3.86	6.0E-64	AI651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3139	16186	29105	4.25	6.0E-64	AW026445.1	EST_HUMAN	wy13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
3139	16186	29106	4.25	6.0E-64	AW026445.1	EST_HUMAN	wy13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
5703	18788	31973	2.43	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5703	18788	31974	2.43	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5725	18819	31898	6.33	6.0E-64	M13976.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5928	19015	32209	0.71	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALOR), mRNA
5928	19015	32210	0.71	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALOR), mRNA
7448	20412	33764	2.85	6.0E-64	11525878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7446	20412	33765	2.85	6.0E-64	11525878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9662	22635	36091	7.07	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
9664	22680	36264	1.78	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
10076	23003	36473	2.44	6.0E-64	S76475.1	NT	tkc [human, brain, mRNA, 2715 nt]
11121	24081	37805	4.48	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11121	24081	37806	4.48	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11358	16196	29105	1.73	6.0E-64	AW026445.1	EST_HUMAN	wf13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
11358	16196	29106	1.73	6.0E-64	AW026445.1	EST_HUMAN	wf13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
12398	25172	31818	9.28	6.0E-64	11526198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
821	13879	26829	3.66	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
821	13879	26830	3.66	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1341	14378	27345	0.93	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1724	14754	27740	1.7	5.0E-64	U98358.1	NT	Human (3)mb1 protein homolog mRNA, complete cds
2837	14509	27483	3.52	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2837	14509	27484	3.52	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3983	17023	29934	7.14	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR63 (CR63) mRNA, partial cds
4132	17184	30053	0.93	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
8125	21062	34460	0.57	4.0E-64	BE794607.1	EST_HUMAN	601590382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944397 5'
11164	24122	37650	1.55	4.0E-64	AW813763.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
11164	24122	37651	1.55	4.0E-64	AW813763.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2208	19223	28243	6.32	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (Tfujivara) Homo sapiens cDNA clone GEN:588E02 5'
3266	16322	28244	0.72	3.0E-64	BE794381.1	EST_HUMAN	601589568F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3457	16503	29422	1.85	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3457	16503	29423	1.85	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6200	19274	32608	1.35	3.0E-64	Z26273.1	NT	H. sapiens isoform 1 gene for L-type calcium channel, exon 28
6475	19540	32788	0.84	3.0E-64	AW500861.1	EST_HUMAN	UHF-BPOp-ak-c-05-Q-U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3073161 5'
6641	19699	32975	2.78	3.0E-64	BF370000.1	EST_HUMAN	RC6-FN0019-230600-011-G11 FN0019 Homo sapiens cDNA
8809	21776	35201	1.78	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8809	21776	35202	1.78	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8840	21807	35225	2.73	3.0E-64	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNABJ
8840	21807	35226	2.73	3.0E-64	BE208521.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
9782	22723	36177	1.54	3.0E-64	AL163246.2	NT	PROTEIN HOMOLOG 2 (HUMAN);
9782	22723	36178	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9872	22825	36278	0.8	3.0E-64	AW977384.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9872	22825	36279	0.8	3.0E-64	AW977384.1	EST_HUMAN	EST389483 MAGe resequences, MAGO Homo sapiens cDNA
11998	24875	38471	1.87	3.0E-64	AL163227.2	NT	EST389483 MAGe resequences, MAGO Homo sapiens cDNA
1090	14134	27086	0.95	2.0E-64	AAG09940.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1398	14432	27401	1.2	2.0E-64	4757701	NT	af09408.s1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1031151 3'
							Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2530	15533		2.05	2.0E-64	A1927030.1	EST_HUMAN	w087b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element ;
2536	15538	28560	3.13	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2536	15538	28561	3.13	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3801	16841	29748	0.67	2.0E-64	AW558145.1	EST_HUMAN	EST370215 IMAGE resequences, IMAGE Homo sapiens cDNA
3801	16841	29749	0.67	2.0E-64	AW558145.1	EST_HUMAN	EST370215 IMAGE resequences, IMAGE Homo sapiens cDNA
6121	19199	32424	2.2	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6370	19438	32881	1.38	2.0E-64	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6632	19690	32969	4.02	2.0E-64	BF668537.1	EST_HUMAN	602123474F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4280395 5'
6745	19800	33080	1.5	2.0E-64	A078387.1	EST_HUMAN	oz29b03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
6869	19912	33208	3.88	2.0E-64	M77185.1	NT	Homo sapiens dopamine receptor D5 pseudogene 1, partial cds
8106	21043	34442	0.57	2.0E-64	11431054	NT	Homo sapiens axitin 2-binding protein 1 (A2BP1) mRNA
8184	21102	34501	0.56	2.0E-64	AV608785.1	EST_HUMAN	QV1-HT0413-010200-059-h12 HT0413 Homo sapiens cDNA
9016	21982	35400	5.69	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1) mRNA
9016	21982	35401	5.69	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1) mRNA
9495	22459	35899	0.43	2.0E-64	11423508	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1) mRNA
9586	22548	35999	0.96	2.0E-64	AU132570.1	EST_HUMAN	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1) mRNA
11114	24074	37597	3.74	2.0E-64	BF528114.1	EST_HUMAN	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1) mRNA
11391	24337	37866	4.59	2.0E-64	A1922911.1	EST_HUMAN	602042882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180558 5'
11391	24337	37867	4.59	2.0E-64	A1922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11833	24716	38301	1.89	2.0E-64	BE268660.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11833	24716	38302	1.89	2.0E-64	BE268660.1	EST_HUMAN	601185078F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542922 5'
12316	25122	31844	1.47	2.0E-64	8587387	NT	601185078F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542922 5'
12744	25393		3.54	2.0E-64	H55162.1	EST_HUMAN	Homo sapiens period (Drosophila) homolog 3 (PER3) mRNA
258	13355	26279	1.48	1.0E-64	AF231919.1	NT	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
1794	14823	27807	17.02	1.0E-64	A1929419.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3024	16081	29004	0.81	1.0E-64	4507334	NT	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:L121696_cds1 PROTHYMOSIN ALPHA (HUMAN) contains element MSR1 repetitive element ;
3522	16568	29492	5.73	1.0E-64	AF198779.1	NT	Homo sapiens synaptophysin 1 (SYNJ1) mRNA
3598	16643	29562	1.38	1.0E-64	AF228527.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3598	16643	29563	1.38	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3917	16957	29870	2	1.0E-64	8922829	NT	Homo sapiens TRIAD3 mRNA, partial cds
							Homo sapiens hypothetical protein FLJ11026 (FLJ11026) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
10424	23348	36831	0.68	1.0E-64	AA042976.1	EST_HUMAN	2k53f08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486587 3'
12288	25104		2.03	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2284	15297	28321	1.84	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2284	15297	28322	1.84	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
11863	24745		35.25	9.0E-65	BF330676.1	EST_HUMAN	QV4-BT0257-081189-017-e03 BT0257 Homo sapiens cDNA
11837	24720	38305	7.27	8.0E-65	A1929244.1	EST_HUMAN	eu88h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to
10515	23437	36936	2.13	7.0E-65	BE081653.1	EST_HUMAN	SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21. ;
1059	14105	27056	2.73	6.0E-65	AV721898.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
1938	14962		12.23	6.0E-65	AA550929.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC08 5'
6721	19777	33058	0.87	6.0E-65	AA503892.1	EST_HUMAN	RI86d10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:989379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
						EST_HUMAN	nh37b07.s1 NCL_CGAP_P15 Homo sapiens cDNA clone IMAGE:954517
9098	22064	35489	2.49	6.0E-65	AW083252.1	EST_HUMAN	xc07b09.x1 NCL_CGAP_C021 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306
9385	22330	35759	4.16	6.0E-65	AA427878.1	EST_HUMAN	LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S. ;contains L1 b2 L1 repetitive element ;
9385	22330	35760	4.16	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9429	22393	35832	1.08	6.0E-65	A1085314.1	EST_HUMAN	zw53b06.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9429	22393	35833	1.08	6.0E-65	A1085314.1	EST_HUMAN	qf18h05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750425 3'
11220	24173	37689	2.59	6.0E-65	BE667816.1	EST_HUMAN	qf18h05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750425 3'
11378	24325	37854	1.51	6.0E-65	BF340825.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
11825	24708	38291	1.3	6.0E-65	AL163210.2	NT	60203772F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185877 5'
632	13697	26817	1.92	5.0E-65	AF064604.1	NT	Homo sapiens chromosome 21 segment HS21C010
1355	14390	27359	1.22	5.0E-65		NT	Homo sapiens KE03 protein mRNA, partial cds
1355	14390	27360	1.22	5.0E-65		NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1355	14390	27360	1.22	5.0E-65		NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2164	15180	28200	1.51	5.0E-65	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3269	16323	29245	2.13	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3269	16323	29246	2.13	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7052	20674	33381	1.18	5.0E-65	4504606	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
10833	23754	37253	1.28	5.0E-65	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
195	13286	26224	2.33	4.0E-65	AL120419.1	EST_HUMAN	DKFZ761G108.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
747	13808	26748	1.29	4.0E-65	AI286488.1	EST_HUMAN	qm48e01.x1 Soares_placenta_8to9weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:1891800 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13808	26749	1.29	4.0E-65	A1268468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8tcsweeks_2NtHP8tcsW Homo sapiens cDNA clone IMAGE:1891800 3'
1080	14124	27077	1.51	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1482	14515	27489	15.66	4.0E-65	4506636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
3971	17011	29925	0.97	4.0E-65	AW993185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA
6279	19351	32585	4.17	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6279	19351	32586	4.17	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7289	20261	33595	0.62	4.0E-65	AY008372.1	NT	Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds
7324	20295	33638	0.84	4.0E-65	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7429	20396	33748	2.46	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7797	20749	34124	0.58	4.0E-65	U40372.1	NT	Human 3', 5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7797	20749	34125	0.58	4.0E-65	U40372.1	NT	Human 3', 5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
8118	21053	34452	0.81	4.0E-65	U39656.1	NT	Human MAP kinase kinase 6 (MKK6) mRNA, complete cds
8174	21144	34549	0.78	4.0E-65	5453765	NT	Homo sapiens nei (chicken)-like 2 (NELL2), mRNA
8174	21144	34550	0.78	4.0E-65	5453766	NT	Homo sapiens nei (chicken)-like 2 (NELL2), mRNA
9501	22465	35805	1.34	4.0E-65	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10946	23866		2.85	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11301	24251	37777	2.89	4.0E-65	AV738764.1	EST_HUMAN	AV738764 CB Homo sapiens cDNA clone CBCCBE05 5'
11434	24378	37918	6.02	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12608	14124	27077	1.79	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
13091	13296	26224	1.6	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
97	13214	26139	3.16	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
98	13214	26139	5.52	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1236	15819		22.13	3.0E-65	X78932.1	NT	Hi.sapiens HZF8 mRNA for zinc finger protein
1840	14867	27866	1.7	3.0E-65	A1000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element ;
3003	16061	28979	0.74	3.0E-65	DB7078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3280	16343	29264	0.68	3.0E-65	4504950	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3734	16776	29668	1.61	3.0E-65	A1000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element ;
4679	17700	30588	1.33	3.0E-65	6912385	NT	Homo sapiens rab5 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
10429	23351	36895	1.42	3.0E-65	BE787366.1	EST_HUMAN	601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11718	23916	37433	8.57	3.0E-65	AA430006.1	EST_HUMAN	z665a06.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3415	18463	28384	8.08	2.0E-65	BF680294.1	EST_HUMAN	602155002F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4289668 5'
6886	19743		4.55	2.0E-65	BE263373.1	EST_HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
7339	20310	33653	27.84	2.0E-65	BF576922.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289285 5'
9197	22163	35562	1.26	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
9197	22163	35563	1.26	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
12238	25069		2.75	2.0E-65	AA307804.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus
12708	25728		1.95	2.0E-65	BF248098.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
940	13611	26530	1.54	1.0E-65	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX6), mRNA
2056	15075	28095	1.07	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3385	18434	28361	0.8	1.0E-65	BE466881.1	EST_HUMAN	h224909.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3208888 3'
4023	17081	28862	1.71	1.0E-65	4504082	NT	Homo sapiens glycylalanine 4 (GPC4) mRNA
4023	17061	28863	1.71	1.0E-65	4504082	NT	Homo sapiens glycylalanine 4 (GPC4) mRNA
4234	17263	30147	2.4	1.0E-65	AW028340.1	EST_HUMAN	w09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4234	17263	30148	2.4	1.0E-65	AW028340.1	EST_HUMAN	w09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5358	18463	31332	0.54	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-09 BT0702 Homo sapiens cDNA
5358	18463	31333	0.54	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-09 BT0702 Homo sapiens cDNA
5554	18851	31595	0.61	1.0E-65	A1243738.1	EST_HUMAN	qh8hp07.x1 Soares, NPL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR:007823
8597	21565	34980	5.47	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8597	21565	34981	5.47	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8623	21591	35009	2.16	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8623	21591	35010	2.16	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8662	21630	35050	2.14	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO100356 5'
8662	21630	35051	2.14	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO100356 5'
9192	22158	35588	1.94	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4289313 5'
9374	22339	35769	2.25	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9374	22339	35770	2.25	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9386	22351		2.52	1.0E-65	11431994	NT	Homo sapiens Insulin 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9832	22681	36136	5.48	1.0E-65	A191716.1	EST_HUMAN	qds6a02.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1739450 3' similar to gb:M29581 ZINC FINGER PROTEIN 8 (HUMAN); contains MER19.1 MER19 repetitive element;
10245	23170	36859	1.28	1.0E-65	AU153793.1	EST_HUMAN	AU153793 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
10665	23687	37086	0.64	1.0E-65	AA069559.1	EST_HUMAN	z75604.r1 Soares, pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10935	23855	37371	1.02	1.0E-66	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11011	23978	37501	7.57	1.0E-65	M26167.1	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
11131	24091	37620	10.37	1.0E-65	4506660	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11465	24408	37855	2.43	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4283313 5'
11545	24486	38040	1.89	1.0E-65	AI621017.1	EST_HUMAN	ts79a08.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb.L15633_ma1
12289	25105		3.13	1.0E-65	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
12391	25168	31615	7.2	1.0E-65	11418322	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12789	25427		1.87	1.0E-65	11418248	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
72	13180	26110	0.94	9.0E-66	AL160311.1	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
72	13190	26111	0.94	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
1356	14391	27361	0.93	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1356	14391	27362	0.93	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1480	14513		6.17	9.0E-66	M87289.1	NT	Human transposon-like element, partial
3916	16958	29868	0.74	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3916	16958	29869	0.74	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4719	17739	30831	0.73	9.0E-66	AL137163.1	NT	Novel human gene mapping to chromosome X
4717	17737	30828	1.58	8.0E-66	AA424304.1	EST_HUMAN	zve0c05.r1 Soares_NIH-MPc_S1 Homo sapiens cDNA clone IMAGE:787048 5'
11675	24641		1.48	7.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
4393	17421	30304	1.01	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
4393	17421	30305	1.01	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
4393	17421	30306	1.01	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
8777	21744		0.62	6.0E-66	BE178563.1	EST_HUMAN	CE18595;
11463	24436	37885	4.18	6.0E-66	X99181.1	NT	PM2-HT0604-030300-001-b06 HT0604 Homo sapiens cDNA
1369	14403	27373	1.94	5.0E-66	BE064410.1	EST_HUMAN	H. sapiens mRNA for ribosomal protein L31
9549	22593	36041	15.54	5.0E-66	11420557	NT	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
791	13850	28797	1.39	4.0E-66	6679816	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
1750	14778	27764	1.16	4.0E-66	AW697798.1	EST_HUMAN	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2288	15301	28325	1.84	4.0E-66	X99211.1	NT	RC1-NN0063-100500-022-e02 NN0063 Homo sapiens cDNA
2481	15485		2.82	4.0E-66	AJ223384.1	NT	H. sapiens DNA for endogenous retroviral like element
4823	17940		3.19	4.0E-66	9635487	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
							Human endogenous retrovirus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5630	18728	31887	3.86	4.0E-68	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate
5835	18925	32109	0.78	4.0E-68	AW939119.1	EST_HUMAN	cyclohydrolase (MTHFD2), mRNA
7038	18368	31255	4.69	4.0E-68	AW965473.1	EST_HUMAN	QV1-DT0089-110200-067-g10 DT0089 Homo sapiens cDNA
7338	20309	33652	7.18	4.0E-68	U78168.1	NT	EST377548 IMAGE resequences, MAGI Homo sapiens cDNA
7891	18726	31887	0.98	4.0E-68		NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
8413	21382	34788	6.46	4.0E-68	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate
8472	21441	34859	1.46	4.0E-68	X57147.1	NT	cyclohydrolase (MTHFD2), mRNA
11020	23985	37512	1.75	4.0E-68	BF507493.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
11706	24871	38248	1.53	4.0E-68	AB023215.1	NT	Human endogenous retrovirus pHE.1 (ERV8)
1424	14457	27432	5.89	3.0E-68	4502098	NT	UI-H-BW1-amr-a-10-0-UI.s1 NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
1424	14457	27433	5.89	3.0E-68	4502098	NT	Homo sapiens mRNA for KIAA0998 protein, partial cds
1989	15020	28027	1.07	3.0E-68	N55323.1	EST_HUMAN	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
1989	15020	28028	1.07	3.0E-68	N55323.1	EST_HUMAN	(SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1989	15020	28029	1.07	3.0E-68	N55323.1	EST_HUMAN	yz27g12.1 Scores_multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to
2718	15712	28729	4.78	3.0E-68	11141880	NT	SW-H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
3134	16191	29101	6.79	3.0E-68	7692223	NT	yz27g12.1 Scores_multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to
5542	18639	31579	0.78	3.0E-68	AB020699.1	NT	SW-H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
5657	18763	31920	0.79	3.0E-68	M13975.1	NT	yz27g12.1 Scores_multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to
5887	18958	32143	1.49	3.0E-68	11417946	NT	SW-H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
5887	18958	32144	1.49	3.0E-68	11417946	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
7660	20620	33985	4.07	3.0E-68	X92211.1	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
9883	22636	36290	0.7	3.0E-68	AF024453.1	NT	Homo sapiens KIAA0892 protein, partial cds
10077	23004	38474	0.62	3.0E-68	11417118	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
10433	23355	36841	0.69	3.0E-68	7019480	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10889	23809	37315	0.97	3.0E-68	AF155659.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
							H. sapiens geminin immunoglobulin heavy chain, variable region, (15-1)
							Homo sapiens mRNA for FLJ00045 protein, partial cds
							Homo sapiens KIAA0433 protein (KIAA0433), mRNA
							Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
							Homo sapiens molybdenum cofactor biosynthesis protein E (MCPPE) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11838	24721	38308	5.1	3.0E-88	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
13109	25929	31847	1.38	3.0E-66	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
53	13173	28082	1.94	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
53	13173	26083	1.94	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
422	13117	26015	0.7	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
422	13117	26016	0.7	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1843	14869	27867	2.18	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2241	15255	28278	2.33	2.0E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
2886	18044	28955	1.38	2.0E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3532	16578	29501	0.79	2.0E-66	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3777	16818	29727	0.9	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4685	17708	30598	36.82	2.0E-66	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4685	17708	30598	36.62	2.0E-66	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
5814	19000	32191	0.82	2.0E-66	AW968854.1	EST_HUMAN	EST380930 IMAGE resequenced, MAGJ Homo sapiens cDNA
5814	19000	32192	0.82	2.0E-66	AW968854.1	EST_HUMAN	EST380930 IMAGE resequenced, MAGJ Homo sapiens cDNA
9199	22165	35595	2.86	2.0E-66	N45480.1	EST_HUMAN	Y59602.1 Soares_multiple_sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:277826 5'
12614	25941		2.61	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
2804	15963	28885	1.58	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2804	15963	28886	1.58	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4412	15963	28885	3.59	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4412	15963	28886	3.59	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5455	18557	31468	5.82	1.0E-66	BE763088.1	EST_HUMAN	802182996F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284151 5'
5875	18964	32154	0.64	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
5875	18964	32155	0.64	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
7125	20058	33364	1.09	1.0E-66	BF326623.1	EST_HUMAN	RC5-BN0183-010900-034-G08 BN0193 Homo sapiens cDNA
8801	21768	35192	1.2	1.0E-66	AA668858.1	EST_HUMAN	aa680604.st NCI CGAP GC01 Homo sapiens cDNA clone IMAGE:827262 3'
9781	22722	36176	0.7	1.0E-66	AA018828.1	EST_HUMAN	z657612.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363118 5'
10737	23659	37153	0.9	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10737	23659	37154	0.9	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10963	23913	37429	0.44	1.0E-66	BE044595.1	EST_HUMAN	hca7n02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:3040563 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11290	24240	37767	2.47	1.0E-66	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11853	24735	38322	1.69	1.0E-66	AW968744.1	EST_HUMAN	EST380820 IMAGE resequences, MAGJ Homo sapiens cDNA
12398	25170		2.76	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
380	13493	28425	2.51	7.0E-67	AW162232.1	EST_HUMAN	au75402 x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1382	14416	27386	1.23	7.0E-67	AA383416.1	EST_HUMAN	EST96812 Testis 1 Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid ZK353
1558	14580	27661	1.19	7.0E-67	W85947.1	EST_HUMAN	zh56b05.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1558	14590	27662	1.19	7.0E-67	W85947.1	EST_HUMAN	zh56b05.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2048	15067	28086	1.02	7.0E-67	7657243	NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
2048	15067	28087	1.02	7.0E-67	7657243	NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
2821	13493	28425	2.78	7.0E-67	AW162232.1	EST_HUMAN	au75402 x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6199	19273	32507	0.96	7.0E-67	10190695	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6401	19469	32716	1.92	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8401	19469	32717	1.92	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6885	19937	33233	1.14	7.0E-67	4885084	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP8B1A), mRNA
7893	20836	34216	1.13	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
7893	20836	34217	1.13	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8666	21834	35065	0.69	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
9284	22260	35681	0.73	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11985	24862	38458	2.45	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
12169	25019	38819	1.92	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12169	25019	38820	1.92	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12839	25323	31789	1.66	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13009	25681		1.44	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA
561	13631	26548	1.19	6.0E-67	X68988.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
788	13855	26802	1.7	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1278	14313	27274	2.06	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
3183	16238	29166	1.16	6.0E-67	4508434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3451	16497	29414	1.33	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3451	16497	29415	1.33	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4152	17183	30069	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4162	17183	30070	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4734	17754	30647	3.55	6.0E-67	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4734	17754	30648	3.55	6.0E-67	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
5242	18250	31121	0.99	6.0E-67	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
5242	18250	31122	0.99	6.0E-67	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
3235	16280	29212	2.02	5.0E-67	AF009860.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
11329	24279		13.19	5.0E-67	BED10038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1331	14366	27335	2.25	4.0E-67	R80819.1	EST_HUMAN	Yn02d11.1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:1493288 3' similar to SW:Z33A_HUMAN
8355	21324	34736	0.89	4.0E-67	A1733032.1	EST_HUMAN	Q08730 ZINC FINGER PROTEIN 33A ;
8725	21693		1.18	4.0E-67	BF357321.1	EST_HUMAN	RC0-HT0694-150900-026-c03 HT0694 Homo sapiens cDNA
11403	24347		1.46	4.0E-67	AA714294.1	EST_HUMAN	rw08a01.s1 NCL CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385
2824	13699	28620	1.18	3.0E-67	AA333788.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN ;
4723	17743	30634	2.52	3.0E-67	AW669159.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' end
4753	17773		1.05	3.0E-67	AL163279.2	NT	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
8522	21490	34905	1.15	3.0E-67	BF196088.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
11588	24526		15.35	3.0E-67	AA927874.1	EST_HUMAN	hr81f05.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
190	13291	26217	0.97	2.0E-67	BE348354.1	EST_HUMAN	Q81085 GTP-RHO BINDING PROTEIN 1 ;
848	13902	26680	0.48	2.0E-67	AW616405.1	EST_HUMAN	cm18b07.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
1107	14151		1.26	2.0E-67	AF167480.1	NT	hw16g09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
1901	14925	27922	1.26	2.0E-67	BE303037.1	EST_HUMAN	CE08617 ;
1901	14925	27923	1.26	2.0E-67	BE303037.1	EST_HUMAN	QV4-ST0234-181106-037-f05 ST0234 Homo sapiens cDNA
2251	15265	28291	0.9	2.0E-67	11422948	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
2251	15265	28292	0.9	2.0E-67	11422948	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
2394	15401	28428	1.16	2.0E-67	AF305981.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
2438	15445	28463	1.36	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3481	16527	29452	3.78	2.0E-67	AA628755.1	EST_HUMAN	Zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:746362 3'
4027	17065	28966	2.7	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6190	19264	32500	0.77	2.0E-67	AL049784.1	NT	Novel human gene mapping to chromosome 13
6247	19320	32550	4.91	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
6428	19494	32746	2.19	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
-	19494	32747	2.19	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6788	19852	33137	0.77	2.0E-67	AL120542.1	EST_HUMAN	DKFZp761A229_r1_761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
8904	21870	35295	0.83	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
8904	21870	35296	0.83	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
9348	22313	35737	1.11	2.0E-67	AW602835.1	EST_HUMAN	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
9348	22313	35738	1.11	2.0E-67	AW602835.1	EST_HUMAN	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
9925	22809	36261	1.05	2.0E-67	AV731333.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
10067	22894	36463	1.01	2.0E-67	AW283624.1	EST_HUMAN	UI-HB12-ahn-e-10-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
10984	23804	37418	0.44	2.0E-67	AA928089.1	EST_HUMAN	086607 s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563541 3'
11249	24202	37724	1.47	2.0E-67	BF685788.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'
11380	24327	37856	1.59	2.0E-67	BF034485.1	EST_HUMAN	601456282F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3868976 5'
11398	26011		2.51	2.0E-67	11436448	NT	Homo sapiens KIA00985 protein (KIA00985), mRNA
11562	24502	38060	1.93	2.0E-67	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11784	23939	37461	1.63	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12808	25434	31741	1.73	2.0E-67	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
253	13350	26276	1.82	1.0E-67	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
709	13771	26705	1.34	1.0E-67	AA702794.1	EST_HUMAN	Z90504.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448016 3'
10587	23509	37001	0.44	1.0E-67	Q93075	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0218
10587	23509	37002	0.44	1.0E-67	Q93075	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0218
2186	15201	28221	2.37	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3983	16923	29831	4.25	8.0E-68	AA209458.1	EST_HUMAN	SW:SAV_SULAC Q07590 SAV PROTEIN ;
3983	16923	29832	4.25	8.0E-68	AA209458.1	EST_HUMAN	Z982h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to
8438	21407	34819	0.57	7.0E-68	AB10505.1	EST_HUMAN	SW:SAV_SULAC Q07590 SAV PROTEIN ;
10816	23737	37240	2.48	6.0E-68	11422088	NT	wb99e03.x1 NCI CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2312860 3'
12811	25438		2.18	6.0E-68	BE612554.1	EST_HUMAN	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
13058	25594	31686	1.52	6.0E-68	BF310675.1	EST_HUMAN	601452067F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3855761 5'
803	15815	26810	0.68	5.0E-68	AF231919.1	NT	601894635F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
803	15815	26811	0.68	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
820	13878	26827	4.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	13878	26828	4.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2791	15783	28799	1.23	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3162	16218	29133	3.08	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4210	17239		0.8	5.0E-68	4829987	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
4518	17543	30429	0.76	5.0E-68	AL157645.1	EST_HUMAN	DKFZp547D207.1 547 (synonym: htr1) Homo sapiens cDNA clone DKFZp547D207.5
6889	19941	33236	0.67	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3l3)-like 1 (RAB3L1), mRNA
6889	19941	33237	0.67	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3l3)-like 1 (RAB3L1), mRNA
2632	15935	28555	0.94	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2632	15935	28556	0.94	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5011	18026		7.63	4.0E-68	P04408	SWISSPROT	GLYCEALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6075	19156	32368	0.67	4.0E-68	AF157063.1	NT	Homo sapiens sedlin (SEDL) gene, exon 4
6939	20163	33485	5.5	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6939	20163	33486	5.5	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7946	20887	34278	0.72	4.0E-68	7681683	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA
9395	22360	35790	5.91	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9395	22360	35791	5.91	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9633	22496	35944	2.83	4.0E-68	AB040918.1	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11345	24295	37821	1.55	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11345	24295	37822	1.55	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
3673	16716	28630	5.02	3.0E-68	AF236092.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
5299	18303	31164	0.93	3.0E-68	AF236092.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9812	21135		5.47	3.0E-68	AI342323.1	EST_HUMAN	q38h02.x1 Scarsa_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR_12 THR repetitive element
10868	23788	37288	2.01	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
13012	25725		1.99	3.0E-68	AW693485.1	EST_HUMAN	QV1-DT0072-010200-056-h06 DT0072 Homo sapiens cDNA
2873	18921		27.9	2.0E-68	D00522.1	NT	Cricetus longicaudatus mRNA for EF-1 alpha, complete cds
4055	17092	29987	0.76	2.0E-68	BE675766.1	EST_HUMAN	T11502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828 HYPOTHETICAL 88.8 KD PROTEIN.
4708	17729	30623	1.86	2.0E-68	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
7059	20081		9.21	2.0E-68	R45088.1	EST_HUMAN	Y38904.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34896 3'
7265	20000	33299	4.51	2.0E-68	BF036316.1	EST_HUMAN	60145951.4F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
7425	20392		0.61	2.0E-68	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7595	20556	33916	0.61	2.0E-68	BF336745.1	EST_HUMAN	IL3-CT0534-180900-273-A01 CT0634 Homo sapiens cDNA
9301	22266	38698	0.67	2.0E-68	Q05859	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
80	13196	26120	0.75	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
296	13390	26318	17.65	1.0E-68	AW819405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2263	15277	28301	1.27	1.0E-68	AB011148.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2263	15277	28302	1.27	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2767	15759	28781	1.04	1.0E-68	AW451832.1	EST_HUMAN	UI-H-B13-alk-4-01-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
4037	17075	29975	1.01	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
5066	18076	30957	0.69	1.0E-68	AA897343.1	EST_HUMAN	ai47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480518 3'
5395	19498	31378	1.8	1.0E-68	7652349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
7938	20880	34270	0.56	1.0E-68	11436716	NT	Homo sapiens sentrin/SUMO-specific protease (SENPT1), mRNA
11196	24153	37894	1.48	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11198	24153	37885	1.48	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11250	24203	37725	3.37	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSM13) mRNA, complete cds
11631	24569	38131	2.13	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKGSH) gene, exon 4-5
11631	24569	38132	2.13	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKGSH) gene, exon 4-5
11975	24852	38449	1.73	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
11975	24852	38450	1.73	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12790	13196	28120	2.19	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
13005	25898	31419	2.07	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13057	25593		1.61	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
22	13142	26040	5.15	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
22	13142	26041	5.15	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1029	14075	27025	0.76	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1029	14075	27026	0.76	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4155	17186	30074	0.97	9.0E-69	4757887	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4175	17206	30092	1.02	9.0E-69	4504010	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD) (GLCLR) mRNA
8241	18249	31120	0.93	9.0E-69	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
11238	24189		5.51	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3397	18446		1.77	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
6487	19552	32802	5.65	7.0E-69	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
8195	21165	34574	15.42	8.0E-69	A182784.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbhL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gbL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8195	21165	34575	15.42	8.0E-69	AI192764.1	EST_HUMAN	q62h01.x1 Scores_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gbL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
9325	22280	35720	1.04	5.0E-69	AA826039.1	EST_HUMAN	cd80a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1372300 3'
521	13592		1.27	4.0E-69	AI873630.1	EST_HUMAN	wm26h1.1.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437125 3'
5855	25646	32130	1.38	4.0E-69	BE561063.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677641 5'
5943	19029	32223	5	4.0E-69	AI764973.1	EST_HUMAN	wh57d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137
6783	19838	33122	2.77	4.0E-69	4557732	NT	O55137 ACYL-CoA THIOESTERASE ;
6783	19838	33123	2.77	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9265	22231	35682	0.55	4.0E-69	AU119634	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
386	13499	26432	3.2	3.0E-69	BE268012.1	EST_HUMAN	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1006263 5'
614	13679	26595	2.56	3.0E-69	AF221712.1	NT	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
2386	15394		0.93	3.0E-69	5729910	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
4818	17639		0.93	3.0E-69	T96234.1	EST_HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
5266	17639		0.93	3.0E-69	T96234.1	EST_HUMAN	ye48h04.r1 Scores_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:121015 5'
5314	18330	38613	1.79	3.0E-69	11418185	NT	ye48h04.r1 Scores_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:121015 5'
5712	18906	31883	0.54	3.0E-69	U14178.1	NT	Homo sapiens eonitase 2, mitochondrial (ACO2), mRNA
6972	20195		0.58	3.0E-69	AJ277557.1	NT	Human type II IL-1 receptor gene, exon 1B
7038	18370	31257	0.6	3.0E-69	11426789	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
7597	20558	33918	0.82	3.0E-69	AF095703.1	NT	Homo sapiens sperm surface protein (HSS), mRNA
7651	20611	33977	1.52	3.0E-69	U62351.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7800	20752	34128	8.4	3.0E-69	AF269075.1	NT	Homo sapiens arm-repeat protein NFRAP/neurojuncin (CTNND2) mRNA, partial cds
8715	21683	35111	1.05	3.0E-69	AW138648.1	EST_HUMAN	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
8120	22086		1.38	3.0E-69	AA376399.1	EST_HUMAN	U1-HB1-acw-g-01-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
9328	22283	35722	0.5	3.0E-69	8928248	NT	EST88807 HSC172 cells I Homo sapiens cDNA 5' end similar to ribosomal protein S18
9768	22709	36164	1.84	3.0E-69	X13223.1	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9891	22844	36301	59.4	3.0E-69	X06233.1	NT	H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
10188	23113	36597	0.71	3.0E-69	5730036	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
11003	23969	37493	3.28	3.0E-69	11432120	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
11190	24146		12.51	3.0E-69	AA376399.1	EST_HUMAN	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
12300	25111		7.34	3.0E-69	11419157	NT	EST88807 HSC172 cells I Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
							Homo sapiens HGC6.2 protein (HGC6.2), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
129	13477	28411	1.06	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
129	13477	28412	1.06	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
404	13477	28411	4.75	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
404	13477	26412	4.75	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1902	14928	27924	1.46	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360074 5'
2856	15916		3.8	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
8900	21868	36289	0.97	2.0E-69	AA114270.1	EST_HUMAN	zm29g01.r1 Stratagene pancreas (H937208) Homo sapiens cDNA clone IMAGE:527088 5'
1714	14744	27728	2.69	1.0E-69	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
5059	18069		0.73	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
8168	19243	32474	0.78	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3988532 5'
8168	19243	32475	0.78	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3988532 5'
8768	19812	33092	4.09	1.0E-69	AW393969.1	EST_HUMAN	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
6992	20215	33544	1.4	1.0E-69	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6992	20215	33545	1.4	1.0E-69	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7011	20137	33453	2.78	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7011	20137	33454	2.78	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7065	20087	33396	0.62	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3810614 5'
7065	20087	33397	0.62	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3810614 5'
10534	23458	36952	4.31	1.0E-69	BE246070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10534	23458	36953	4.31	1.0E-69	BE246070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10631	23553	37053	1.48	1.0E-69	AB014807.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10779	23700	37198	0.53	1.0E-69	BF528429.1	EST_HUMAN	602043782F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4181325 5'
11210	24172		2.78	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
12234	25066	38167	1.89	1.0E-69	BF125987.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12648	25331		6.78	1.0E-68	AI809894.1	EST_HUMAN	wf64e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element; contains element 1 MIR repetitive element;
2339	15890	28370	1.61	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1008023
4401	17429	30314	2.11	8.0E-70	L77566.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1830	14857	27854	2.26	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1830	14857	27855	2.26	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1947	14971	27989	1.87	7.0E-70	AA282956.1	EST_HUMAN	z15f04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2078	15095		2.97	7.0E-70	5031668	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA.

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4252	17281	30162	4.29	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5560	18667	31602	5.36	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5560	18667	31603	5.36	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7110	20044	33346	2.38	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
8046	20982	34378	0.74	7.0E-70	11417306	NT	Homo sapiens tlin immunoglobulin domain protein (myosin) (TTID), mRNA
8774	21741	35162	2.43	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8774	21741	35163	2.43	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
9072	22038	35462	4.26	7.0E-70	M74099.1	NT	Human displacement protein (GCAAT) mRNA
9072	22038	35463	4.26	7.0E-70	M74099.1	NT	Human displacement protein (GCAAT) mRNA
9512	22475	35919	2.79	7.0E-70	X69841.1	NT	Human PBX3 mRNA
9512	22475	35920	2.79	7.0E-70	X69841.1	NT	Human PBX3 mRNA
9790	21113	34513	3.51	7.0E-70	AF163715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9816	21138	34542	2.05	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9816	21138	34543	2.05	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
10014	22941	36407	0.93	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
10661	23583	37079	0.6	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10661	23583	37080	0.6	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11923	24804	38398	2.36	7.0E-70	11526316	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11923	24804	38397	2.36	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
12893	25982	31414	13.53	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa I)
13071	25605	31698	34.82	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa I)
872	13928	26896	2.38	6.0E-70	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2147	15163	28179	1.7	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2516	15519	28542	1.17	6.0E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2569	15987	28577	1.76	5.0E-70	7682307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2559	15987	28578	1.76	5.0E-70	7682307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12243	25073		2.52	5.0E-70	BE166034.1	EST_HUMAN	MF3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
6918	19669	33285	1.24	4.0E-70	T06037.1	EST_HUMAN	EST03926 Fetal brain, Stralagene (cat#939206) Homo sapiens cDNA clone HFBDN25
6961	20186	33510	0.78	4.0E-70	AW793228.1	EST_HUMAN	CN4-UM0003-010300-105-908 UM0003 Homo sapiens cDNA
6961	20186	33511	0.78	4.0E-70	AW793228.1	EST_HUMAN	CN4-UM0003-010300-105-908 UM0003 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1593	14625	27598	1.56	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-e12 BT0522 Homo sapiens cDNA
1593	14625	27599	1.56	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-e12 BT0522 Homo sapiens cDNA
5701	18796	31970	0.63	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5701	18796	31971	0.63	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6055	19136	32346	1.1	3.0E-70	AI831975.1	EST_HUMAN	W80403.X1 NCL_CGAP_GLL.1 Homo sapiens cDNA clone IMAGE:2388005 3'
6509	19573	32826	1.27	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302806 5'
6509	19573	32827	1.27	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302806 5'
10487	23369	36883	0.55	3.0E-70	BE502973.1	EST_HUMAN	h281h02.X1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
40	13180	28063	2.14	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
690	13753	26680	14.23	2.0E-70	N42161.1	EST_HUMAN	W07a10.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
690	13753	26681	14.23	2.0E-70	N42161.1	EST_HUMAN	W07a10.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
706	13768	26704	1.39	2.0E-70	AI246899.1	EST_HUMAN	q551h01.X1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1023	14069	27020	1.23	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1188	14228	27184	1.73	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1188	14228	27185	1.73	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1664	14696	27671	1.53	2.0E-70	AA180093.1	EST_HUMAN	zp45h05.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
1664	14696	27672	1.53	2.0E-70	AA180093.1	EST_HUMAN	zp45h05.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
1757	14786	27771	1.73	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2328	15339		5.47	2.0E-70	AA054010.1	EST_HUMAN	zf48g04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:191599 5'
3641	16694	29600	1.06	2.0E-70	H37988.1	EST_HUMAN	yp58b04.r1 Soares gene mapping to chromosome X
3833	18873	29774	0.86	2.0E-70	AL133207.2	NT	Novel human gene mapping to chromosome X
4079	17114	30010	5.63	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
4221	17250	30135	0.86	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4221	17250	30136	0.86	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
5593	18689	31658	9.14	2.0E-70	X72862.1	NT	H. sapiens gene for schwannomin (CS8)
5593	18689	31659	9.14	2.0E-70	X72862.1	NT	H. sapiens gene for schwannomin (CS8)
6328	19398	32640	1.1	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6780	19844	33128	3.84	2.0E-70	D12625.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
9824	19878	33167	11.3	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6824	19878	33168	11.3	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7190	18421	31223	1.44	2.0E-70	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA
7633	20593	33956	0.58	2.0E-70	AF288207.1	NT	Homo sapiens cysteinyl-tRNA synthetase mRNA, complete cds, alternatively spliced
8251	21220	34629	5.38	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
8564	21532	34952	0.45	2.0E-70	11423599	NT	Homo sapiens amylo-1,8-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA
9007	21973		0.76	2.0E-70	H47659.1	EST_HUMAN	yp79g02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193682 5'
9524	22487	35935	0.95	2.0E-70	11526355	NT	Homo sapiens dynein p62 subunit (LOC51184), mRNA
10497	23419	36918	1.42	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10963	23883	37396	0.49	2.0E-70	AB033042.1	NT	Homo sapiens mRNA for KIAA1216 protein, partial cds
11408	24352	37884	3.11	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11408	24352	37885	3.11	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11956	24835	38431	11.5	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
12637	25321	31786	2.84	2.0E-70	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12637	25321	31787	2.84	2.0E-70	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3404	18463		3.08	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9635	22579		0.78	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:418024 5'
10158	23083		0.84	1.0E-70	AA442292.1	EST_HUMAN	zv54c03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
11281	24231	37757	8.6	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLBGB10 5'
6054	19135	32344	7.1	8.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6054	19135	32345	7.1	8.0E-71	AI143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE.; O14045 PHOSPHOTRANSFERASE.;
7231	20253	33587	1.98	8.0E-71	A1654903.1	EST_HUMAN	wb52c05.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;
11852	20253	33587	3.67	9.0E-71	A1654903.1	EST_HUMAN	wb52c05.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;
9425	22389		3.62	8.0E-71	AA171451.1	EST_HUMAN	zp21d11.r1 Stragene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL.;
10967	23887	37398	0.45	8.0E-71	AW273920.1	EST_HUMAN	xv24d01.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR:O54730
7601	20562	33923	8.17	7.0E-71	AA442230.1	EST_HUMAN	O54730 TRANSPLANTABILITY ASSOCIATED PROTEIN 1; zv60h06.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:758076 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9026	21992	35412	1.61	7.0E-71	AA705457.1	EST_HUMAN	z91a06.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
11659	24594	38168	1.76	7.0E-71	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2220	15234	28258	8.79	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4145	17177	30066	1.1	5.0E-71	AW818405.1	EST_HUMAN	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
5981	19066	32264	2.02	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6819	19873	33162	1.15	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
7105	20039	33341	0.72	5.0E-71	7692209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7167	18398	31243	0.84	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7167	18398	31244	0.84	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7353	20323	33671	0.69	5.0E-71	11431580	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7753	20708	34075	1.62	5.0E-71	M38106.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7974	20913	34304	0.84	5.0E-71	11526445	NT	Homo sapiens MAGUK protein p55T, Protein Associated with Lns 2 (LOC51678), mRNA
8007	20945	34340	22.85	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8868	21835	35256	0.61	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8868	21835	35257	0.61	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
10271	23196		2.45	5.0E-71	X13467.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
11325	24275	37603					Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11525	24466	38020	2.01	5.0E-71	11438089	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC63325), mRNA
12198	26043	38624	1.81	5.0E-71	11417892	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
104	13220	26145	1.04	4.0E-71	4507692	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
350	13439	26363	56.4	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
350	13439	26364	56.4	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2897	15956	28873	1.9	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4459	17485	30372	4.75	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5022	18036	30821	6.04	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
6368	21337		1.34	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone PLACE1002775 5'
11051	24014	37538	2.84	3.0E-71	AA557683.1	EST_HUMAN	nl45h10.61 NC1 CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element;
1234	14271	27231	5.56	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
5393	18496	31374	8.35	2.0E-71	D87482.1	NT	Homo sapiens mRNA for KIAA0272 gene, partial cds
5393	18496	31375	8.35	2.0E-71	D87482.1	NT	Human mRNA for KIAA0272 gene, partial cds
7160	18392	31236	0.57	2.0E-71	AL042439.1	EST_HUMAN	DKFZp434D1721_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1721 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9359	22324	35752	0.5	2.0E-71	BF195585.1	EST_HUMAN	7n85c11.x1 NCL CGAP_OV18 Homo sapiens cDNA clone IMAGE:3571221 3' similar to TR:Q9Z165
10950	23870	37382	4.19	2.0E-71	AF095703.1	NT	Q9Z165 PUTATIVE FOUR REPEAT ION CHANNEL ; Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10950	23870	37383	4.19	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
11053	24018	37539	3.41	2.0E-71	BE018477.1	EST_HUMAN	bb81a08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN
11907	24788	38377	2.27	2.0E-71	R56626.1	EST_HUMAN	P54727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B ;
12315	25121		7.13	2.0E-71	T95489.1	EST_HUMAN	y77c11.1 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:164772 5' ye43a09.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120520 5'
639	13705	26928	1.69	1.0E-71	A1077927.1	EST_HUMAN	oy15e03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element ;
940	13993	26945	1.58	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1102	14146	27096	6.21	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1343	14378	27347	9.86	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2084	15111	28131	1.29	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2084	15111	28132	1.29	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2703	15699	28714	4.81	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3610	16655	29572	5.11	1.0E-71	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3610	16655	29573	5.11	1.0E-71	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3662	16705	28619	1.18	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3662	16705	28620	1.18	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3764	16798	29707	1.56	1.0E-71	AF218804.1	NT	Homo sapiens atracitin precursor (ATRIN) gene, exon 19
4497	17522	30409	2.16	1.0E-71	D28478.1	NT	Homo sapiens atracitin precursor (ATRIN) gene, exon 19
4622	17643	30531	0.88	1.0E-71	H23176.1	EST_HUMAN	Human mRNA for KIAA0045 gene, complete cds ym66h10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52528 5'
6906	19968	33256	1.38	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog-like 2 (GCN5L2), mRNA
7292	20264	33598	1.26	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7633	20496	33857	12.67	1.0E-71	U60793.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8486	21454	34871	0.76	1.0E-71	AF105287.1	NT	Homo sapiens glycican-6 (GPC6) mRNA, complete cds
8509	21477	34890	2.14	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8789	21766	35177	4.49	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8780	21756	35178	4.49	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
9584	22546	36097	0.83	1.0E-71	S72393.1	NT	CSNK2A1=casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
10387	23280	36767	9.49	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
10428	23350		3.08	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10804	23824	37336	1.52	1.0E-71	11433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
11137	24097		2.43	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
11228	24181	37706	2.12	1.0E-71	11418803	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11481	24424	37973	2.27	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11481	24424	37974	2.27	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12681	25349		3.13	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
407	13480	26414	1.23	9.0E-72	A1857635.1	EST_HUMAN	wk95g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
407	13480	26415	1.23	9.0E-72	A1857635.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
6232	19308	32538	0.89	8.0E-72	BF03752.1	EST_HUMAN	wk95g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:3862451 5'
11444	24387	37927	2.55	8.0E-72	11424480	NT	601458747F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862451 5'
11444	24387	37928	2.55	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
11444	24387	37929	2.55	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
4139	17170	30056	1.24	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4139	17170	30057	1.24	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4139	17170	30058	1.24	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7331	20302	33846	2.87	7.0E-72	S41694.1	NT	(pseudogene) PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
12800	25428		1.52	7.0E-72	F26259.1	EST_HUMAN	HSPD13670 HK3 Homo sapiens cDNA clone s4000051G02
8727	21695		4.9	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
65	13184	26102	4.86	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
65	13184	26103	4.86	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	13184	26102	13.05	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	13184	26103	13.05	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1141	14184		2.76	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7138	20114	33427	1.65	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003761 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8163	21101	34500	0.55	5.0E-72	AA316632.1	EST_HUMAN	EST188312 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to FAC1
9129	22085	35523	4.14	6.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ;contains element MSR1 repetitive element ;
10320	23244	36724	0.56	5.0E-72	AV724632.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAKB01 5'
11573	24511	38067	2.74	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11573	24511	38068	2.74	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
12389	25929		2.52	6.0E-72	BE926645.1	EST_HUMAN	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
4860	17877		1.12	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dj1057B20.2 (DJ1057B20.2), mRNA
5540	18637	31577	0.75	4.0E-72	AF170025.1	NT	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
6709	19765	33045	0.83	4.0E-72	T87947.1	EST_HUMAN	y493a01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
7639	20669	33963	1.28	4.0E-72	5729867	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
10143	23069	36545	1.24	4.0E-72	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10758	23679	37174	0.49	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
10758	23679	37175	0.49	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
							qh67-c02.x1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to TR:Q14498 Q14498 SPLICING FACTOR. [1] ;contains Alu repetitive element;contains element L1 repetitive element ;
10786	23707	37208	1.24	4.0E-72	A1249796.1	EST_HUMAN	aa2309.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11616	24554	38115	1.54	4.0E-72	AA465388.1	EST_HUMAN	aa2309.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11616	24554	38116	1.54	4.0E-72	AA465388.1	EST_HUMAN	aa2309.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11857	24739	38324	5.09	4.0E-72	H79421.1	EST_HUMAN	y428403.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
11988	24865	38461	1.72	4.0E-72	T81910.1	EST_HUMAN	y429409.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
12729	25392	31748	4.28	4.0E-72	AJ27546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
21	13141	26039	1.99	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
904	13959		1.23	3.0E-72	AA723823.1	EST_HUMAN	ah63a06.s1 Soares testis NHT Homo sapiens cDNA clone 1310290 3'
1159	14201	27152	5.57	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1159	14201	27153	5.57	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1198	14238	27193	0.71	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1198	14238	27194	0.71	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1523	14555	27528	1.45	3.0E-72	BE242161.1	EST_HUMAN	TCAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1252
3090	16148	29052	13.29	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3292	16345	29265	2.41	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3836	16876	29778	2.52	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4576	17598	30492	3.77	3.0E-72	11416196	NT	[human, precursor B-cell line REH, mRNA, partial, 211 nt]
4800	17817	30710	1.31	3.0E-72	AF167572.1	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4800	17817	30711	1.31	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
5149	18158	31037	1.02	3.0E-72	AW969677.1	EST_HUMAN	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
5598	18694		1.06	3.0E-72	4759093	NT	EST371747 MAGE resequences, MAGF Homo sapiens cDNA
6092	19171	32386	1.91	3.0E-72	AF073367.1	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6092	19171	32387	1.91	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6290	19362	32600	4.78	3.0E-72	AB028004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6290	19362	32601	4.78	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6767	19821	33103	3.89	3.0E-72	4826887	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
7838	20785	34160	1.87	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
8516	21484	34898	1.07	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
10797	23718	37220	7.09	3.0E-72	X98289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
11912	24793	38383	3.23	3.0E-72	11424091	NT	Homo sapiens CD37 antigen (CD37), mRNA
11912	24793	38384	3.23	3.0E-72	11424091	NT	Homo sapiens CD37 antigen (CD37), mRNA
12078	24950	38646	3.56	3.0E-72	AF190864.1	NT	Homo sapiens ADP-ribosylation factor binding protein GGA3 (GGA3) mRNA, complete cds
6069	19150	32362	1.53	2.0E-72	11426671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
9451	22415	35852	0.62	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9451	22415	35853	0.62	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
11092	24052	37575	2.4	2.0E-72	AA789277.1	EST_HUMAN	aj28609.s1 Soares testis_NHT Homo sapiens cDNA clone 1391608 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
12726	25379	31745	6.47	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
5961	18950	32136	3.76	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6711	19767	33046	1.24	1.0E-72	11321678	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6711	19767	33047	1.24	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6788	26688	33126	1.3	1.0E-72	AV751818.1	EST_HUMAN	AV751818 NP2 Homo sapiens cDNA clone NPDAIE11 5'
7889	20842	34224	3.72	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7899	20842	34225	3.72	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9949	22876	36338	7.79	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
9949	22876	36339	7.79	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1455	14488	27463	1.53	9.0E-73	AW374968.1	EST_HUMAN	MRQ-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
6156	19231	32462	0.94	9.0E-73	11525983	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
11297	24247		18.46	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1039	14084	27035	0.93	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCJ CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q59050
5660	18756	31924	0.79	8.0E-73	4505798	NT	Q59050 HYPOTHETICAL PROTEIN MJ1656.
6724	19780	33059	5.01	8.0E-73	11428469	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
8432	21401	34814	2.3	8.0E-73	AF113129.1	NT	Homo sapiens lysozyme homolog (LOC57151), mRNA
						NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9708	22661	36117	7.24	8.0E-73	BE019900.1	EST_HUMAN	bb62a08.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
10097	23023	38497	2.34	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10097	23023	38498	2.34	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
12010	24887	38483	3.54	8.0E-73	AF084520.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 mRNA, complete cds
12785	26418	31735	3.45	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
1136	14176	27130	1.3	7.0E-73	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3312	16365	29285	1	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4981	17996		1.74	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
159	13262		2.28	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7378	20348	33689	3.58	6.0E-73	BE166574.1	EST_HUMAN	QVQ-HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5326	18432	31184	2.11	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM441), mRNA
1344	14379	27348	1.16	3.0E-73	AW843789.1	EST_HUMAN	CMO-CH0044-260100-164-08 CN0044 Homo sapiens cDNA
1879	14804	27804	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1878	14804	27905	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
6856	19009	33204	0.86	3.0E-73	AA136403.1	EST_HUMAN	zn95604.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:565950 3' similar to gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
9111	22077	35503	0.54	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071 5'

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9111	22077	35504	0.54	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071 5'
11047	24011		1.65	3.0E-73	X99660.1	NT	H. sapiens SH3GLP2 pseudogene, 5' end
13017	25567		1.35	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13021	25569		1.97	3.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
852	13908	26868	1.9	2.0E-73	AF138897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1963	14985		2.95	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2306	15318		1.58	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3196	16251	29170	3.89	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3561	16607	28527	0.77	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3561	16607	28528	0.77	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
6577	19637	32902	0.7	2.0E-73	AF088824.1	NT	Mus musculus rho/rao-interacting citron kinase (Crik) mRNA, complete cds
6577	19637	32903	0.7	2.0E-73	AF088824.1	NT	Mus musculus rho/rao-interacting citron kinase (Crik) mRNA, complete cds
6627	19685	32964	6.38	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6858	19911	33208	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6858	19911	33207	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
8092	21028	34427	0.59	2.0E-73	M94048.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
8099	21035	34435	0.77	2.0E-73	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
9890	22843	36299	0.55	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9890	22843	36300	0.55	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10788	23709	37211	1.12	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10863	23783	37284	1.69	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10863	23783	37285	1.69	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
11107	24067	37589	1.49	2.0E-73	11431598	NT	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-adenylin ear containing, ARF-binding protein 2 (KIAA1080), mRNA
11395	24341	37872	2.64	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11395	24341	37873	2.64	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11420	24364	37899	1.81	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12581	14985		1.81	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1798	14827	27814	2.81	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
6495	19559	32810	1.2	1.0E-73	BE151283.1	EST_HUMAN	CM1-HT0282-11169-042-h10 HT0282 Homo sapiens cDNA
9857	22793	36244	1.47	1.0E-73	AI147427.1	EST_HUMAN	qg61b07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element MER22 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value:	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11778	23934	37455	2.1	1.0E-73	BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
742	13803	26742	1.47	8.0E-74	4557426	NT	Homo sapiens GD39-like 4 (CD39L4) mRNA
6021	18104	32308	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
6021	19104	32307	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
1668	14987	27889	4.43	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3339	16990	29311	2.01	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9598	22602	36051	2.25	7.0E-74	BE967432.1	EST_HUMAN	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5'
12784	25417	31734	4.84	7.0E-74	BE266305.1	EST_HUMAN	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'
1124	14168	27120	5.19	6.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
1631	14664	27639	1.03	6.0E-74	AW263177.1	EST_HUMAN	xt78y07.x1 Soares NFL_T_G9C_S1 Homo sapiens cDNA clone IMAGE:2700686 3'
2324	15335	28357	7.92	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805453 5'
2324	15335	28358	7.92	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805453 5'
2875	15934	28852	1.12	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709366 3'
2875	15934	28853	1.12	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709366 3'
3728	16768	28679	1.28	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3728	16768	29680	1.28	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5065	18075	30955	4.18	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5065	18075	30956	4.18	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5439	18541	31451	3.08	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
906	13981	26917	2.09	5.0E-74	AW020989.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2713	15707	31492	3.68	5.0E-74	AW362756.1	EST_HUMAN	PMO-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5481	18581	31492	1.76	5.0E-74	11426417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5887	18976	32168	12.05	5.0E-74	X89870.1	NT	H.sapiens mRNA for TPOR18 protein
5938	19024	32218	7.23	5.0E-74	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6013	19086	32296	2.71	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6013	19086	32297	2.71	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7080	20101	33412	2.18	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7932	20101	33412	0.54	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8371	21340	34751	3.05	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
11087	24048	37670	4.06	6.0E-74	Y09420.1	NT	H.sapiens mRNA for HIP-1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11087	24048	37571	4.06	5.0E-74	Y09420.1	NT	H.sapiens mRNA for HIP-1
279	13374	28303	1.85	4.0E-74	D87675.1	NT	Homo sapiens DNA for anyfold precursor protein, complete cds
853	13909	26867	5.8	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1979	15000	28002	2.21	4.0E-74	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1979	15000	28003	2.21	4.0E-74	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2086	15103	28120	2.38	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2086	15103	28121	2.38	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2142	15159	28175	1.51	4.0E-74	AB032394.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2434	15441	28459	0.91	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3107	16184	28076	5.45	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
4091	17123	30018	1.23	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4587	17609	30504	2.06	4.0E-74	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4646	17667	30554	0.99	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5055	18067	30849	0.74	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
8895	21861		21.61	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
9727	22755	36209	2.57	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #938205) Homo sapiens cDNA clone HHCPF91
10703	23625	37122	2.69	3.0E-74	AA601493.1	EST_HUMAN	nc17g05.61 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
959	14012	28665	58.94	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
959	14012	28666	58.94	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1179	14220	27176	0.9	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-147D
1249	14285	27251	1.32	2.0E-74	AI950528.1	EST_HUMAN	wx51907.x1 NC1_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
1599	14631	27606	3.54	2.0E-74	4885198	NT	Q08379 GOLGIN-95; contains element MER22 repetitive element;
1599	14631	27607	3.54	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2609	15608	28632	3.02	2.0E-74	AI657280.1	EST_HUMAN	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
5042	18055	30933	3.67	2.0E-74	AL355092.1	NT	PT2.1_16_G11.7 tumor2 Homo sapiens cDNA 3'
5042	18055	30934	3.67	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5046	18059	30938	0.93	2.0E-74	J02963.1	NT	Novel human gene mapping to chromosome 22
5896	25647	32174	2.03	2.0E-74	BE711134.1	EST_HUMAN	Human platelet glycoprotein IIb mRNA, 3' end
							RC8-H10678-220500-011-C03 HT0678 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5999	25650	32280	1.93	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/INY-CO-38), mRNA
5999	25650	32281	1.93	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/INY-CO-38), mRNA
6077	25650	32280	2.58	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/INY-CO-38), mRNA
6077	25650	32281	2.58	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/INY-CO-38), mRNA
7310	20281	33621	1.14	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
8272	21241	34652	1.35	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
9737	22765	36220	8.08	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12058	24631	38528	1.72	2.0E-74	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
12621	25252		3.11	2.0E-74	AA196181.1	EST_HUMAN	z996a06.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
55	13175	26096	2.22	1.0E-74	7657334	NT	Homo sapiens Mitochondrial-related kinase (MINK), mRNA
337	13428	26348	3.95	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
500	13572	26494	1.1	1.0E-74	8622829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
507	13578	26499	8.18	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
603	13670	26584	2.15	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1001	14052	27004	2.21	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2235	15249	28273	3.58	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3156	16212	29127	2.83	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3943	16993	29898	0.78	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3943	16993	29898	0.78	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3992	17032	29941	5.75	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4092	17126	30019	0.96	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-103 BT0642 Homo sapiens cDNA
4296	17325	30205	0.71	1.0E-74	BE467769.1	EST_HUMAN	hcz73h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12
5217	18228	31100	1.36	1.0E-74	D83327.1	NT	CE17351 ;
6863	19916	33210	0.97	1.0E-74	M89914.1	NT	Homo sapiens DORR1 mRNA, partial cds
7898	20832	34211	1.17	1.0E-74	11417977	NT	Homo sapiens neurofibromin (NF1) gene, complete cds
8391	21390	34767	1.1	1.0E-74	BE549105.1	EST_HUMAN	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8391	21390	34768	1.1	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9157	22123	35552	3.96	1.0E-74	AF214562.1	NT	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9186	22152	35581	0.71	1.0E-74	BF351951.1	EST_HUMAN	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
10600	23522	37015	0.55	1.0E-74	AJ251660.1	NT	MRO-HT0559-230500-021-a03 HT0559 Homo sapiens cDNA
10600	23522	37016	0.55	1.0E-74	AJ251660.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10847	23767	37266	1.51	1.0E-74	11420549	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
12100	24971	38568	1.5	1.0E-74	AB007841.1	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
							Homo sapiens mRNA for KIAA0472 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12154	25012	38616	3.9	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12235	25067		7.14	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12848	25458		1.52	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2852	15849		6.34	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12543	25266		1.81	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2329	15340	28382	1.16	8.0E-75	AI817415.1	EST_HUMAN	wk38a08.x1 NCJ_CGAP_P22 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4
5201	18210	31084	0.91	5.0E-75	BE841305.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
8075	21012	34411	0.51	5.0E-75	AA573446.1	EST_HUMAN	MRO-SN0040-080600-008-g08 SN0040 Homo sapiens cDNA
8075	21012	34411	0.51	5.0E-75	AA573446.1	EST_HUMAN	nk99d03.s1 NCJ_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:1028933 3'
9259	22225	35654	1.13	5.0E-75	BE272325.1	EST_HUMAN	nk99d03.s1 NCJ_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:1028933 3'
9472	22436	35874	0.84	5.0E-75	AA132611.1	EST_HUMAN	601126068F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989885 5'
9549	22512	35961	0.89	5.0E-75	BE661855.1	EST_HUMAN	2017e08.r1 Stratagene clone (#37204) Homo sapiens cDNA clone IMAGE:587174 5'
9549	22512	35962	0.89	5.0E-75	BE661855.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687488 5'
9728	22756	38209	1.42	5.0E-75	BF690254.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
10594	23516	37007	2.9	5.0E-75	AI638623.1	EST_HUMAN	tt31c12.x1 NCJ_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361
112	13223	25147	1.68	4.0E-75	BE081333.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN ;
459	13532		2.68	4.0E-75	N36757.1	EST_HUMAN	QV1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
1780	14809	27706	1.73	4.0E-75	AW897230.1	EST_HUMAN	y99h08.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:269055 5'
2861	15921	28841	4.5	4.0E-75	BE408464.1	EST_HUMAN	GMO-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
3512	16558	29482	0.93	4.0E-75	BE408464.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
5607	18703	31859	0.65	4.0E-75	11417946	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
5607	18703	31860	0.55	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6400	19468	32715	6.35	4.0E-75	5579457	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6923	19873	33270	1.61	4.0E-75	11417946	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (EIF3S8), mRNA
6923	19873	33271	1.61	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
11044	24008	37534	15.05	4.0E-75	7669505	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
1004	14055	27007	4.38	3.0E-76	AF157623.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1005	14055	27007	3.22	3.0E-76	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1853	14879	27875	2.36	3.0E-75	AB011153.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2430	15437	28454	5.12	3.0E-76	4759153	NT	Homo sapiens mRNA for KIA0581 protein, partial cds
3034	16092	28010	1.08	3.0E-76	AL163201.2	NT	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
							Homo sapiens chromosome 21 segment HS21C001

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3203	16258	29177	1.13	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3381	16411	28334	0.95	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3361	16411	28335	0.95	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3752	16794	29705	0.78	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4197	17228	30118	1.03	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4469	17492	30379	0.71	3.0E-75	7662421	NT	Homo sapiens KIAA0671 protein (KIAA0671), mRNA
5323	18429	31179	1.15	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
5323	18429	31180	1.15	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6657	18714	32891	0.51	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6657	18714	32892	0.51	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6935	20159	33479	1.76	3.0E-76	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6935	20159	33480	1.76	3.0E-75	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7342	20313	33658	4.47	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7342	20313	33657	4.47	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7884	20828	34204	2.82	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7884	20828	34205	2.82	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
9336	22301	35730	1.21	3.0E-75	11420804	NT	Homo sapiens snail 1 (Drosophila homolog), zinc finger protein (SNAI1), mRNA
10037	22964	36431	0.95	3.0E-75	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
10908	23828	37341	4.16	3.0E-75	11436430	NT	Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), mRNA
12085	24957	38552	1.73	3.0E-75	6715588	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12085	24957	38553	1.73	3.0E-75	6715588	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
5755	18850		1.41	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386
9103	22069	35495	2.56	2.0E-76	A1311783.1	EST_HUMAN	POL/ENV GENE ; gc91e02.x1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7 t1
2311	15323	28346	7.79	1.0E-76	AW168135.1	EST_HUMAN	PTX7 repetitive element ; H.sapiens ERCC2 gene, exons 1 & 2 (partial)
2857	18015	28943	3.35	1.0E-75	X52221.1	NT	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
4718	17738	30630	0.85	1.0E-75	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504272 5'
5224	18232	31107	0.7	1.0E-75	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3922303 5'
7843	20780	34165	0.76	1.0E-75	BE082528.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
7843	20780	34166	0.76	1.0E-75	BE082528.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8757	21724		12.42	1.0E-75	AA399270.1	EST_HUMAN	z57h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:M13932 40S
8783	22724	36179	4.03	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
8783	22724	36180	4.03	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
11229	24182		3.79	1.0E-75	AA664377.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
11428	24372	37810	2.13	1.0E-75	AF223391.1	NT	ac77b08.s1 Siralagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
12438	18232	31107	1.72	1.0E-75	BE894192.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
46	13168	26070	2.23	9.0E-76	AI652648.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
46	13166	26071	2.23	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
2425	15432		0.96	9.0E-76	AA702415.1	EST_HUMAN	TRAP1 ;
10261	23186	36670	37.43	9.0E-76	M12937.1	NT	wb30b10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
937	13660	26941	0.98	8.0E-76	4504374	NT	TRAP1 ;
937	13690	26942	0.98	8.0E-76	4504374	NT	z65b07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'
2921	15979	28904	1.28	8.0E-76	7706724	NT	Human ferritin Heavy subunit mRNA, complete cds
6295	19367	32608	4.79	8.0E-76	11421442	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
7731	20686	34049	1.41	8.0E-76	11435215	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
7816	20765	34141	0.97	8.0E-76	11419212	NT	Homo sapiens modulator (Sur2), mRNA
8639	21607	35030	0.64	8.0E-76	11416961	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
8453	22417	35855	0.45	8.0E-76	AB046784.1	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
10744	23666	37161	1.41	8.0E-76	M13792.1	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
11028	23991	37518	4.09	8.0E-76	10442821	NT	Homo sapiens ALM-1 protein (LOC51151), mRNA
12767	25408		2.29	8.0E-76	11417862	NT	Homo sapiens mRNA for KIAA1544 protein, partial cds
777	13636	26782	1.41	7.0E-76	5016092	NT	Human adenosine deaminase (ADA) gene, complete cds
3305	16358	29277	25.65	7.0E-76	AF056490.1	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
3311	16364	29284	8.23	7.0E-76	4505052	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
4399	17427	30311	4.52	7.0E-76	4507184	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DL2) mRNA
4399	17427	30312	4.52	7.0E-76	4507184	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
1238	14274		12.96	6.0E-76	BE396253.1	EST_HUMAN	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
11793	23948	37469	2.36	6.0E-76	BE273201.1	EST_HUMAN	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
							Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
							601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
							601142233F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1960	14982	27983	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1960	14982	27984	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1960	14982	27985	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3220	16275	29199	1.01	4.0E-76	BE814098.1	EST_HUMAN	QV3-BN0047-270700-283-g06 BN0047 Homo sapiens cDNA
5342	18447	31200	1.08	4.0E-76	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
10384	23306	38783	6.89	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178G01 5'
10384	23308	38784	6.89	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178G01 5'
630	13695	26614	1.94	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
630	13695	26615	1.94	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1603	14635	27811	9.36	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1603	14635	27812	9.36	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3442	16489	29407	5.03	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3442	16489	29408	5.03	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
4105	17139	30034	14.72	3.0E-76	BE346693.1	EST_HUMAN	h67f12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151823 3' similar to TR:O94886 O94886 KIAA0792 PROTEIN. ;
5301	18304	31165	0.88	3.0E-76	AV702981.1	EST_HUMAN	AV702981 ADB Homo sapiens cDNA clone ADBBSC02 5'
5309	18327	38612	2.12	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized Infant brain cDNA Homo sapiens cDNA clone c-zq404 3'
5822	18912	32095	1	3.0E-76	AA160611.1	EST_HUMAN	z073c07.r1 Stratagene pancreas (#337208) Homo sapiens cDNA clone IMAGE:592524 5' similar to gb:L32976 MIXED LINEAGE KINASE 1 (HUMAN);
6102	19181	32400	0.71	3.0E-76	AW027705.1	EST_HUMAN	w75605.x1 Soares_thymus_NHFT1 Homo sapiens cDNA clone IMAGE:2635368 3'
6504	19568	32820	8.03	3.0E-76	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
8480	21458	34876	0.83	3.0E-76	N42671.1	EST_HUMAN	y20g10.r1 Soares_melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:271842 5'
10074	23001	36471	3.32	3.0E-76	AW299353.1	EST_HUMAN	xs49h01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
10098	23024	36499	1.08	3.0E-76	AA442309.1	EST_HUMAN	z654d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
10098	23024	36500	1.08	3.0E-76	AA442309.1	EST_HUMAN	z654d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
12143	25760	31619	2.43	3.0E-76	AW967984.1	EST_HUMAN	EST380059 MAGe resequences, MAGJ Homo sapiens cDNA
12248	25971	31301	4.4	3.0E-76	AW966455.1	EST_HUMAN	EST386526 MAGe resequences, MAGD Homo sapiens cDNA
281	13376	26305	1.46	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
342	13431	26352	2.6	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
342	13431	26353	2.6	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
461	13534		1.14	2.0E-76	4557962	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
592	13659	26573	1.12	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1032	14078	27031	1.37	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1537	14570	27542	1.74	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1537	14570	27543	1.74	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1945	14969	27987	1.03	2.0E-76	AA253954.1	EST_HUMAN	z660h11.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2854	15914	28837	3.73	2.0E-76	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3308	16361	29281	1.87	2.0E-76	AA445992.1	EST_HUMAN	z64602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
3308	16361	29282	1.87	2.0E-76	AA445992.1	EST_HUMAN	z64602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
4551	17584	30476	1.01	2.0E-76	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4984	17999	30898	7.6	2.0E-76	AW879618.1	EST_HUMAN	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5382	18496		0.97	2.0E-76	AF127845.1	NT	Grilla grillis olfactory receptor (GGO18) gene, partial cds
5700	18795	31869	5.35	2.0E-76	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7643	20603	33968	0.55	2.0E-76	11421328	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7668	20627	33991	0.76	2.0E-76	11426808	NT	Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA
7924	20867	34255	1.66	2.0E-76	11427410	NT	Homo sapiens TPOR88 protein (HSTPCR88P), mRNA
10645	23567	37084	7.03	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63150), mRNA
11266	24218	37742	2.64	2.0E-76	7649807	NT	Homo sapiens HIRA interacting protein 4 (dnaj-like) (HIRIP4), mRNA
4326	17355	30241	3.37	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4328	17355	30242	3.37	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5523	18622	31557	6.74	1.0E-76	BE796537.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6372	19440		0.64	1.0E-76	AA333207.1	EST_HUMAN	EST37301 Embryo, 8 week 1 Homo sapiens cDNA 5' end
7109	20043	33345	4.09	9.0E-77	BE889525.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
12923	25499		1.36	9.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3836753 5'
189	13289	28215	1.35	8.0E-77	R83144.1	EST_HUMAN	yp11h02.r1 Soares breast 3NbrHst Homo sapiens cDNA clone IMAGE:187165 5' similar to SP-ANKB_HUMAN_Q01484 ANKYRIN, BRAIN VARIANT 1 ;
4550	17573	30463	1.26	8.0E-77	BF205181.1	EST_HUMAN	601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
5528	18627	31663	1.83	8.0E-77	4506230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Moc34 homolog) (PSMD7) mRNA
11716	24679	38257	1.92	8.0E-77	AA019770.1	EST_HUMAN	z662602.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11716	24679	38258	1.82	8.0E-77	AA019770.1	EST_HUMAN	z662602.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
12800	25484	31732	4.66	8.0E-77	R00245.1	EST_HUMAN	ye6904.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element ;
1946	14970	27968	2.43	7.0E-77	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2421	15428	28451	1.88	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2421	15428	28452	1.88	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
262	13358	26283	4.64	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1144	14187	27138	20.18	6.0E-77	AW957753.1	EST_HUMAN	EST1398823 IMAGE resequences, IMAGE Homo sapiens cDNA
1545	14578	27551	3.97	6.0E-77	AI204066.1	EST_HUMAN	qe77h12x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1240	14278	27236	2.34	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1362	14398	27387	1.41	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2695	15691	28709	1.03	5.0E-77	AF162866.1	NT	Homo sapiens toubied-like kinase 1 (TLK1) mRNA, complete cds
2774	15768	28786	0.96	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3534	16580	29504	0.64	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
4732	17752	30644	0.92	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4732	17752	30645	0.92	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4975	17990	30845	3.64	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
6951	20175	33499	0.84	5.0E-77	M19875.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7348	20511	33859	0.52	5.0E-77	X88296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
7849	20511	33859	0.67	5.0E-77	X88296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8711	21679	35104	1.22	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8711	21679	35105	1.22	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9928	22811	36284	3	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9928	22811	36285	3	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10857	23777	37276	0.82	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10857	23777	37277	0.82	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
1989	15010	28015	1.26	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1989	15010	28016	1.26	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10852	23574	37069	0.71	3.0E-77	H65167.1	EST_HUMAN	yu64g01.r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238508 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -
10852	23574	37070	0.71	3.0E-77	H65167.1	EST_HUMAN	yu64g01.r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238508 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -
10858	23888	37399	0.66	3.0E-77	AI017333.1	EST_HUMAN	ov31h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
10968	23888	37400	0.66	3.0E-77	AI017333.1	EST_HUMAN	ov31h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
11222	24175	37701	3.68	3.0E-77	BF359917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 M10078 Homo sapiens cDNA
1354	14389	27358	1.66	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1428	14462	27439	2.31	2.0E-77	AW99712.1	EST_HUMAN	RC3-BN0053-170200-011-101 BN0053 Homo sapiens cDNA
2102	15119	28140	1.01	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2113	15130	28150	2.46	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2600	15898	28620	2.28	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2600	15898	28621	2.28	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4064	17100	29892	1.25	2.0E-77	BE044316.1	EST_HUMAN	h043b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4442	17468	30357	0.68	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4442	17468	30358	0.68	2.0E-77	AI613519.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
							O65245 F21E10.7 PROTEIN ;
4802	17819	30713	2.32	2.0E-77	AA653025.1	EST_HUMAN	ns68g12.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1]; contains element MSR1 repetitive element ;
5158	17468	30357	0.65	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
5158	17468	30358	0.65	2.0E-77	AI613519.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
5065	19146	32358	2.06	2.0E-77	BE298940.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
6296	19368	32607	1.62	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
7380	20350	33701	14.21	2.0E-77	AI833003.1	EST_HUMAN	ai74a09.x1 Barslead colon HPLR87 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151. [1];
8874	21841	35264	0.75	2.0E-77	AI362707.1	EST_HUMAN	qy70c09.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F29D11.1 CE05765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN ;
9886	22839	36295	5.84	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
9886	22839	36296	5.84	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10354	23278	36753	0.5	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
10354	23278	36754	0.5	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
45	13165	26068	0.94	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
45	13165	26069	0.94	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
272	13368	26284	1.33	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
272	13368	26285	1.33	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	15853	26891	2.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	15853	26892	2.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2450	15455	28477	1.73	1.0E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3058	16115	28028	2.01	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4380	17408	30289	3.92	1.0E-77	7708299	NT	Homo sapiens CGI-80 protein (LOC51626), mRNA
4525	17550	30438	0.73	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
4552	17575	30465	16.98	1.0E-77	AJ229041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4680	17701	30589	2.11	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4721	17741	30632	0.72	1.0E-77	A1273014.1	EST_HUMAN	q09g04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110.3
5000	17550	30438	0.95	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
5219	17550	30438	0.68	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
5246	18254		1.12	1.0E-77	AL163247.2	NT	Homo sapiens chromosome 21 segment H521C047
6038	19120	32324	1.61	1.0E-77	AF086844.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6038	19120	32325	1.61	1.0E-77	AF086844.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6165	19240	32471	1.39	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6590	19650	32821	1.26	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7254	19889	33286	14.51	1.0E-77	5981412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7928	20871	34280	0.91	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
8040	20977	34373	0.69	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9620	22564	36013	0.65	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
9620	22564	36014	0.65	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10800	23810	37316	0.92	1.0E-77	AB028396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10890	23810	37317	0.92	1.0E-77	AB028396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10916	23836	37352	3	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280899-011-b05 CT0254 Homo sapiens cDNA
6589	19849	32819	2.93	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
6589	19849	32920	2.93	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
86	13202	26126	2.14	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
86	13202	26127	2.14	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3325	16378	29297	8.56	6.0E-78	BF344101.1	EST_HUMAN	602016926F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4152511 5'
6712	19768		2.34	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
219	13319	26244	1.79	5.0E-78	11422488	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2569	15570	28590	5.46	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B6A.6
3396	16445	29372	3.94	5.0E-78	M55586.1	NT	CE22121 ; Human collagenase type IV (CLG4) gene, exon 6
5486	18586	31497	2.45	5.0E-78	AF038536.1	NT	Human sapiens Best's macular dystrophy related protein mRNA, partial cds
5655	18761	31917	24.78	5.0E-78	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68KD (TGFB1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7361	20331	33681	2.22	5.0E-78	AW953120.1	EST_HUMAN	EST365180 MAGE resequences, MAGB Homo sapiens cDNA
9438	22402	35840	6.85	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
9439	22403	35841	3.51	5.0E-78	BE960836.1	EST_HUMAN	801848051F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3931887 5'
11614	24552	38112	1.64	5.0E-78	BE241639.1	EST_HUMAN	TCAAP1E0686 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0686
11614	24552	38113	1.64	5.0E-78	BE241639.1	EST_HUMAN	TCAAP1E0686 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0686
1139	14182	27133	1.88	4.0E-78	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
1521	14553	27524	2.74	4.0E-78	AL355941.1	NT	Novel human gene mapping to chromosome 22
1656	14688	27663	1.11	4.0E-78	A1985094.1	EST_HUMAN	wr97b12.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2465615 3' similar to SW:WAP_PIG O46655 WHEY ACIDIC PROTEIN PRECURSOR ;
2326	15337	28360	3.31	4.0E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4350	17377	30255	1.47	4.0E-78	7656876	NT	Homo sapiens synovial (LOC30816), mRNA
4807	17824	30719	2.16	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4807	17824	30720	2.16	4.0E-78	4505808	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5802	18951	32137	1.13	4.0E-78	11420732	NT	Homo sapiens SFRS3 protein kinase 2 (SRPK2), mRNA
6297	19369	32608	0.61	4.0E-78	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
6297	19369	32609	0.61	4.0E-78	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
6725	19781	33060	0.59	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7733	20698	34052	0.58	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9205	22171	35601	1.68	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9205	22171	35602	1.66	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9723	22761	36204	0.64	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10811	23732	37233	1.97	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10811	23732	37234	1.97	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11749	24634	38213	1.65	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
11893	24764	38350	5.69	4.0E-78	X05944.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12126	24995	38599	2.38	4.0E-78	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
12797	25426	31739	3.89	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
162	13265	28189	2.77	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
162	13265	28189	2.77	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
162	13265	28189	2.77	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
3776	16818		0.94	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
3829	16869	29771	0.88	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	16869	29771	0.79	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
10649	23571		5.79	3.0E-78	BE144758.1	EST_HUMAN	GM0-H10-041089-065-c07 HT0180 Homo sapiens cDNA
11326	24276	37804	1.8	3.0E-78	BE156318.1	EST_HUMAN	QVO-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
3138	16195		4.1	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4042	17080		1.43	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
7705	20692	34027	1.24	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BKO-aaj-g-10-Q-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7705	20662	34028	1.24	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BKO-aaj-g-10-Q-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
8003	20942	34335	3.2	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
8375	21344	34755	2.54	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBFWF09 5'
8795	21762	35183	1.51	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8795	21762	35184	1.51	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
11416	24360	37895	2.5	2.0E-78	AI97837.1	EST_HUMAN	q150H05.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1889961 3' similar to WP.R90.1
11458	24401	37949	2.03	2.0E-78	N66951.1	EST_HUMAN	CE06325 PROTEIN KINASE ;
5378	18482	31357	3.22	1.0E-78	11417304	EST_HUMAN	z948f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
7144	18376	31264	0.87	1.0E-78	AV648699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
8499	21467		2.95	1.0E-78	U52373.1	NT	AV648699 GLC Homo sapiens cDNA clone GLCBMC01 3'
12323	25125	31847	1.81	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
4727	17747	30638	3.81	9.0E-79	11625891	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4899	17916	30807	3.55	9.0E-79	BE000837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
5507	18607	31537	16.13	9.0E-79	AB028070.1	NT	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
6474	19539	32785	2.49	9.0E-79	5454145	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6772	19827	33109	0.87	9.0E-79	11430822	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
7573	25684		1.05	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
7825	20773	34150	0.84	9.0E-79	11421735	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7825	20773	34151	0.84	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L16.1), mRNA
7875	20819	34197	0.55	9.0E-79	D30688.1	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L16.1), mRNA
8689	21657	35079	0.5	9.0E-79	11417260	NT	Human T-cell mRNA for glycyl tRNA synthetase, complete cds
8689	21657	35080	0.5	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9418	22383	35821	5.53	9.0E-79	J02853.1	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9418	22383	35822	5.53	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9735	22763	36218	0.66	9.0E-79	D87875.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
10730	23652	37145	0.66	9.0E-79	11438843	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
							Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10784	23705	37204	1.53	9.0E-79	AF082346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10784	23705	37205	1.53	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11408	24350	37882	4.27	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11841	24724	38310	2.97	9.0E-79		NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
11841	24724	38311	2.97	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
12115	24985	38586	2.71	9.0E-79	7662451	NT	Homo sapiens KIAA1035 protein (KIAA1035), mRNA
13000	25556	31720	1.55	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3755	16787	29708	1.33	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6195	18204	31078	0.66	8.0E-79	8867387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
3268	18320	29242	7.24	7.0E-79	BE619848.1	EST_HUMAN	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
12170	25020		2.63	6.0E-79	AA869829.1	EST_HUMAN	z194604.s1 Soares fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:462558 3' similar to
11824	24707	38280	4.57	5.0E-79	AL163282.2	NT	TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
3161	18246		1.35	4.0E-79	8922325	NT	Homo sapiens chromosome 21 segment HS21C082
313	13405	26331	1.48	3.0E-79	AF114488.1	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
979	14030	26984	2.02	3.0E-79	AF232708.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3115	16172	29082	1.82	3.0E-79	U09410.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein [(Cin) gene, complete cds
8435	18537	31446	6.05	3.0E-79	AF110322.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5812	18902	32085	1.61	3.0E-79	AB020868.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5841	18931	32115	0.95	3.0E-79	BE789470.1	EST_HUMAN	Homo sapiens mRNA for KIAA0892 protein, partial cds
5841	18931	32116	0.95	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5863	18952	32138	4.05	3.0E-79	11426770	NT	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5863	18952	32139	4.05	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6909	19961	33257	0.8	3.0E-79	BE256893.1	EST_HUMAN	Homo sapiens netrin 1 (NTN1), mRNA
7282	19997	33294	3.31	3.0E-79	AB014520.1	NT	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7282	19997	33295	3.31	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8504	21472	34886	1.58	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
8758	22989	36156	0.57	3.0E-79	10835036	NT	Homo sapiens tetrapeptide repeat domain 3 (TTC3), mRNA
10712	23634		0.64	3.0E-79	AV698115.1	EST_HUMAN	Homo sapiens tetrapeptide repeat domain 3 (TTC3), mRNA
287	13382		2.05	2.0E-79	H63129.1	EST_HUMAN	AV698115 GKC Homo sapiens cDNA clone GKCAHE11 5'
635	13701	26822	1.29	2.0E-79	BE378926.1	EST_HUMAN	y48f03.s1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:208541 3'
928	13981	26935	1.35	2.0E-79	4757841	NT	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
985	14036	26980	4.78	2.0E-79	4885234	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
985	14036	26991	4.78	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
							Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1036	14082		1.02	2.0E-79	AI523747.1	EST_HUMAN	h18n07.x1 NC1 CGAP_P128 Homo sapiens cDNA clone IMAGE:2118685 3'
1804	14832	27619	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1804	14832	27620	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1893	14918	27914	0.92	2.0E-79	7662258	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2158	15174	28193	4.97	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2158	15174	28194	4.97	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2202	15217	28237	0.91	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (FAF1 gene)
3933	19973	29887	0.83	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4193	17224	30113	1.15	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (FAF1 gene)
4716	17736	30528	0.97	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5754	18848		1.25	2.0E-79	AA312223.1	EST_HUMAN	EST182926 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, coesmid B0303.15
5815	18905	32088	0.88	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6371	19439	32682	1.07	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7153	18385	31273	0.7	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7373	20343	33694	1.74	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7373	20343	33695	1.74	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8437	21408	34818	1.13	2.0E-79	4508442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8862	21829	35252	2.55	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9118	22084	35512	0.46	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9118	22084	35513	0.46	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9357	22322	35749	1.1	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (H. sapiens) (LOC63991), mRNA
10452	23374	36885	3.12	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10452	23374	36886	3.12	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
11368	24315	37840	3.86	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
11368	24315	37841	3.86	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
11666	24902		2.62	2.0E-79	AB036532.1	NT	Homo sapiens p58B2 gene for ribonucleotide reductase, exon 9 and complete cds
12207	18350	31295	3.21	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12293	25107	31837	4.8	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12524	25254	31804	2.41	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6739	25668		3.26	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6862	19905	33200	0.51	1.0E-79	AI613480.1	EST_HUMAN	y37e08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623 TEKTIN C1.;
6862	19905	33201	0.51	1.0E-79	AI613480.1	EST_HUMAN	TEKTIN C1.;
8587	21555	34971	0.73	1.0E-79	BE394211.1	EST_HUMAN	601311517F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632909 5'
11944	24824	35419	2.64	1.0E-79	BF087405.1	EST_HUMAN	QV2-H10540-120900-358-a05 HT0540 Homo sapiens cDNA
3161	16217	28131	6.25	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3161	16217	29132	6.25	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
10373	23266	36772	1.02	9.0E-80	BE798803.1	EST_HUMAN	601561652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5'
11606	24544	38104	8.28	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
11606	24544	38105	8.28	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3616	16660		1.22	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7862	20806	34183	2.95	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7862	20806	34184	2.95	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
8757	22698	36154	1.14	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8757	22698	36155	1.14	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7166	18397	31242	0.58	7.0E-80	AF127882.1	NT	Callithrix jacchus olfactory receptor (CJAB0) gene, partial cds
901	13956	26913	0.7	6.0E-80	AI422197.1	EST_HUMAN	#58d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
1650	14682	27655	2.17	6.0E-80	U64898.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2307	15319	28338	1.17	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2307	15319	28339	1.17	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4314	17343	30225	1.1	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4314	17343	30226	1.1	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5899	18986	32177	1.32	6.0E-80	11421462	NT	Homo sapiens maleate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6194	19288	32503	3.12	6.0E-80	AJ404488.1	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6355	19424	32666	3.81	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6403	19471		0.93	6.0E-80	7662393	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
6455	19520	32770	0.88	6.0E-80	M18533.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
9176	22142	35568	3.06	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9176	22142	35569	3.06	6.0E-80	11528484	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9373	22338	35768	1.56	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9714	22687	38125	0.94	6.0E-80	AF161495.1	NT	Homo sapiens HSPC146 mRNA, complete cds
9841	22777	38233	0.47	6.0E-80	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
10220	23145	36634	1.55	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
11289	24239	37768	2.49	6.0E-80	11427368	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11558	24498	38054	20.37	6.0E-80	AF28730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
12051	24924	38521	1.64	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
12304	25787		2.39	6.0E-80	AF240785.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12506	25243		6.41	6.0E-80	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfoltransferase, exon 1, 2, 3, 4, 5
12994	26914		4.47	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
590	13657	26572	2.89	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
836	13893	26948	1.49	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
836	13893	26949	1.49	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1193	14233		0.96	5.0E-80	X81647.1	NT	H. sapiens ncx1 gene (exon 12)
1450	14483		2.21	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2369	15377	28400	1.92	5.0E-80	U89358.1	NT	Human (3)mbt protein homolog mRNA, complete cds
2437	15444	28462	6.37	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2806	15798	28816	5	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4069	17105	29998	1.28	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4069	17105	29998	1.26	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4391	18006	30894	1.53	5.0E-80	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
8700	21668	35091	1.14	5.0E-80	9910283	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9613	22817	36068	15.19	4.0E-80	F26915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
218	13318		9.37	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4738	17758	30653	1.45	3.0E-80	BF085009.1	EST_HUMAN	PMD-GN0018-04900-002-E03 GN0018 Homo sapiens cDNA
4945	17961		3.11	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
5919	19005	32197	2.02	3.0E-80	A1091675.1	EST_HUMAN	cc23612.x1 Soares_NSF_F8_9W_OT_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:O35790 O35790 PIG-L.
1814	14841	27832	4.7	2.0E-80	R35321.1	EST_HUMAN	Y065a08.f1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38060 5'
1877	14902	27902	1.49	2.0E-80	A1444821.1	EST_HUMAN	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2071	15088	28106	5.1	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1323 5'
6374	19442	32894	0.69	2.0E-80	A1923972.1	EST_HUMAN	wn49c10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6374	19442	32685	0.69	2.0E-80	A1823972.1	EST_HUMAN	w149c10.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'
6977	20200	33530	1.01	2.0E-80	AA582952.1	EST_HUMAN	nn80d01.s1 NCL_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1090177 3'
7098	20032	33335	1.51	2.0E-80	11421930	NT	Homo sapiens Golgi transport complex protein (90 kDa) (GTC90), mRNA
7463	20429	33798	0.81	2.0E-80	T75215.1	EST_HUMAN	y88f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22851 5' similar to SP:K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B ;
8514	22477	35922	1.22	2.0E-80	AW964270.1	EST_HUMAN	EST376343 IMAGE resequences, MAGH Homo sapiens cDNA
10126	23052	36530	0.97	2.0E-80	AJ007379.1	NT	Homo sapiens GGT gene, exon 6
11216	24169	37697	8.06	2.0E-80	AA393362.1	EST_HUMAN	z70f12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
340	13429		2.11	1.0E-80	AL163303.2	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
800	13859	26806	1.95	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 segment HS21C103
1971	14992		2.82	1.0E-80	AJ732658.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
4857	17874	30762	0.78	1.0E-80	N99520.1	EST_HUMAN	nm01112x5 NCL_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR repetitive element ;
5400	18503		3.62	1.0E-80	BE386615.1	EST_HUMAN	z839g07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294972 5' similar to contains Alu repetitive element;
6083	19163	32376	6.24	1.0E-80	L10347.1	NT	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
6646	19704	32980	1.3	1.0E-80	5174640	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7414	20381	33732	1.09	1.0E-80	AJ224172.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
7824	20772	34148	2.6	1.0E-80	A1948731.1	EST_HUMAN	Homo sapiens mRNA for lipophilin B
7824	20772	34149	2.6	1.0E-80	A1948731.1	EST_HUMAN	wq25c05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
8573	21541	34961	1.17	1.0E-80	11421211	NT	wq25c05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
9048	22014	35437	0.92	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9048	22014	35438	0.92	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9840	22584	36032	1.26	1.0E-80	AF245219.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9840	22584	36033	1.26	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10791	23712	37214	1.12	1.0E-80	D63479.2	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
11013	23978	37503	1.72	1.0E-80	11641276	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11013	23978	37504	1.72	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
11443	24386	37926	1.67	1.0E-80	8923939	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
12578	25287	37779	2.27	1.0E-80	11417901	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11488	24431	37980	9.7	8.0E-81	BE394525.1	EST_HUMAN	Homo sapiens manningia (disrupted in balanced translocation) 1 (MN1), mRNA
7484	20430	33787	2.87	7.0E-81	A1822115.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
							z891c08.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299918 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4414	17441	30331	4.98	6.0E-81	BE256829.1	EST_HUMAN	60111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4414	17441	30332	4.98	6.0E-81	BE256829.1	EST_HUMAN	60111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5365	18460	31329	1.65	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5365	18460	31330	1.65	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7845	20792	34168	0.56	6.0E-81	AF038660.1	NT	Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
9592	22554	36004	1.17	6.0E-81	AA360017.1	EST_HUMAN	EST69129 Fetal lung II Homo sapiens cDNA 5' end
12707	25364	31768	2.68	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
12707	25364	31769	2.68	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2226	15240	28265	2.27	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8765	21723	35146	1.57	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8765	21723	35147	1.57	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10006	22833	36396	0.81	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
10006	22833	36397	0.81	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11008	24789	38378	1.84	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
703	13765	28700	1.21	4.0E-81	A1521435.1	EST_HUMAN	th80e12.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:212702 3' similar to TR:Q85560 Q85560
1839	14866	27865	1.36	4.0E-81	AW776912.1	EST_HUMAN	hm98d02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COOPG_BOVIN
3186	16241	29159	4.49	4.0E-81	AB037768.1	NT	P53620 COATOMER GAMMA SUBUNIT ; Homo sapiens mRNA for KIAA1345 protein, partial cds
3644	16687	29602	0.89	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815
4187	17218	30104	1.85	4.0E-81	AF263306.1	NT	STRIATIN ; Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4187	17218	30105	1.85	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4419	17446	30337	1.1	4.0E-81	8923209	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
7492	20457	33815	0.93	4.0E-81	4757893	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2), mRNA
7629	20589	33952	0.69	4.0E-81	11420544	NT	Homo sapiens ets variant gene 1 (ETV1), mRNA
8630	21598	35018	2	4.0E-81	X06989.1	NT	Human mRNA for amyloid A4(761) protein
8880	21856	35276	3.34	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
8880	21856	35277	3.34	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9581	22543	35994	3.82	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10461	23383	36876	1.82	4.0E-81	11426281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10531	23453	36950	0.67	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
10531	23453	36951	0.67	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11519	24460	38010	3.39	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
11519	24460	38011	3.39	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
12200	25853	31439	3.45	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12200	25853	31439	3.45	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12737	25389	31753	1.71	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12737	25389	31754	1.71	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12878	25472	31729	3.69	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1272	14307	27286	10.2	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1272	14307	27287	10.2	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2380	15388	28412	1.65	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3004	16062	28980	5.19	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3004	16062	28981	5.19	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2844	15904	28828	2.48	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2844	15904	28829	2.48	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3787	16928	28735	0.88	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
8290	21299	34670	0.53	2.0E-81	8923839	NT	Homo sapiens hypothetical protein (LOC55586), mRNA
13032	16828	28735	2.55	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
4543	17566	30453	3.12	1.0E-81	AA040370.1	EST_HUMAN	z445h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to
4675	17696	30583	9.34	1.0E-81	BE047996.1	EST_HUMAN	PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly;
5308	18326	38611	3.31	1.0E-81	U87928.1	NT	tz45c04.y1 NCI CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291526 5'
5427	18530	31409	3.6	1.0E-81	11432966	NT	Human aconitase hydratase (ACO2) gene, exon 3
5427	18530	31410	3.6	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5590	18676	31639	0.83	1.0E-81	AA255569.1	EST_HUMAN	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
6737	18831	32009	3.37	1.0E-81	U52351.1	NT	z85d08.r1 Soares_NbHPU_S1 Homo sapiens cDNA clone IMAGE:682475 5' similar to SW:PRI2_HUMAN
5737	18831	32010	3.37	1.0E-81	U52351.1	NT	P49843 DNA PRIMASE 58 KD SUBUNIT
6269	19342	32575	1.55	1.0E-81	BF074641.1	EST_HUMAN	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
6696	19756	33032	0.58	1.0E-81	11420965	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
6699	19756	33033	0.56	1.0E-81	11420965	NT	602137804F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
							Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
							Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
							Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6902	18954	33251	1.26	1.0E-81	AJ133269.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	20868	34382	7.53	1.0E-81	11432866	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
10134	23060	36537	7.65	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930228 5'
10134	23060	36538	7.65	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
10328	23252	36731	4.63	1.0E-81	BE964367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885483 5'
							ac14406.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:YB36_YEAST P38128 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION. ;
10463	23385	36878	1.09	1.0E-81	AA630784.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10465	23387	36880	3.01	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10465	23387	36881	3.01	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10874	23784	37298	1.7	1.0E-81	AW897550.1	EST_HUMAN	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA
11425	24369	37905	2.9	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0008-250599-019 CT0008 Homo sapiens cDNA
11425	24369	37908	2.9	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0008-250599-019 CT0008 Homo sapiens cDNA
11428	24373	37911	6.55	1.0E-81	AW798187.1	EST_HUMAN	RC3-UM0046-290200-011-a06 UM0046 Homo sapiens cDNA
11429	24373	37912	6.55	1.0E-81	AW798187.1	EST_HUMAN	RC3-UM0046-290200-011-a06 UM0046 Homo sapiens cDNA
11951	24734	38321	2.11	1.0E-81	BF204253.1	EST_HUMAN	601857714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12414	25185	31822	4.59	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
13	13133	26031	0.94	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
107	13133	26031	2.07	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
263	13359	26284	2.7	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
815	13873	26821	14.95	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
888	13943	26901	1.44	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1487	14520	27493	1.36	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1666	14688	27674	1.7	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4114	17148	30040	0.62	8.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4272	17301	30181	0.75	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1444	14477	26789	2.53	7.0E-82	BF036327.1	EST_HUMAN	601488531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
2777	16769	26789	1.8	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
12053	24926	38524	1.75	7.0E-82	AA683747.1	EST_HUMAN	ae68604.s1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:969342 3'
1680	14712	27680	25.07	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5574	18870	31632	0.89	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-108 HT0540 Homo sapiens cDNA
5574	18870	31633	0.89	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-108 HT0540 Homo sapiens cDNA
5851	18941	32126	0.59	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12025	24901	38488	7.32	4.0E-82	AI937300.1	EST_HUMAN	wp75e09.x1 NC1_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2487624 3' similar to TR:075276
12657	25337		3.69	4.0E-82	AF029701.2	NT	075276 PKD1 ; Homo sapiens presenilin-1 gene, exons 1 and 2
277	13373	26301	16.34	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
704	13766	26701	2.78	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
788	13947	26794	10.4	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
871	13927	26885	6.11	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1062	14108		53.62	3.0E-82	AA725848.1	EST_HUMAN	al23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1357	14392	27363	1.01	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-502 PT0001 Homo sapiens cDNA
1462	14495	27469	2.51	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1917	14941	27937	1.95	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
2023	15043	28095	1.2	3.0E-82	4501922	NT	Homo sapiens adenylyate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1) mRNA
3285	16339		2.31	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
8492	21460	34877	2.7	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8902	21868	35292	0.77	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8902	21868	35293	0.77	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
10183	23108	36590	3.98	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10183	23108	36591	3.98	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
12108	24978	38577	1.6	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
12108	24978	38578	1.6	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
599	13696	28579	1.96	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
599	13696	28580	1.96	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1694	14724	27707	2.13	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117.1 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434M117 5'
2991	16049	29970	0.78	2.0E-82	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3850	16899	29802	1.07	2.0E-82	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4052	17089	29984	0.65	2.0E-82	U76833.1	NT	Human integral membrane serine protease Sepsase mRNA, complete cds
4261	17290	30171	1.07	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4588	17610	30505	1.09	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4588	17610	30506	1.09	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4904	17921	30813	3.21	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5117	18127	31002	1.53	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5117	18127	31003	1.53	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5546	18643	31583	3.46	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6299	19371	32610	4.99	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7945	26004		0.88	2.0E-82	A1476428.1	EST_HUMAN	hm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
8104	21041	34440	0.89	2.0E-82	8823130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8589	21557	34973	0.48	2.0E-82	11431845	NT	Homo sapiens nucleotide binding protein 1 (E.coli MinD like) (NUBP1), mRNA
8848	21616	35038	1.94	2.0E-82	11321570	NT	Homo sapiens silt (Drosophila) homolog 3 (SLIT3), mRNA
9017	21983	35402	0.47	2.0E-82	7657340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
9017	21983	35403	0.47	2.0E-82	7657340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
10468	23390	36884	1.66	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10468	23390	36885	1.66	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11600	24538	38095	3.95	2.0E-82	11471791	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11600	24538	38096	3.95	2.0E-82	11471791	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11638	24575	38140	2.31	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11638	24575	38141	2.31	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
12227	25082		1.94	2.0E-82	N94950.1	EST_HUMAN	z531d10.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
12760	25403		4.39	2.0E-82	AA011278.1	EST_HUMAN	z01g09.t1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
13064	25588		1.53	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA
594	13661	26574	1.27	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1213	14251		1.09	1.0E-82	BE885108.1	EST_HUMAN	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1290	14325	27286	2.11	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-f10 BT0310 Homo sapiens cDNA
1291	14326	27287	1.07	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0539 protein, partial cds
9294	22260	36689	1.09	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
10011	22938	36403	0.56	1.0E-82	AB014582.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10609	23528		1.24	1.0E-82	BF515938.1	EST_HUMAN	UI-H-BW1-aca-f03-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084063 3'
11097	24057	37681	1.87	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9065	22031	35454	4.87	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
10637	23559	37058	0.62	9.0E-83	BE253347.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1412	14445	27417	1.55	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1691	15820	27702	4.08	8.0E-83	N66951.1	EST_HUMAN	zaf8r12.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
1359	14394	27364	0.99	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271299-068-h11 L10016 Homo sapiens cDNA
2876	15935		1.92	7.0E-83	AA594655.1	EST_HUMAN	nc12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4853	17870		7.64	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TRC:Q9Y316 Q9Y316
6169	19244	32476	0.73	7.0E-83	11426657	NT	DJ207H1.1;
403	13476	26410	3.07	6.0E-83	M33320.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
1802	14830	27817	1.08	6.0E-83	AW573088.1	EST_HUMAN	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-28
3030	16088	29008	0.64	6.0E-83	AW816405.1	EST_HUMAN	h31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034.;
3064	16121		0.97	6.0E-83	AF231919.1	NT	QV4-ST0234-181189-037-05 ST0234 Homo sapiens cDNA
3063	16140	29051	1.03	6.0E-83	AA701457.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3575	16620	29541	2.54	6.0E-83	11430241	NT	z59c05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:495080 3'
5167	18176	31054	1.2	6.0E-83	4827033	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5368	18471	31342	1.53	6.0E-83	4507968	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 18 (TNFSF18) mRNA
6139	19215	32444	1.32	6.0E-83	AJ010770.1	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
7745	20699	34065	2.1	6.0E-83	11422024	NT	Homo sapiens hyperion gene, exons 1-50
10035	22982	36430	2.5	6.0E-83	4505314	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
10127	23053	36531	0.76	6.0E-83	11430947	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10127	23053	36532	0.76	6.0E-83	11430947	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
11859	24741		2.01	6.0E-83	AA496105.1	EST_HUMAN	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
12179	25027		5.85	6.0E-83	AF240786.1	NT	ab14610.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element;
945	13898		1.42	5.0E-83	U17883.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2066	15823		1	5.0E-83	AF006305.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
3652	16695	28610	0.97	6.0E-83	AL133207.2	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3926	16966	29879	1.02	5.0E-83	4855190	NT	Novel human gene mapping to chromosome X
5115	18125	31000	14.32	5.0E-83	4557013	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
5115	18125	31001	14.32	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5245	18253	31124	0.93	5.0E-83	4505802	NT	Homo sapiens phosphatidylinositol 3-kinase, catalytic, gamma polypeptide (PIK3CG) mRNA
641	13707	28628	2.28	4.0E-83	AF224699.1	NT	Homo sapiens marnosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3525	16571	29494	1	4.0E-83	BE898078.1	EST_HUMAN	(UBE2D3) genes, complete cds
999	14050		6.39	3.0E-83	AA368311.1	EST_HUMAN	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
							EST79542 Placenta 1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2788	15780		1.82	3.0E-83	AA632654.1	EST_HUMAN	np87c07.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:113292 similar to contains THR12 THR
6730	19786		0.72	3.0E-83	A1217223.1	EST_HUMAN	repetitive element ;
1816	14843	27834	1.88	2.0E-83	AA993492.1	EST_HUMAN	q773g06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755682 3'
1816	14843	27835	1.88	2.0E-83	AA993492.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
1942	14866	27963	3.01	2.0E-83	N66951.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
2894	15924	28943	1.36	2.0E-83	BE828694.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
3282	16336		2.14	2.0E-83	11430834	NT	Q92614 MYELOBLAST KIAA0216 ;
3788	16829		0.87	2.0E-83	AL163202.2	NT	Q92614 MYELOBLAST KIAA0216 ;
4363	17390	30272	9.78	2.0E-83	AF202879.1	NT	Q92614 MYELOBLAST KIAA0216 ;
4681	17702	30590	6.03	2.0E-83	7706398	NT	Q92614 MYELOBLAST KIAA0216 ;
4681	17702	30591	6.03	2.0E-83	7706398	NT	Q92614 MYELOBLAST KIAA0216 ;
5343	18448	31319	0.94	2.0E-83	U06879.1	NT	Q92614 MYELOBLAST KIAA0216 ;
5547	18644	31584	1.09	2.0E-83	11024711	NT	Q92614 MYELOBLAST KIAA0216 ;
5547	18644	31585	1.09	2.0E-83	11024711	NT	Q92614 MYELOBLAST KIAA0216 ;
5845	19031	32224	0.54	2.0E-83	11428081	NT	Q92614 MYELOBLAST KIAA0216 ;
6076	19157	32369	1.21	2.0E-83	BE885401.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
7669	20628	33992	5.47	2.0E-83	AF129533.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8103	21039	34438	0.52	2.0E-83	BF105097.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
8175	21145	34551	0.55	2.0E-83	AB001025.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8175	21145	34552	0.55	2.0E-83	AB001025.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8319	21288	34702	1.48	2.0E-83	U66707.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8657	21625	35045	2.5	2.0E-83	AF011920.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8657	21625	35046	2.5	2.0E-83	AF011920.1	NT	Q92614 MYELOBLAST KIAA0216 ;
9852	22879	36342	0.46	2.0E-83	5453881	NT	Q92614 MYELOBLAST KIAA0216 ;
9852	22879	36343	0.46	2.0E-83	5453881	NT	Q92614 MYELOBLAST KIAA0216 ;
10242	23167	36654	0.43	2.0E-83	BF128748.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
10394	23316	36795	2.53	2.0E-83	M22094.1	NT	Q92614 MYELOBLAST KIAA0216 ;
10394	23316	36796	2.53	2.0E-83	M22094.1	NT	Q92614 MYELOBLAST KIAA0216 ;
10475	23397	36895	1.2	2.0E-83	AU117659.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
10549	23471	36966	0.74	2.0E-83	AW505600.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
11185	24150	37681	3.48	2.0E-83	11438448	NT	Q92614 MYELOBLAST KIAA0216 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11272	24224	37749	1.84	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
11272	24224	37750	1.84	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
12802	25429		4.91	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1410	14443	27414	1.56	1.0E-83	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-kebacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1410	14443	27415	1.56	1.0E-83	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-kebacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1453	14486	27481	0.93	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1453	14486	27482	0.93	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
2865	15882	28681	1.16	1.0E-83	BE883860.1	EST_HUMAN	601607375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3198	16253	29173	0.65	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIA00868), mRNA
3882	16922	29830	3.33	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4273	17302	30182	2.31	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-iscmerase, exon 3
6854	19907	33203	1.53	1.0E-83	A1027614.1	EST_HUMAN	ov69508.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM
3810	16850	29758	3.98	7.0E-84	BE901209.1	EST_HUMAN	PROTEIN (HUMAN);
1298	14333	27294	4.11	6.0E-84	BE838864.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1298	14333	27295	4.11	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2407	15414	28438	5.78	6.0E-84	AA776574.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
5311	18328		1.9	6.0E-84	AL042863.2	EST_HUMAN	aa86a03.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5596	18692	31662	1.69	6.0E-84	AA897339.1	EST_HUMAN	DKFZp434H0322_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'
5743	18837	32018	1.09	6.0E-84	11426718	NT	ai47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338
5743	18837	32018	1.09	6.0E-84	11426718	NT	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5743	18837	32018	1.09	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
5743	18837	32019	1.09	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
7714	20671	34038	3.36	6.0E-84	BE810371.1	EST_HUMAN	PMO-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
7855	20896	34289	0.89	6.0E-84	AF038391.1	NT	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
8408	21377	34783	2.05	6.0E-84	BE770198.1	EST_HUMAN	PM4-F70054-160600-004-af0 F70054 Homo sapiens cDNA
715	13777	26712	0.81	5.0E-84	AA382811.1	EST_HUMAN	EST86094 Testis I Homo sapiens cDNA 5' end
3027	16084		1.54	6.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
6227	19301	32534	0.49	5.0E-84	AA167678.1	EST_HUMAN	zq39e07.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632100 5' similar to TR:G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11871	24753	38334	2.06	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11864	24843	38437	2.29	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11864	24843	38438	2.29	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1409	14442	27413	1.68	4.0E-84	AF685321.1	EST_HUMAN	wa7604.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN O43847 NARDILYSIN PRECURSOR;
4987	18002	30891	0.99	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
4988	18003	30892	2.19	4.0E-84	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5335	18440	31163	0.53	4.0E-84	AF022835.1	NT	Homo sapiens multidrug resistance protein (MRP), exon 13
5642	18738	31902	1.28	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5642	18738	31903	1.28	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6309	19467	32714	1.89	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7809	20852	34239	12.53	4.0E-84	11421328	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9262	22228	35658	0.9	4.0E-84	4557523	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9262	22228	35659	0.9	4.0E-84	4557523	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
11263	24215	37739	5.34	4.0E-84	AB032856.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
316	13408	26334	1.92	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1157	14188	27148	5.95	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1977	14998	28000	1.24	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2024	15044	28057	3.11	3.0E-84	AL066880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3604	16849	28565	1.15	3.0E-84	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3762	16803	29715	6.26	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
11228	24179		17.2	3.0E-84	AF083801.1	EST_HUMAN	wu20405.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb1.05093 80S RIBOSOMAL PROTEIN L18A (HUMAN);
2115	15132	28153	5.68	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2115	15132	28154	5.68	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2954	16012	28939	7.98	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
2973	16031	28954	1.35	2.0E-84	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
5604	18700	31671	0.88	2.0E-84	BF511575.1	EST_HUMAN	UH-H-B14-act-a-02-0-J1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
5604	18700	31672	0.88	2.0E-84	BF511575.1	EST_HUMAN	UH-H-B14-act-a-02-0-J1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
6793	19847	33132	0.88	2.0E-84	H63370.1	EST_HUMAN	y56611.s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:208324 3'
8392	21381		1.62	2.0E-84	AI298674.1	EST_HUMAN	qm87c09.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1895728 3'
8728	21698	35121	0.56	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8728	21698	35122	0.56	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9701	22654	38108	0.99	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
10089	23015	36491	0.55	2.0E-84	H22841.1	EST_HUMAN	yn49a11.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:51383 5' similar to SP:APOH_RAT P26844 BETA-2-GLYCOPROTEIN I;
12445	25206	31829	3.28	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupskl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4060261 3' similar to TR:Q8UGS3 Q8UGS3 DJ756G23.1;
12445	25206	31830	3.28	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupskl_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4060251 3' similar to TR:Q8UGS3 Q8UGS3 DJ756G23.1;
312	13404	26330	1.44	1.0E-84	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
551	13621	26541	15.79	1.0E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
721	13783	27292	1.16	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1296	14331	27292	3.1	1.0E-84	AA984379.1	EST_HUMAN	ant5b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'
2070	15087	28105	2.34	1.0E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3526287 5'
2232	15246	28269	1.27	1.0E-84	11427187	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3764	16806	28717	2.47	1.0E-84	AA720851.1	EST_HUMAN	nm12e06.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4446	17472	30360	3.92	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
4728	17748	30639	2.66	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4728	17748	30640	2.66	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
4949	17472	30360	2.12	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
6029	19112	32314	0.66	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
6314	19385	32627	1.38	1.0E-84	S73482.1	NT	uterine water channel=28 kDa erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
7084	20086	33394	1.44	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7084	20086	33395	1.44	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7314	20285	33626	2.66	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7708	20665	34032	4.72	1.0E-84	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7814	20763	34139	0.63	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7859	20763	34139	2.13	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
9893	22846	36533	2.91	1.0E-84	6031684	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
10128	23054	31285	0.62	1.0E-84	AF224511.1	NT	Homo sapiens Ca2+-binding protein CABP3 (CABP3) gene, exon 6 and partial cds
10150	18337	31285	2.65	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10150	18337	31286	2.65	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
12121	20285	33626	2.67	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
12324	25126		2.03	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12436	26201	31825	2.32	1.0E-84	11418185	NT	Homo sapiens acinlase 2, mitochondrial (ACO2), mRNA
898	14020		1.9	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1074	14119	27069	2.21	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1074	14119	27070	2.21	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1581	14614	27586	1.31	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1581	14614	27587	1.31	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1684	14715	27595	2.95	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4280	17309	30188	1.11	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4913	17930	30821	1.05	9.0E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4950	17965	30855	1	9.0E-85	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
1138	14181	27132	13.33	7.0E-85	L05034.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11958	24837		9.76	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11745	24830	38209	2.51	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11745	24830	38210	2.51	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2340	15350	28371	1.67	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5528	18625	31560	1.37	6.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882402 5'
5528	18625	31561	1.37	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882402 5'
13030	18344		6.19	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I isoform (CACNA1I) mRNA, complete cds
6271	19344	32576	1.42	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6271	19344	32577	1.42	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
7013	20139	33456	0.58	4.0E-85	AI628119.1	EST_HUMAN	684901.X1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2285908 3'
10937	23857		1.35	4.0E-85	BE079263.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
12875	25772		1.31	4.0E-85	Z18867.1	EST_HUMAN	HSDHEGC03 Stralagene cDNA library Human heart, cat#936208 Homo sapiens cDNA clone HSDHEGC03
1302	14338	27301	1.02	3.0E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1795	14824	27808	3.9	3.0E-85	T97495.1	EST_HUMAN	y53309.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
4935	17951	30842	1.37	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4935	17951	30843	1.37	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5475	18576	31485	0.65	3.0E-85	11436001	NT	Homo sapiens lacrima proline rich protein (LPRP), mRNA
6204	19278	32511	0.66	3.0E-85	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6257	19330	32560	5.69	3.0E-85	7662309	NT	Homo sapiens KIA00793 gene product (KIA00793), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6257	19330	32561	5.69	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
7140	20116		7.73	3.0E-85	AJ404498.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7628	20586	33949	0.88	3.0E-85		NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621), mRNA
8204	21174	34584	1.94	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8853	21820	35240	1.06	3.0E-85	11525829	NT	Homo sapiens CGI-81 protein (LOC51108), mRNA
9329	22294	35723	3.37	3.0E-85	11430989	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9661	22818	36272	1.03	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB2), mRNA
9661	22818	36273	1.03	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB2), mRNA
10849	23769	37268	1.16	3.0E-85	AF098642.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11834	24717	38303	1.72	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
12919	25485		2.14	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
964	14016	28970	0.87	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Mx2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1041	14087	27039	2.52	2.0E-85	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1418	14461	27424	8.49	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1418	14461	27425	8.49	2.0E-85	5174776	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2239	15253	28277	1.8	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2834	14375		14.69	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3035	16093	29011	1.16	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4361	17388	30270	4.83	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4948	17964	30854	0.93	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5178	18187	31064	1.37	2.0E-85	4502212	NT	Homo sapiens arginase, liver (ARG1) mRNA
9628	22572	36022	2.67	2.0E-85	AI760820.1	EST_HUMAN	wf67108.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element MSR1 repetitive element
10007	22934	36398	0.94	2.0E-85	AI014459.1	EST_HUMAN	MSR1 repetitive element
10626	23547	37048	1.31	2.0E-85	AI086384.1	EST_HUMAN	wd49d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331461 3'
2285	15307		2.51	1.0E-85	BE794306.1	EST_HUMAN	wm94412.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2403	15410	28434	6.6	1.0E-85	BE618392.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2403	15410	28435	6.6	1.0E-85	BE618392.1	EST_HUMAN	601482817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
8091	21027	34426	0.52	1.0E-85	BE062951.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
10140	23066	36542	2.41	1.0E-85	BE257817.1	EST_HUMAN	MRO-BT0264-221169-002-f03 BT0264 Homo sapiens cDNA
10671	23493	36985	0.83	1.0E-85	AW81325.1	EST_HUMAN	601109738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360553 5'
11269	24221	37745	2.01	1.0E-85	AA778785.1	EST_HUMAN	RC1-ST0196-081099-011-d05 ST0196 Homo sapiens cDNA
							Z145f03.a1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11269	24221	37746	2.01	1.0E-85	AA778785.1	EST_HUMAN	245703.s1 Soares_telar_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:463245 3'
11342	24282	37816	2.46	1.0E-86	BF311552.1	EST_HUMAN	801897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
11342	24292	37817	2.46	1.0E-85	BF311552.1	EST_HUMAN	601997003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
12064	24937	38533	2.37	1.0E-85	AI198420.1	EST_HUMAN	q166a07.x1 NCL_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:1860468 3'
12328	25289	31780	3.47	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12583	25289	31780	3.37	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1426	14459		12.78	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
6249	19322	32552	1.27	8.0E-86	11424140	NT	Homo sapiens similar to GDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
12004	24881	38477	1.57	8.0E-86	4503224	NT	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
936	13989	26939	0.83	7.0E-86	AA860801.1	EST_HUMAN	q188f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
936	13989	26940	0.83	7.0E-86	AA860801.1	EST_HUMAN	q188f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6320	19391	32631	0.85	7.0E-86	9966888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6320	19391	32632	0.85	7.0E-86	9966888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7169	18400	31246	6.12	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
9096	22062	35487	4.12	7.0E-86	L38557.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15
10058	22985		1.49	7.0E-86	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10116	23042	36522	1.67	7.0E-86	11526307	NT	Homo sapiens DGeorge syndrome critical region gene 6 (DGCR6), mRNA
1297	14332	27293	3.29	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
212	13312	26241	1.75	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
6151	19228	32455	10.99	4.0E-86	BE295843.1	EST_HUMAN	601072594F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
11572	13312	26241	2.44	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
5877	18772	31944	6.64	3.0E-86	AW340946.1	EST_HUMAN	x292h12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8605	21573	34988	1.12	3.0E-86	AV722329.1	EST_HUMAN	AV722329 HTB Homo sapiens cDNA clone HTBBS004 5'
10581	23503	36996	3.26	3.0E-86	BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
10581	23503	36996	3.26	3.0E-86	BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11764	23919	37437	5.6	3.0E-86	AI659240.1	EST_HUMAN	tu18b02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2251371 3'
11842	24725	38312	1.55	3.0E-86	AV690469.1	EST_HUMAN	AV690469 GKC Homo sapiens cDNA clone GKCBSE02 5'
12295	25784		1.35	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
286	13362	26286	1.83	2.0E-86	AA306284.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
414	13487		2.72	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1184	14234	27189	2.88	2.0E-86	N58977.1	EST_HUMAN	yz19a08.r1 Soares_multiple_sclerosis_2NBHMSHP Homo sapiens cDNA clone IMAGE:283478 5'
2201	15216	28236	2.54	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2277	15290	28315	1.14	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3426	16474	28383	1.47	2.0E-86	AW966142.1	EST_HUMAN	EST378215 IMAGE resequences, MAGI Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3759	16800	29711	2.55	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3759	16800	29712	2.55	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4070	17106		3.01	2.0E-86	AW515742.1	EST_HUMAN	hdb7g08.x1 NCI_QGAP_G08 Homo sapiens cDNA clone IMAGE:2916542 3'
4828	17845	30745	3.3	2.0E-86	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5972	19057	32267	1.53	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5972	19057	32268	1.53	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7277	25672	33314	0.81	2.0E-86	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8343	21312	34725	0.77	2.0E-86	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8861	21828		0.53	2.0E-86	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8920	21886	35312	2.44	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8920	21886	35313	2.44	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9254	22220	35651	1.48	2.0E-86	10863976	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9673	22628	36080	2.12	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10814	23735	37237	2.88	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10814	23735	37238	2.88	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10869	23789	37289	1.63	2.0E-86	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
12732	25385	31750	2.92	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12901	25485		6.37	2.0E-86	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
1601	14633	27609	1.28	1.0E-86	48268955	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1), mRNA
3176	16231	29147	1.52	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3249	16304	29228	2.61	1.0E-86	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3307	16360	29279	2.18	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3307	16360	29280	2.18	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3966	17006	29921	1.01	1.0E-86	7708161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3966	17006	29922	1.01	1.0E-86	7708161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4293	17322	30202	5.56	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4651	17672	30559	1.12	1.0E-86	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
5632	18728	31889	1.44	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5430	18533		1.78	9.0E-87	AI150703.1	EST_HUMAN	q577c09.x1 Soares_fetal_hear_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7681	20639	34001	1.73	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7681	20639	34002	1.73	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
480	13552	26480	82.98	8.0E-87	X62245.1	NT	O. cuniculus mRNA for elongation factor 1 alpha
2304	16316	28336	3.11	7.0E-87	BF083211.1	EST_HUMAN	7a8502.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2304	16316	28337	3.11	7.0E-87	BF083211.1	EST_HUMAN	7a8502.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6540	19802	32864	1.01	7.0E-87	AF080338.1	EST_HUMAN	MRO-NT0039-020500-004-a11 NT0039 Homo sapiens cDNA
8531	21499	34915	2.59	7.0E-87	BF352776.1	EST_HUMAN	IL3-HT0619-060700-188-D10 HT0619 Homo sapiens cDNA
9809	21132	34535	0.66	7.0E-87	BE712961.1	EST_HUMAN	IL5-HT0702-160600-103-d06 HT0702 Homo sapiens cDNA
10431	23363	36837	3.41	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
10431	23363	36838	3.41	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
10834	25703	37708	0.48	7.0E-87	AI081555.1	EST_HUMAN	ox59h01.st Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660657 3'
11237	24190	37709	10.09	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
11237	24190	37709	10.09	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
3588	16584	29507	0.76	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
6561	19621	32886	1.84	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
11079	24041		6.13	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1162	14204	27157	1.86	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
12585	14204	27157	2	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
867	14019	26972	0.98	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1176	14217	27172	15.32	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
2045	15064	28084	1.49	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
3478	16524	29448	1.57	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23) (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
5307	18310	31167	0.98	4.0E-87	4759073	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 16 (SCYA16) mRNA
5307	18310	31168	0.98	4.0E-87	4759073	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 16 (SCYA16) mRNA
5521	18620	31554	5.85	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5844	18934	32118	0.55	4.0E-87	JB5429.1	NT	Human transcription factor NFATx3 mRNA, complete cds
6163	19238	32469	4.54	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBA4051
7933	20875	34264	0.5	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7933	20875	34265	0.5	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8050	20987	34363	0.61	4.0E-87	L48524.1	NT	Homo sapiens tuberin (TSC2) gene, exon 10
9583	22545	35986	0.47	4.0E-87	AF223470.1	NT	Homo sapiens KIAA0971-1 protein (KIAA0971-1) mRNA, complete cds

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11500	24443	37994	5.12	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
12678	25839	31428	1.47	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12678	25839	31429	1.47	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12835	25444		3.11	4.0E-87	11417812	NT	Homo sapiens putative receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2787	15778	28796	4.73	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2959	16017		0.79	2.0E-87	BF327920.1	EST_HUMAN	QV0-BN0148-050600-254-a03 BN0148 Homo sapiens cDNA
3768	16838	29745	0.9	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
4951	17866	30856	1.64	2.0E-87	BF37631.1	EST_HUMAN	CM0-TN0038-150900-652-n08 TN0038 Homo sapiens cDNA
4988	18013	30900	0.68	2.0E-87	BE175478.1	EST_HUMAN	RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
5744	18838	32020	8.67	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5744	18838	32021	8.67	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6480	19525		3.73	2.0E-87	BE567193.1	EST_HUMAN	601341393F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5'
6857	19910	33205	1.12	2.0E-87	N48128.1	EST_HUMAN	y21e07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
6948	20172	33495	0.64	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDSG04 3'
7379	20349	33700	1.31	2.0E-87	BE294932.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7436	20403	33757	0.81	2.0E-87	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7686	20844	34008	37.21	2.0E-87	N48128.1	EST_HUMAN	w21e07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
7851	20892	34284	36.03	2.0E-87	N48128.1	EST_HUMAN	w21e07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
8738	21706	35130	13.21	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
10144	23070		5.58	2.0E-87	BE531136.1	EST_HUMAN	601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3810539 5'
1186	15818		3.71	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
3723	16766	28677	4.15	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3746	16788	29700	2.03	1.0E-87	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
5152	18102	31042	1.98	1.0E-87	J50949.1	NT	Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds
6352	19421	32682	1.94	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6352	19421	32663	1.94	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7383	20353	33704	0.84	1.0E-87	AF039517.1	NT	Homo sapiens corticotrophin-releasing factor type 1 receptor gene, exon 8
7383	20353	33705	0.84	1.0E-87	AF039517.1	NT	Homo sapiens corticotrophin-releasing factor type 1 receptor gene, exon 8
7389	20358	33710	1.03	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7628	20588	33951	1.17	1.0E-87	11431580	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7783	20736	34108	0.85	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
8068	21005	34403	0.54	1.0E-87	4505528	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
8453	21422	34837	11.12	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9260	22226	35655	0.97	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9260	22228	35656	0.97	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9991	22918	36384	6.68	1.0E-87	BE818183.1	EST_HUMAN	RO6-BN0278-050700-012-E02 BN0276 Homo sapiens cDNA
9991	22918	36385	6.68	1.0E-87	BE818183.1	EST_HUMAN	RO6-BN0278-050700-012-E02 BN0276 Homo sapiens cDNA
10739	23661	37155	3.11	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' end
11084	24045	37567	1.78	1.0E-87	5729867	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
12675	25978		1.48	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1108	14152	27102	6.48	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1351	14386	27355	2.56	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
1351	14386	27356	2.56	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
2130	15147	28162	1.14	9.0E-88	7661701	NT	Homo sapiens DKFZP586P1522 protein (DKFZP586P1522), mRNA
3642	16685	29601	0.99	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4288	17327	30207	3.27	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4298	17327	30208	3.27	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
5038	18051	30931	1	9.0E-88	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9375	22340	35771	3.69	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1845	14871		1.13	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2647	15944	28669	5.45	5.0E-88	N88399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3013	16071	28991	0.91	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3023	16080	29002	0.77	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3023	16080	29003	0.77	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3400	16449		2.75	5.0E-88	AI693217.1	EST_HUMAN	w468h08.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element/contains element MER22 MER22 repetitive element ;
6936	20160	33481	3.32	5.0E-88	H10932.1	EST_HUMAN	ym06b10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5'
8261	21230	34639	2.44	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9666	22619	36070	0.57	5.0E-88	BF680206.1	EST_HUMAN	602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5'
12435	14871		1.73	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
1332	14367	27336	1.49	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1332	14367	27337	1.49	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
5185	18194	31069	0.81	4.0E-88	BF670714.1	EST_HUMAN	602149762F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290975 5'
7454	20420	33775	1.35	4.0E-88	11416586	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11818	24701	38282	3.12	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11818	24701	38283	3.12	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
733	13794	28731	0.85	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1829	14856		1.78	3.0E-88	4508020	NT	Homo sapiens Zinc finger protein 259 (ZNF259), mRNA
2958	16016	28944	2.91	3.0E-88	N66951.1	EST_HUMAN	z48f12.s1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:295823 3'
4268	17298	30175	0.93	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4268	17298	30176	0.93	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4504	17529		3.94	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
6372	18477	31350	2.45	3.0E-88	11429567	NT	Homo sapiens valosin-containing protein (VCP), mRNA
5686	18761	31630	4.05	3.0E-88	9956938	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5789	18881	32063	3.82	3.0E-88	11420697	NT	Homo sapiens v-rat simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6285	19357	32593	0.95	3.0E-88	11417370	NT	Homo sapiens Interleukin 13 (IL13), mRNA
6553	25662	32877	0.77	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6553	25662	32878	0.77	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7267	20002	33302	15.04	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7788	20741	34114	6.35	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
8253	21222	34632	10.99	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8538	21508	34923	1.28	3.0E-88	AF034374.1	NT	Homo sapiens myoblast fusion factor biosynthesis protein A and myoblast fusion factor biosynthesis protein C mRNA, complete cds
9789	21112	34512	2.14	3.0E-88	11526262	NT	Homo sapiens v-rat simian erythroid leukemia virus E26 oncogene related (ERG), mRNA
10288	23213	36686	0.74	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10288	23213	36697	0.74	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10316	23240	38721	0.99	3.0E-88	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12086	24958	38554	3.65	3.0E-88	4557502	NT	Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN) mRNA
12421	25191		7.12	3.0E-88	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1037	14083	27033	61.87	2.0E-88	7305198	NT	Homo sapiens Gelsolin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1628	14681	27637	1.66	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
1765	14784	27779	4.07	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
4455	17481	30369	1.86	2.0E-88	5031668	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
6016	16099	32300	5.17	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aea-d-04-0-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6016	16099	32301	5.17	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aea-d-04-0-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6802	19858	33141	23.82	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6802	19858	33142	23.82	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7329	20300	33644	1.29	1.0E-88	AI969034.1	EST_HUMAN	wg70a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2478606 3'
7390	20369	33711	3.91	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCI_CGAP_GC61 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2
8476	21445	34882	0.47	1.0E-88	AF135183.1	NT	CE00851 ; Homo sapiens Recq helicase 5 (RECQ5) gene, alternative splice products, complete cds
9597	22801	36050	1.09	1.0E-88	AA190368.1	EST_HUMAN	zp87c02.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:827170 5' similar to
9938	22895	36327	2.73	1.0E-88	AL043314.2	EST_HUMAN	SW-POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN ; DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
11773	23928	37449	3.86	1.0E-88	AA991479.1	EST_HUMAN	os91g03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612766 3' similar to gb:M16342
12640	25324		1.91	1.0E-88	AL163246.2	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN); Homo sapiens chromosome 21 segment HS21C046
11298	24248	37774	3.66	9.0E-89	11421238	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
2745	15738	28765	1.74	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
7118	20052	33356	1.21	8.0E-89	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
433	13507	26440	1.21	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
433	13507	26441	1.21	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4919	17936	30828	2.95	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4987	17982	30872	4.02	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E246 5'
5505	18605	31534	1.22	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete CDS
5505	18605	31535	1.22	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete CDS
6477	19542	32780	0.77	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
6477	19542	32780	0.77	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
7741	20895	34060	1.42	7.0E-89	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
8211	21180	34589	0.57	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8211	21180	34590	0.57	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8823	21780	35212	3.88	7.0E-89	J02823.1	NT	Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds
10897	23817	37324	1.26	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10897	23817	37325	1.25	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10913	23833	37347	1.11	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10913	23833	37348	1.11	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
1025	14071	27022	1.23	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2223	15237	28281	1.17	6.0E-89	4505124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2440	15447	28464	0.99	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L3 (UBE2L3) mRNA
2440	15447	28465	0.99	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L3 (UBE2L3) mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4667	17688	30573	4.04	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4667	17688	30574	4.04	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5111	18121	30995	3.41	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5111	18121	30996	3.41	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
7842	20789	34164	0.84	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-080600-219-g03 NT0022 Homo sapiens cDNA
2888	15947	28863	1.1	3.0E-89	AW976161.1	EST_HUMAN	EST388280 MAGe resequences, MAGN Homo sapiens cDNA
7347	20317	33663	1.25	3.0E-89	AI217359.1	EST_HUMAN	qh17b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844915 3'
11151	24111	37638	1.79	3.0E-89	N57357.1	EST_HUMAN	yw66e11.1 Soares_placenta_8to9weeks_2NbpHP8to9W Homo sapiens cDNA clone IMAGE:269148 5' similar to SW_P14K_HUMAN P42356 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
127	13481	28416	0.68	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
127	13481	28417	0.68	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
408	13481	28418	0.64	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
408	13481	28417	0.64	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
531	13602	28520	0.93	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2892	15981	28867	1.71	2.0E-89	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb.J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
3565	16611	29632	0.65	2.0E-89	AA756149.1	EST_HUMAN	ah70603.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
3565	16611	29633	0.65	2.0E-89	AA756149.1	EST_HUMAN	ah70603.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4169	17200	30086	1.41	2.0E-89	AF098997.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4180	17211	30098	4.98	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4180	17211	30099	4.98	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4376	17404	30284	0.83	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4524	17549	30437	1.1	2.0E-89	AJ07378.1	NT	Homo sapiens GGT gene, exon 5
5416	18519	31900	1.39	2.0E-89	BE541744.1	EST_HUMAN	607066996F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5558	18655	32167	1.89	2.0E-89	U03095.1	NT	Homo sapiens gene for LECT2, complete cds
5888	18975	32167	1.89	2.0E-89	U03095.1	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
6335	19404	32644	0.67	2.0E-89	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7931	20874	34263	4.07	2.0E-89	U81004.1	NT	Human GT24 (GT24) mRNA, partial cds
8268	21235	34546	2.9	2.0E-89	1142880.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8760	21727	35149	0.94	2.0E-89	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
9608	22612	36095	0.67	2.0E-89	AB037754.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10169	23094	36572	1.11	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
10169	23094	36573	1.11	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
11701	24866	38243	2.63	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11896	24777	38363	3.64	2.0E-89	11433873	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
12028	24902	38497	1.63	2.0E-89	U10692.1	NT	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds
11903	24784	38372	5.65	1.0E-89	BF196052.1	EST_HUMAN	h87d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
11903	24784	38373	5.65	1.0E-89	BF196052.1	EST_HUMAN	h87d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
8569	21537	34957	1.77	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8569	21537	34958	1.77	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1054	14110	27059	1.93	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1055	14110	27059	2.43	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1333	15884	27338	4.85	8.0E-90	BE670561.1	EST_HUMAN	7636f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1333	15884	27339	4.85	8.0E-90	BE670561.1	EST_HUMAN	7636f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8906	21872	35298	0.78	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-508 HT0598 Homo sapiens cDNA
11374	24321	37848	1.68	8.0E-90	AA705222.1	EST_HUMAN	z82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
11374	24321	37849	1.68	8.0E-90	AA705222.1	EST_HUMAN	z82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
837	13894		3.74	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8767	21734		2.07	7.0E-90	AA782977.1	EST_HUMAN	ai63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
9317	22282	35712	1.82	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9317	22282	35713	1.82	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10495	23417	36916	2.08	7.0E-90	H68849.1	EST_HUMAN	y86g04.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10495	23417	36916	2.08	7.0E-90	H68849.1	EST_HUMAN	y86g04.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10821	23742	37243	0.58	7.0E-90	BF528089.1	EST_HUMAN	602071208F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214257 5'
3081	16138	29049	0.88	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
3081	16138	29050	0.88	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4254	17283	30164	9.77	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4254	17283	30165	9.77	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6097	19176	32393	3.07	6.0E-90	U77700.1	NT	Homo sapiens HsGON1 mRNA, partial cds
6097	19176	32394	3.07	6.0E-90	U77700.1	NT	Homo sapiens HsGON1 mRNA, partial cds
8670	21638	35081	3.16	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8670	21638	35082	3.16	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
156	13259		25.61	5.0E-90	AB035344.1	NT	Homo sapiens TCE6 gene, exon 1-10b
1197	14237	27192	1.94	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1836	14863	27680	1.33	5.0E-90	AI222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSPETIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
1836	14863	27681	1.33	5.0E-90	AI222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSPETIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
2582	15583	28582	2.8	5.0E-90	AF114487.1	NT	Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds
4571	17593	30487	1.32	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4593	17814	30508	0.7	5.0E-90	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5672	18787	31839	2.88	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6690	18785		0.61	5.0E-90	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
5777	18869	32052	1.34	5.0E-90	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
6860	18767	31939	2.22	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6894	19946	33242	0.73	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6894	19946	33243	0.73	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7423	20390	33741	2.09	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7423	20390	33742	2.09	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7813	20762	34138	8.82	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
8636	21604	35028	4.98	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10039	22866	36433	1.13	5.0E-90	11419429	NT	Homo sapiens similar to ectorucleotide pyrophosphatasephosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10644	23566	37063	0.74	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10777	23698	37196	0.53	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10777	23698	37197	0.53	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10813	23734	37236	5.86	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class 1, type 8A, member 2 (ATP8A2), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10871	23791	37291	0.67	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10871	23791	37292	0.67	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
12872	25506		2.89	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12920	25498		4.66	5.0E-90	AF523366.1	EST_HUMAN	ar79h05.x1 Barslead aorta HPLR60 Homo sapiens cDNA clone IMAGE:2128761 3'
302	13396	26323	2.82	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
302	13396	26324	2.82	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1088	14132	27084	4.74	4.0E-90	4505318	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1698	14728	27711	8.84	4.0E-90	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
4696	17707	30600	6.15	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4835	17882	30761	2.4	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4856	17873	30761	1.96	4.0E-90	M95967.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 8
12134	25003	38610	1.75	4.0E-90	D31124.1	EST_HUMAN	HJML12582 Human fetal lung Homo sapiens cDNA 5'
8185	21155	34563	1.72	3.0E-90	BF516168.1	EST_HUMAN	UI-HBW1-amy-b-04-Q-UJ.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
8185	21155	34564	1.72	3.0E-90	BF516168.1	EST_HUMAN	UI-HBW1-amy-b-04-Q-UJ.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11951	24850	38426	67.56	3.0E-90	BE563833.1	EST_HUMAN	601335244FT NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
215	13315	26243	5.41	2.0E-90	BE537913.1	EST_HUMAN	601087378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1177	14218	27173	46.4	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1177	14218	27174	46.4	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3859	16898	29801	2.03	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1713410 3'
4714	17734	30627	1.17	2.0E-90	AB006627.1	NT	similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3 ;
4947	17963	30853	9.22	2.0E-90	5729855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5870	18959	32147	0.57	2.0E-90	11525901	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5870	18959	32148	0.57	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5879	18968	32159	4.7	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
10149	23075	36550	8.23	2.0E-90	11427320	NT	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:O75208 O75208 HYPOTHETICAL 35.5 KD PROTEIN. ;
10149	23075	36551	8.23	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10319	23243	36722	1.27	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10319	23243	36723	1.27	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11798	23953	37475	5.5	2.0E-90	11024711	NT	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
							Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
276	13372	26300	3.99	1.0E-90	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
374	16812	26389	1.13	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
375	16812	26389	2.04	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
698	13768	26689	2.55	1.0E-90	AJ237689.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
698	13758	26690	2.55	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
731	13792	26728	17.02	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
731	13762	26728	17.02	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1112	14158		2.23	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1309	14345	27310	2.89	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1309	14345	27311	2.89	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1676	14708		1.76	1.0E-90	BE379884.1	EST_HUMAN	601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5'
1918	14942	27638	2.77	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila))-like (LOC57167), mRNA
2868	15928	28846	7.85	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3865	16904	29810	0.72	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3865	16904	29811	0.72	1.0E-90	AB020710.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL-1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
4453	17479	30387	1.17	1.0E-90	AF167340.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
5270	18277	31140	1.7	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
5270	18277	31141	1.7	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5758	18881	32031	1.76	1.0E-90	AB074533.1	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
5936	19022	32216	0.99	1.0E-90	11426910	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7276	20011	33313	0.67	1.0E-90	U91834.1	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7626	20489	33851	0.6	1.0E-90	6006002	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
7634	20876	34266	2.63	1.0E-90	11426758	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9173	22139	35565	3.96	1.0E-90	11422088	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9648	22592		1.08	1.0E-90	AF163884.1	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9670	22623	36075	1.38	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9670	22623	36076	1.38	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
10990	23910	37424	0.53	1.0E-90	X55545.1	NT	H. sapiens cDNA for CREB protein
10990	23910	37425	0.53	1.0E-90	X55545.1	NT	H. sapiens cDNA for CREB protein
11021	23986	37513	2.13	1.0E-90	R25888.1	EST_HUMAN	yg44d1.12 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:35477 5'
4224	17263	30140	6.09	8.0E-91	D12234.1	EST_HUMAN	HUIM000S381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8649	21617	35039	4.36	7.0E-91	11419234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
10983	23585	37083	0.87	7.0E-91	AB04151.1	EST_HUMAN	CM-BT043-090299-075 BT043 Homo sapiens cDNA
3488	16334	29459	1.71	5.0E-91	AA702794.1	EST_HUMAN	z90b04.s1 Scores_fetal_liver_infls_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4544	17567	30454	1.05	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4544	17567	30455	1.05	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
6770	19825	33108	1.19	5.0E-91	AB79995.1	EST_HUMAN	au49109.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW:ASPG_FLAME_Q47898 N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR:
8547	21515	34833	1.65	5.0E-91	BF314682.1	EST_HUMAN	G01801624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
9113	22079	35506	1.28	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
9113	22079	35507	1.28	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
12892	25479		2.28	5.0E-91	AI193586.1	EST_HUMAN	qe70111.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR_b2 MIR MIR repetitive element:
3215	16270	29192	1.41	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3215	16270	29193	1.41	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
11276	24228	37755	3.24	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12377	25159	31811	1.55	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12377	25159	31858	1.55	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
1621	14654	27630	5.97	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1621	14654	27631	5.97	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3350	16401	29323	1.76	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3476	16622	29445	3.84	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3476	16622	29446	3.84	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3802	16842	29750	1.47	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4821	17842	30530	4.36	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5016	18030	30915	1.3	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5016	18030	30916	1.3	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5770	18882	32041	1.43	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19.8kD) (HE1), mRNA
6437	18503		2.97	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6735	18791	33071	3.34	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6735	19791	33072	3.34	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7900	20843	34226	4.07	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7900	20843	34227	4.07	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8278	21247	34659	0.44	3.0E-91	6801589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9123	22089	36517	2.51	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9643	22587	36036	0.8	3.0E-91	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11235	24188	37707	2.53	3.0E-91	AB032179.2	NT	Homo sapiens EHM2 mRNA, complete cds
11536	24477	38026	2.3	3.0E-91	AB028003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11536	24477	38027	2.3	3.0E-91	AB028003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
12620	25314	31784	1.48	3.0E-91	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12950	18335	31174	3.88	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12950	18335	31175	3.88	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
60	13170	26078	2.39	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1250	14286	27252	7.11	1.0E-91	AW449746.1	EST_HUMAN	UJ-H-B13-aks-d-01-UJ.s1 NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2735280 3'
5487	18587	31498	0.73	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
7020	20146	33464	1.9	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
7020	20146	33466	1.9	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
8161	21099	34498	0.59	1.0E-91	M20463.1	NT	Human nucleus-encoded mitochondrial aldehyde dehydrogenase 2 (ALDH2) gene, exon 10
1246	14283	27246	6.04	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1246	14283	27247	6.04	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5538	18635	31576	2.94	9.0E-92	J03007.1	NT	Human Na ⁺ /K ⁺ ATPase alpha-subunit mRNA, partial cds
5688	18781	31953	2.18	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
6596	19856	32928	3.86	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
8180	21160	34569	0.47	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8190	21160	34570	0.47	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8717	21885	35112	1.73	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8717	21885	35113	1.73	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9629	22573	36023	1.69	9.0E-92	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
92	13208	28132	3.76	8.0E-92	W26367.1	EST_HUMAN	263 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
285	13380	26308	4.52	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
1838	14865	27893	1.08	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
1838	14865	27894	1.06	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6140	18149	31028	0.7	8.0E-92	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
6466	18568	31478	0.84	8.0E-92	AB046820.1	NT	TR:O60302 O60302 KIAA0555 PROTEIN. ;contains element MER22 repetitive element ; Homo sapiens mRNA for KIAA1600 protein, partial cds
5576	18672	31635	0.81	8.0E-92	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6697	19754	33031	1.19	8.0E-92	AJ000979.1	NT	Homo sapiens MOP-4 gene
6701	19758	33036	0.79	8.0E-92	AF179428.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
8164	21092	34491	1.16	8.0E-92	AF251025.2	NT	Homo sapiens double FYVE-containing protein 1 mRNA, complete cds
8428	21397	35155	0.56	8.0E-92	11418961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8768	21735	35155	3.52	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8768	21735	35156	3.52	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8869	21836	35258	0.66	8.0E-92	11426569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
9417	22382	35820	2.48	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10386	23308	36786	1.86	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
11155	24114	37640	3.34	8.0E-92	AF074393.1	NT	Homo sapiens nuclear ribogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11888	24654	38233	1.72	8.0E-92	4503340	NT	Homo sapiens dihydroilpoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
27	13147	26046	1.69	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
238	15836	26262	0.89	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
238	15836	26263	0.89	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
593	13660	27283	1.22	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Sepsase truncated isoform mRNA, complete cds
1285	14320	27283	1.14	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2197	15212	28230	3.62	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2197	15212	28231	3.62	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2570	15571	28591	1.27	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2735	15729	28743	2.96	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2763	15765	28776	1.31	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3356	18314	29327	0.97	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3356	18314	29328	0.97	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4617	17638	30528	1.44	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4617	17638	30529	1.44	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5040	18053	30832	0.91	7.0E-92	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5333	18439	31181	5.57	7.0E-92	AA446206.1	EST_HUMAN	z668d12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'
1591	14623		1.08	5.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606018 5'
9847	22783		0.42	5.0E-92	W27688.1	EST_HUMAN	36a7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
2776	15768	28788	2.03	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
5976	19091	32262	4.55	3.0E-92	AA378338.1	EST_HUMAN	EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
11116	24076	37599	5.32	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
11116	24076	37600	5.32	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
28	13148	26047	1.09	2.0E-92	4501898	NT	Homo sapiens actinin A receptor, type IIB (ACVR2B) mRNA
180	13280	26205	3.9	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D.J462023.2), mRNA
180	13280	26206	3.9	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D.J462023.2), mRNA
750	13811	28753	1.25	2.0E-92	BE259180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
750	13811	28754	1.25	2.0E-92	BE259180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1727	14767		1.4	2.0E-92	S78653.1	NT	mg-mae-related [human, Genomic, 2416 nt]
1953	14976	27976	1.73	2.0E-92	AB18119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1953	14976	27977	1.73	2.0E-92	AB18119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN;
2064	15082	28101	6.36	2.0E-92	4506860	NT	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2668	15665	28684	21.32	2.0E-92	5912457	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN;
3627	16670	29582	1.17	2.0E-92	AF231919.1	NT	Homo sapiens syndecan 4 (emphiglycan, ryudocan) (SDC4) mRNA
3627	16670	29583	1.17	2.0E-92	AF231919.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3698	16741	29654	5.32	2.0E-92	5803180	NT	Homo sapiens chromosome 21 unknown mRNA
4318	17347	30231	1.4	2.0E-92	M10976.1	NT	Homo sapiens chromosome 21 unknown mRNA
5029	18043		2.37	2.0E-92	AL040437.1	EST_HUMAN	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
5953	18944	32128	0.53	2.0E-92	AF016535.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6434	19500		13.83	2.0E-92	4504766	NT	DKFZp434C0414_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0414 5'
6768	19822	33104	2.24	2.0E-92	AB028891.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
7701	20659		0.81	2.0E-92	U67780.1	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
7730	20659		0.71	2.0E-92	U67780.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
9207	22173	35604	1.91	2.0E-92	AW340174.1	EST_HUMAN	Human NPY Y1-like receptor pseudogene mRNA, complete cds
							Human NPY Y1-like receptor pseudogene mRNA, complete cds
							hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:Q02711
							Q02711 PRO-POL-OUTPASE POLYPROTEIN;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11112	24072	37594	4.68	2.0E-92	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
11389	24335	37864	4.54	2.0E-92	5803103	NT	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
12716	25370	31773	3.75	2.0E-92	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12983	15685	28684	2.95	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1867	14892	27890	1.77	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1867	14892	27891	1.77	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2087	16104	28122	34.86	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8590	21558	34974	0.77	1.0E-92	BE439825.1	EST_HUMAN	HTM1-289F HTM1 Homo sapiens cDNA
9519	22482	35927	3.43	1.0E-92	AI380356.1	EST_HUMAN	Q1602.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element; contains element MER17 repetitive element;
9519	22482	35928	3.43	1.0E-92	AI380356.1	EST_HUMAN	Q1602.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element; contains element MER17 repetitive element;
2044	15063	28083	2.77	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2058	15077		11.43	9.0E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end similar to ribosomal protein L29
2655	15652		1.44	9.0E-93	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3628	16671	29584	1.44	9.0E-93	BE388571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
11959	24838		35.01	9.0E-93	11418528	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
6585	19645	32913	0.52	8.0E-93	AW014042.1	EST_HUMAN	UJ-H-B10-aah-h-06-0-UJ.st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6585	19645	32914	0.52	8.0E-93	AW014042.1	EST_HUMAN	UJ-H-B10-aah-h-06-0-UJ.st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6744	19799	33079	3.82	8.0E-93	BF036364.1	EST_HUMAN	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3868908 5'
248	13343	26268	9.15	7.0E-93	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3091	16149	29063	1.56	6.0E-93	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6086	19175	32391	0.59	6.0E-93	11450204	NT	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
6086	19175	32392	0.59	6.0E-93	11450204	NT	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
6838	19891	33186	0.99	6.0E-93	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7101	20035	33338	1.14	6.0E-93	AF085771.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
1381	14415	27385	3.77	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1406	14439	27408	4.78	5.0E-93	AI674184.1	EST_HUMAN	wc08c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'
1406	14439	27409	4.78	5.0E-93	AI674184.1	EST_HUMAN	wc08c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'
1471	14504		1.02	5.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3247	16302	29226	3.91	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
5897	18984	32175	0.9	5.0E-93	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
6230	19304		1.22	5.0E-93	AF045555.1	NT	Homo sapiens wbcscr1 (WBCSCR1) and wbcscr5 (WBCSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7982	20921	34312	3.32	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8952	21918	35343	0.56	5.0E-93	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8952	21918	35344	0.56	5.0E-93	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9981	22808	36373	2.06	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10168	23081	36569	1.33	5.0E-93	5032166	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10430	23352	36836	1.59	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
11174	24131	37681	2.48	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12627	25622	31677	2.56	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
13096	25622	31677	1.32	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
88	13204		7.06	4.0E-93	AA459933.1	EST_HUMAN	z50e09.s1 Soares, testis NHT Homo sapiens cDNA clone IMAGE:796588 3' similar to SW:CLPA_RAT
445	13518	28450	1.25	4.0E-93	4557879	NT	P37397 CALPONIN, ACIDIC ISOFORM ;
445	13518	26451	1.25	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
773	13832	26777	1.38	4.0E-93	7657454	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
773	13832	26778	1.38	4.0E-93	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1187	14227	27183	1.62	4.0E-93	8923658	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1994	15015	28022	4.21	4.0E-93	AF047677.1	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
2916	16613	28638	1.08	4.0E-93	7656972	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
3580	16625	29546	0.94	4.0E-93	7705396	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
4078	17113	30009	2.01	4.0E-93	4504654	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
6058	16625	29546	0.93	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5727	18821	32001	4.28	4.0E-93	T46864.1	EST_HUMAN	yb94c12.r1 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN ,
11468	24411	37950	13.22	4.0E-93	AV692051	EST_HUMAN	AV692051 GK Homo sapiens cDNA clone GKCDR07 5'
3665	16708	29622	9.21	3.0E-93	BF690830.1	EST_HUMAN	60224654F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332036 5'
3665	16708	29623	9.21	3.0E-93	BF690830.1	EST_HUMAN	60224654F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332036 5'
4283	17282		1.23	3.0E-93	AF226896.1	NT	Homo sapiens tensin mRNA, complete cds

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5881	18970	32181	0.56	3.0E-93	AI553853.1	EST_HUMAN	tr29g03.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169076 3'
5881	18970	32182	0.56	3.0E-93	AI553853.1	EST_HUMAN	tr29g03.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169076 3'
6715	19771	33051	1.55	3.0E-93	11426182	NT	Homo sapiens GON5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
11152	24112	37637	3.04	3.0E-93	AI824829.1	EST_HUMAN	wb02a05.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304489 3'
192	13293	26219	8.05	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
192	13293	26220	8.05	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
323	13415	26340	12.88	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
324	13415	26340	8.91	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2140	15157	28173	1.15	2.0E-93	U40763.1	NT	Human Ck1-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2494	15497	28523	2.03	2.0E-93	BE252082.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5491	18591	31502	5.04	2.0E-93	AW984385.1	EST_HUMAN	EST1376458 IMAGE resequences, MAGH Homo sapiens cDNA
5502	18602	31531	0.78	2.0E-93	4758153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5621	18717		0.63	2.0E-93	BF351459.1	EST_HUMAN	QV3-H10513-230300-126-H04 HT0513 Homo sapiens cDNA
5720	18814	31893	1.08	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
5734	18828	32006	0.7	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-86
6841	19894		1.06	2.0E-93	AW502002.1	EST_HUMAN	UI-PF-BN0-aks-g-09-0-UI17 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
12620	28251		3.14	2.0E-93	AA126735.1	EST_HUMAN	z29c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
12601	28303		2.69	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12853	25461		3.49	2.0E-93	BF036327.1	EST_HUMAN	601488531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
103	13219	26143	1.92	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
103	13219	26144	1.82	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
519	13690	26510	16.6	1.0E-93	7657076	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
602	13669	26583	5.09	1.0E-93	AI146755.1	EST_HUMAN	oy64b08.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384
873	13928	26987	4.11	1.0E-93	D87675.1	NT	ZINC FINGER PROTEIN ;
1241	14277	27237	8.85	1.0E-93	8923270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1241	14277	27238	8.85	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
2344	15354	28375	1.27	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HLEO1) mRNA, complete cds
2471	15475	28499	9.52	1.0E-93	AF055086.1	NT	Homo sapiens MHC class I region
2833	14334	27298	2.05	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3332965 5'
2833	14334	27297	2.05	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3332965 5'
2946	16003	28928	2.18	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3229	16284		1.3	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4480	17486	30373	1.99	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5846	18742	31907	1.66	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5646	18742	31808	1.66	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5859	18949	32135	1.02	1.0E-93	AF227198.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6022	19105	32308	10.93	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6321	19392	32633	0.91	1.0E-93	7662241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
6969	20184	33507	2.08	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7462	20428	33785	3.07	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8803	21571	34987	1.97	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8888	21854	35274	1.12	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEMD protein
8998	21962	35387	1.29	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9379	22344	35776	0.47	1.0E-93	AB023228.1	NT	Homo sapiens mRNA for KIAA1011 protein, partial cds
9379	22344	35776	0.47	1.0E-93	AB023228.1	NT	Homo sapiens mRNA for KIAA1011 protein, partial cds
9807	21130	34533	1.85	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9946	22873	36333	1.04	1.0E-93	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9946	22873	36333	4.08	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
10083	23010	36482	0.71	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
10504	23428	36924	0.63	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
12647	25405		2.11	1.0E-93	AJ230125.1	NT	Homo sapiens dyranodine receptor 3 (RYR3), mRNA
12763	25405		2.11	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12847	25457		3.14	1.0E-93	11417858	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
10956	23876		1.25	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3986	17026	28937	2.15	6.0E-94	AF142492.1	NT	Homo sapiens transcription enhancer factor-6 mRNA, complete cds
5441	18543	31454	3.23	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5441	18543	31455	3.23	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6166	19241	32472	3.08	5.0E-94	AA72434.1	EST_HUMAN	z887g06.s1 Soares_fetal_heart_Nb2H19W Homo sapiens cDNA clone IMAGE:409594 3'
7206	20230	33562	1.34	5.0E-94	A016800.1	EST_HUMAN	o833d05.s1 Soares_total_fetus_Nb2H19W Homo sapiens cDNA clone IMAGE:1623369 3'
8966	21952	35376	0.82	5.0E-94	BF528115.1	EST_HUMAN	602042163F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180023 5'
11318	24268	37795	2.81	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11318	24268	37796	2.81	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
12497	25965	31318	6.07	5.0E-94	T89398.1	EST_HUMAN	Yd88B04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:116239 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13048	25588		1.9	5.0E-04	9588724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
1859	14885		9.09	4.0E-04	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2698	15693	28682	1	4.0E-04	4505008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
4748	17768	30684	2.95	4.0E-04	AI591312.1	EST_HUMAN	tw11f10.x1 NCL CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2559403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE ;
6612	19670	32947	1.96	4.0E-04	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6612	19670	32948	1.96	4.0E-04	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7097	20031		0.99	4.0E-04	27388.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
11782	23937	37458	1.83	4.0E-04	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
613	13678	26694	2.23	3.0E-04	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
722	13784	28718	1.02	3.0E-04	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1754	14783	27767	1.12	3.0E-04	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1754	14783	27768	1.12	3.0E-04	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1787	14816	27801	4.2	3.0E-04	4557566	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
5764	18856	32037	3.32	3.0E-04	11490268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6274	19347	32579	0.99	3.0E-04	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6594	19654	32926	4.91	3.0E-04	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
8088	21024	34423	0.52	3.0E-04	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8540	21508	34925	1.03	3.0E-04	AF152309.1	NT	Homo sapiens probocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8934	21900	35327	4.93	3.0E-04	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
9950	22877	36340	4.37	3.0E-04	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
11438	24379	37919	3.76	3.0E-04	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
11987	24864	38460	2.17	3.0E-04	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
10110	23036	36514	0.66	2.0E-04	AI910393.1	EST_HUMAN	w30h11.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
10110	23036	36515	0.66	2.0E-04	AI910393.1	EST_HUMAN	w30h11.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
150	13253	26182	2.81	1.0E-04	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3105	16162	28073	2.24	1.0E-04	BE253433.1	EST_HUMAN	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3362559 5'
3105	16162	28074	2.24	1.0E-04	BE253433.1	EST_HUMAN	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3362559 5'
4386	17414	30299	1.18	1.0E-04	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6191	19265	32501	0.65	1.0E-04	AE000269.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6397	19465	32711	0.81	1.0E-04	AL040518.1	EST_HUMAN	DKFZp434G0314_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G0314 5'
6406	19474	32722	0.77	1.0E-04	H08270.1	EST_HUMAN	y87f02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:45053 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6683	19725	33000	0.56	1.0E-04	AV725992.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone H7CBEF05 5'
8450	21419	34833	0.56	1.0E-04	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8450	21419	34834	0.56	1.0E-04	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9611	22615	36087	2.57	1.0E-04	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
10146	23072	36547	1.93	1.0E-04	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872099 5'
11405	24349	37881	2.77	1.0E-04	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11646	24583	38151	1.94	1.0E-04	AI272244.1	EST_HUMAN	ep22a02.x1 Schiller oligodendroglioma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q62845
12050	24923	38520	3.39	1.0E-04	11418871	NT	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ;
12615	13253	26182	1.43	1.0E-04	BE295714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
12887	13263	26182	1.31	1.0E-04	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1473	14503	27480	1.3	9.0E-05	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3170	16225	29140	1.19	9.0E-05	7662027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3170	16225	29141	1.19	9.0E-05	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5479	18579	31489	1.38	9.0E-05	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5479	18579	31490	1.38	9.0E-05	X82569.1	NT	M.musculus glyt1 gene (exons 1c and 2)
8595	21563	34977	1.61	9.0E-05	AF274753.1	NT	M.musculus glyt1 gene (exons 1c and 2)
4567	17590	30482	1.82	8.0E-05	AI700998.1	EST_HUMAN	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4567	17590	30483	1.82	8.0E-05	AI700998.1	EST_HUMAN	we08e04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
7136	20112	33425	0.83	8.0E-05	11419376	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7452	20418	33773	1.55	8.0E-05	11426529	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7452	20418	33774	1.55	8.0E-05	11426529	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
8539	21507	34924	2.02	8.0E-05	AF032697.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
9720	22748	36199	1.97	8.0E-05	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
9720	22748	36200	1.97	8.0E-05	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
10207	23132	36619	2.67	8.0E-05	5174644	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
10238	23163	37008	3.08	8.0E-05	AB037816.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10595	23517	37008	0.8	8.0E-05	9845523	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
11813	24598	38279	2.21	8.0E-05	10864024	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
12820	25442		29.02	8.0E-05	AA629056.1	EST_HUMAN	Homo sapiens mRNA for KIAA1395 protein, partial cds
							Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
							Homo sapiens HGF-binding transcription factor Zhangfei (ZF), mRNA
							zu84d01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.1t L1
							repetitive element ;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
275	13371	28298	6.59	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
275	13371	28299	6.59	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4394	17422	30307	4.55	7.0E-95	M95708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4443	17469		1.26	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5090	18100	30976	1	7.0E-95	M95929.1	NT	Human homeobox protein (PHOX1) mRNA, 3' end
9572	22534	35985	0.82	4.0E-95	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
12013	24890	38487	1.93	4.0E-95	AW950834.1	EST_HUMAN	EST1382704 MAGC resequences, MAGA Homo sapiens cDNA
12013	24890	38488	1.93	4.0E-95	AW950834.1	EST_HUMAN	EST1382704 MAGC resequences, MAGA Homo sapiens cDNA
12065	24938	38534	1.79	4.0E-95	BF371302.1	EST_HUMAN	RC6-FN0114-090800-011-B07 FN0114 Homo sapiens cDNA
5517	18617	31560	1.61	3.0E-95	BF526041.1	EST_HUMAN	602071146F1 NCI_OGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'
5757	25644	32030	0.64	3.0E-95	4503354	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA
7593	20554	33913	1	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGC resequences, MAGC Homo sapiens cDNA
7593	20554	33914	1	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGC resequences, MAGC Homo sapiens cDNA
9710	22663	36119	1.75	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9710	22663	36120	1.75	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10104	23030	36508	0.69	3.0E-95	BF213446.1	EST_HUMAN	601845212F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070451 5'
1651	14683	27656	2.18	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1651	14683	27657	2.18	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1958	14980	27982	2.13	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1961	14983	27986	1.36	2.0E-95	BE393673.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658882 5'
2433	15440	28457	1.43	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2433	15440	28458	1.43	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2473	15477	28500	3.35	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2620	15523	28545	1.2	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
3171	16226	29142	2.48	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3577	16522	29542	2.93	2.0E-95	7706900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3577	16522	29543	2.93	2.0E-95	7706900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3631	16674	29587	0.93	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3763	16805	29716	1.09	2.0E-95	AI290264.1	EST_HUMAN	qin01c02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4
4368	17416	30300	1.69	2.0E-95	7667185	NT	CE03705; Homo sapiens hypothetical protein (HS322B1A), mRNA
5077	18087	30967	2.92	2.0E-95	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5557	18654	31598	4.36	2.0E-95	7705784	NT	Homo sapiens CGI-48 protein (LOC31098), mRNA
5557	18654	31599	4.36	2.0E-95	7705784	NT	Homo sapiens CGI-48 protein (LOC31098), mRNA
5782	18674	32055	1.22	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5782	18674	32056	1.22	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5827	18917	32101	0.87	2.0E-95	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6255	19338	32571	3.71	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6592	19652	32923	1.01	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6592	19652	32924	1.01	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6722	19778	33057	2.39	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9), mRNA, complete cds
6928	20152	33471	1.37	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9498	22462	35903	2.51	2.0E-95	11421785	NT	Homo sapiens ribophorin II (RPN2), mRNA
10747	23669	37166	0.54	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
11078	24040	37554	1.72	2.0E-95	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A), mRNA
12011	24888	38484	2.35	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12011	24888	38485	2.35	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12587	25291	31782	2.69	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12984	25546	31718	6.81	2.0E-95	11418184	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5698	18791	31962	7.21	1.0E-95	AA284651.1	EST_HUMAN	z23h04.r1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:714007 5' similar to
5698	18791	31963	7.21	1.0E-95	AA284651.1	EST_HUMAN	z23h04.r1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:714007 5' similar to
7757	20710	34079	4.21	1.0E-95	BF370000.1	EST_HUMAN	TR:G1067084 G1067084 F58H2.6 ;
7757	20710	34080	4.21	1.0E-95	BF370000.1	EST_HUMAN	z23h04.r1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:714007 5' similar to
8536	21504	34922	1.58	9.0E-96	BE897259.1	EST_HUMAN	TR:G1067084 G1067084 F58H2.6 ;
442	15840	26447	1.38	8.0E-96	BE907607.1	EST_HUMAN	TR:G1067084 G1067084 F58H2.6 ;
442	15840	26448	1.38	8.0E-96	BE907607.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
5593	16935	28448	2.28	8.0E-96	AW836047.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3929	16959	28682	1.06	7.0E-96	AF231820.1	NT	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3329	16380	26301	0.64	6.0E-96	AL163201.2	NT	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3494	16541	26465	16.12	6.0E-96	M26873.1	NT	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5'
5722	18816	31995	0.82	6.0E-96	11422842	NT	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
							601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
							PMO-LT0019-090300-002-409 LT0019 Homo sapiens cDNA
							Homo sapiens chromosome 21 unknown mRNA
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
							Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIA T6), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11872	24754	38335	2.59	6.0E-98	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11872	24754	38336	2.59	6.0E-98	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11918	24799	38390	2.78	6.0E-98	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
320	13412	28336	3.08	5.0E-98	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
843	13899	26855	3.47	5.0E-98	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
843	13899	26856	3.47	5.0E-98	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2626	16625	29013	1.23	5.0E-98	11416787	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
3039	16097	29013	0.71	5.0E-98	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
4940	17956		0.93	5.0E-98	X60812.1	NT	H. sapiens DNA for monoamine oxidase type A (7) (partial)
5233	18241	31113	0.93	5.0E-98	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
6807	19861	33148	1.15	5.0E-98	AF14973.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6870	19923	33219	0.5	5.0E-98	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
6949	20173	33496	4.02	5.0E-98	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6949	20173	33497	4.02	5.0E-98	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7219	20241	33576	0.78	5.0E-98	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7758	20711	34081	0.7	5.0E-98	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8443	21412	34825	6.11	5.0E-98	M88347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8443	21412	34826	6.11	5.0E-98	M88347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
12076	24948	38543	1.51	5.0E-98	7661973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4219	17248		7.1	3.0E-98	H68656.1	EST_HUMAN	yr87h12.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5'
415	13488		4.65	2.0E-98	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
748	13809	26750	1.12	2.0E-98	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4790	17808	30700	1.39	2.0E-98	BE148074.1	EST_HUMAN	RCS-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
7696	20654	34017	0.58	2.0E-98	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
7696	20654	34018	0.58	2.0E-98	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
9332	22297		6.83	2.0E-98	AV689461.1	EST_HUMAN	AV689461 GKO Homo sapiens cDNA clone GKCFCMD07 5'
12285	25102		3.08	2.0E-98	AW249440.1	EST_HUMAN	2818351.1 Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818351 5'
672	13736	26863	2.47	1.0E-98	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1796	14825	27809	2.35	1.0E-98	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1796	14825	27810	2.35	1.0E-98	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
2237	15251	28274	1.04	1.0E-98	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
2237	15251	28275	1.04	1.0E-98	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
7158	18390	31234	1.15	1.0E-98	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7250	19985	33283	0.55	1.0E-96	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8555	21523	34941	1.35	1.0E-96	7691803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8555	21523	34942	1.35	1.0E-96	7691803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
9066	22032	35455	24.51	1.0E-96	11418428	NT	Homo sapiens similar to actonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
9202	22168	35598	2.21	1.0E-96	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10520	23442	36939	0.91	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
10520	23442	36940	0.91	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
12272	18332	31169	1.59	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12272	18332	31170	1.59	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3338	18389	29310	0.65	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
7806	20756		3.82	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
9286	22252	35682	0.85	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
9286	22252	35683	0.85	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10959	23879	37391	0.71	6.0E-97	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
10959	23879	37392	0.71	6.0E-97	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
11734	24620	38198	3.43	6.0E-97	X15804.1	NT	Human mRNA for alpha-actinin
8348	21317	34732	2.27	6.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323_r1_434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434N0323 5'
8482	21450	34868	13.95	5.0E-97	AA118026.1	EST_HUMAN	z097e12.s1 Soares NIH-MPUs_S1 Homo sapiens cDNA clone IMAGE:767768 3' similar to TR:G1304125
10034	22981	36428	2.61	6.0E-97	BF154912.1	EST_HUMAN	G1304125 PMS4 MRNA ;
11873	24765	38337	1.75	5.0E-97	BE148597.1	EST_HUMAN	RCO-BT0812-250300-032-a09 BT0812 Homo sapiens cDNA
11873	24765	38338	1.75	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
938	13991	26943	2.4	4.0E-97	BE004438.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
948	14001	26953	1.87	4.0E-97	AB030176.1	NT	CNO-BN0106-170300-293-a08 BN0106 Homo sapiens cDNA
948	14001	26954	1.87	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
1925	14949	27845	0.99	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
5845	18741	31908	0.66	4.0E-97	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
5956	19041	32239	0.52	4.0E-97	4557326	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
5956	19041	32240	0.52	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (hNR2A) mRNA, complete cds
5956	19041	32240	0.52	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (hNR2A) mRNA, complete cds
6997	20123	33437	5.9	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
6997	20123	33438	5.9	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
7217	20239	33573	1.35	4.0E-97	7710125	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7270	20005	33305	0.94	4.0E-97	1142155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8474	21443	34860	0.98	4.0E-97	4557708	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8701	21669	36092	1.62	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8826	21892	35320	0.49	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
8967	21833	36358	0.78	4.0E-97	11423233	NT	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA
9603	22607	36056	1.36	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9603	22607	36057	1.36	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10803	23724	37226	0.79	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
11498	24441	37891	2.15	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11498	24441	37882	2.15	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
12467	25216	28266	7.99	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
243	13341	28266	1.01	3.0E-97	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
875	13931	26889	2.71	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
875	13931	26890	2.71	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1435	15868	27446	1.72	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2445	15825	28470	1.57	3.0E-97	U96255.1	NT	Human beta-prime-adaplin (BAM22) gene, exon 7
3185	16240	29158	2.22	3.0E-97	K02212.1	NT	Human alpha-1-antitrypsin gene (S variant), complete cds
3274	16328	29249	1.01	3.0E-97	5174478	NT	Homo sapiens pericentrioh (PCNT) mRNA
4815	17632	30730	18.16	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6587	19627	32892	2.5	1.0E-97	BE566486.1	EST_HUMAN	RCO-HT0258-211199-011-g05 HT0258 Homo sapiens cDNA clone IMAGE:3681821 5'
6789	21122	34525	0.51	1.0E-97	AW379978.1	EST_HUMAN	RCO-HT0258-211199-011-g05 HT0258 Homo sapiens cDNA
9789	21122	34528	0.51	1.0E-97	AW379978.1	EST_HUMAN	RCO-HT0258-211199-011-g05 HT0258 Homo sapiens cDNA
10122	23048	36527	1.46	1.0E-97	R10887.1	EST_HUMAN	y38c08.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:129134 3'
11062	24025	37649	3.07	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11062	24025	37650	3.07	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11639	24576	38142	1.67	1.0E-97	AA553761.1	EST_HUMAN	nk29g02.s1 NC1 CGAP_Cot1 Homo sapiens cDNA clone IMAGE:1014962 3'
11796	23951	37472	35.59	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11796	23951	37473	35.59	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
902	13957	26914	1.43	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1281	14316	27278	2.02	9.0E-98	8930392	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6435	19501		0.63	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
7507	20472	33832	0.55	9.0E-98	7561871	NT	Homo sapiens leucyl-RNA synthetase, mitochondrial (KIAA0028), mRNA
7617	20577	33940	0.56	9.0E-98	11419408	NT	Homo sapiens A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), mRNA
8257	21226	34636	5.5	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8257	21226	34637	5.5	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8471	22435	35873	2.01	9.0E-98	X09889.1	NT	Human mRNA for amyloid A4(751) protein
9579	22541	35991	1.44	9.0E-98	11321560	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9847	22591	36040	1.49	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9894	22847		0.83	9.0E-98	AF057728.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9722	22750	36202	1.16	9.0E-98	4507070	NT	Homo sapiens SWI/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9722	22750	36203	1.16	9.0E-98	4507070	NT	Homo sapiens SWI/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10623	23545	37045	0.5	9.0E-98	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
11346	24286	37823	2.06	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11346	24286	37824	2.06	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11407	24351	37883	1.75	9.0E-98	11418982	NT	Homo sapiens mitogen-activated protein kinase kinase 7 (MAP3K7), mRNA
26	13146		2.24	8.0E-98	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1562	14594	27568	1.49	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1562	14594	27569	1.49	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1739	14769	27764	2.73	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1739	14769	27765	2.73	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3607	16652	29569	0.97	8.0E-98	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
3607	16652	29570	0.97	8.0E-98	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
3808	16849	29757	6.45	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
6201	19275	32509	2.74	5.0E-98	BE885873.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908097 5'
2188	15203	28223	1.23	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3,4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2816	15814	28639	1.19	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2759	15751		3.63	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7131	20107	33418	0.7	3.0E-98	9956946	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7134	20110	33422	1.63	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7134	20110	33423	1.63	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
9104	22070	35496	3.59	3.0E-98	H46998.1	EST_HUMAN	y917g09.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9652	22595	36043	0.65	3.0E-98	8922096	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10243	23168	36855	1.51	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
10243	23168	36856	1.51	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
10839	23759	37259	0.89	3.0E-08	BE900454.1	EST_HUMAN	601673686F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
11299	24249	37775	2.09	3.0E-08	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
12951	25835		1.4	3.0E-08	BE382519.1	EST_HUMAN	601297955F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628213 5'
13039	25581		2.4	3.0E-08	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
737	13798	26737	0.94	2.0E-08	BE261694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2092	15109	28128	3.36	2.0E-08	BE294281.1	EST_HUMAN	601172558F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2247	15261	28288	1.49	2.0E-08	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4325	17354	30240	0.75	2.0E-08	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4368	17395	30274	2.9	2.0E-08	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4864	17881	30767	1.22	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4864	17881	30768	1.22	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5450	18552	31484	4.26	2.0E-08	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6811	19865	33153	1.09	2.0E-08	4505798	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7885	20829	34208	1.08	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7885	20829	34207	1.08	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8955	21921	35347	3.8	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8955	21921	35348	3.8	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
9039	22005	35425	0.57	2.0E-08	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9039	22005	35426	0.57	2.0E-08	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9895	22848	36305	2.7	2.0E-08	X12684.1	NT	H sapiens arginase gene exon 3 (EC 3.5.3.1)
10778	23699		1.25	2.0E-08	7705968	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
11942	24922	38418	1.58	2.0E-08	AF273048.1	NT	Homo sapiens CTCL tumor antigen s620-9 mRNA, complete cds
405	13478	26413	23.04	1.0E-08	AI862007.1	EST_HUMAN	U36504.X1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN
455	13528	26458	2.12	1.0E-08	AW998611.1	EST_HUMAN	P29316 60S RIBOSOMAL PROTEIN L23A.1
1813	14840	27831	13.58	1.0E-08	N49818.1	EST_HUMAN	PMO-BN0085-100300-001-c08 BN0085 Homo sapiens cDNA
5390	18493	31370	3.54	1.0E-08	AA195854.1	EST_HUMAN	y23705.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2435585 5' similar to
5849	18745	31912	1.07	1.0E-08	BE390627.1	EST_HUMAN	PIR:S54204 S54204 ribosomal protein L29 - human ;
5849	18745	31913	1.07	1.0E-08	BE390627.1	EST_HUMAN	z99809.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G808562
							G808562 NEBULIN.1
							601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606992 5'
							601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606992 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
9350	22315	35740	5.28	1.0E-98	AF141349.1	Homo sapiens beta-tubulin mRNA, complete cds
9350	22315	35741	5.28	1.0E-98	AF141349.1	Homo sapiens beta-tubulin mRNA, complete cds
5917	19003	32195	0.84	9.0E-99	AI805004.1	QV-BT073-191298-012 BT073 Homo sapiens cDNA
5917	19003	32196	0.84	9.0E-99	AI905004.1	QV-BT073-191298-012 BT073 Homo sapiens cDNA
6158	19233	32455	3.77	9.0E-99	AW96635.1	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
11458	24399	37946	3.71	9.0E-99	AI479829.1	tm69h07.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
11458	24399	37947	3.71	9.0E-99	AI479829.1	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11460	24403	37951	2.19	9.0E-99	BF359879.1	tm69h07.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
11743	24628	38207	1.84	9.0E-99	AA134604.1	PM2-MT0037-250700-003-G04 MT0037 Homo sapiens cDNA
9078	22044	35487	1.18	8.0E-99	8635487	zn90402.1 Stratiogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to
5933	19019	32214	9.72	7.0E-99	AF035908.1	TR.G662994 G662994 GPI-ANCHORED PROTEIN P137 ;
11793	24814	38410	1.99	7.0E-99	AF001886.1	Human endogenous retrovirus, complete genome
472	13544	26473	0.84	6.0E-99	U10991.1	Homo sapiens oscillin (hLn) gene, exon 5
4779	17799	30690	0.97	6.0E-99	4502660	Homo sapiens G2 protein mRNA, partial cds
6752	19808	33087	0.96	6.0E-99	7706136	Homo sapiens CD34 antigen (CD34) mRNA
6835	19888	33182	0.81	6.0E-99	L43610.1	Homo sapiens GAP-like protein (LOC51306), mRNA
6835	19888	33183	0.81	6.0E-99	L43610.1	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8441	21410	34823	1.06	6.0E-99	X99101.1	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8460	21429	34846	0.52	6.0E-99	6601589	H sapiens mRNA for estrogen receptor
9117	22083	35511	2.24	6.0E-99	AB036429.1	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9215	22181	35612	3.79	6.0E-99	AF080255.1	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
9215	22181	35613	3.79	6.0E-99	AF080255.1	Homo sapiens fadester protein mRNA, complete cds
9275	22241	35669	0.64	6.0E-99	11431994	Homo sapiens fadester protein mRNA, complete cds
9275	22241	35670	0.64	6.0E-99	11431994	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
11074	24036	37560	3.32	6.0E-99	11526269	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
11763	23938	37459	1.98	6.0E-99	9910279	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
11763	23938	37460	1.98	6.0E-99	9910279	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
1982	15003	28006	1.37	5.0E-99	Y11365.1	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
4596	17617	30511	1.46	5.0E-99	AF009660.1	H sapiens IMPA gene, exon 8
12496	25238		5.2	5.0E-99	BE890177.1	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8694	21632		5.74	3.0E-99	M95586.1	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
						Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1244	14281		16.34	2.0E-99	AW274792.1	EST_HUMAN	xp0906x1 NCL_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3272	16326	29248	1.19	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4574	17598	30480	1.85	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7936	20878	34268	0.67	2.0E-99	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
9055	22021	35446	12.17	2.0E-99	W23507.1	EST_HUMAN	2b46d06.r1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
9507	22470	35914	0.65	2.0E-99	R78254.1	EST_HUMAN	y81b09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145825 5'
11440	24383	37923	2.66	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
315	13407	26333	1.5	1.0E-99	AF114487.1	NT	Homo sapiens intersecin long isoform (ITSN) mRNA, complete cds
379	13463	26393	1.04	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1419	14452	27426	1.98	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1559	14591	27593	1.52	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1559	14591	27593	1.52	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1944	14968	27966	1.18	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1944	14968	27966	1.18	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3101	16158	29070	1.6	1.0E-99	J03171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-R) mRNA, complete cds
4407	17435	30320	2.26	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4407	17435	30321	2.26	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5836	18926	32110	0.59	1.0E-99	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
6976	20199	33528	1.77	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6976	20199	33529	1.77	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7346	25680	33682	0.61	1.0E-99	X98022.1	NT	H sapiens EG-AP gene exon 2
9554	22516		0.86	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
9878	22831	36285	1.99	1.0E-99	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN;
11473	24416	37965	1.89	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11473	24416	37966	1.89	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11705	24670	38247	2.17	1.0E-99	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12253	25078						Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	13123	26021	1.83	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	13123	26021	1.19	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
69	13187	26105	1.3	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
69	13187	26106	1.3	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
87	13203	26128	0.67	1.0E-100	AW275237.1	EST_HUMAN	xv78b11.x1 NCL_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3'
170	13272	26197	2.52	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
317	13409	26335	0.98	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
343	13432	26354	2.53	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Striatagene (cat933206) Homo sapiens cDNA clone HFBGCR32
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
437	13511		2.36	1.0E-100	AF003528.1	NT	G.gorilla DNA for ZNF80 gene homolog
490	13553		4.8	1.0E-100	X89631.1	NT	RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA
510	13581	26502	1.4	1.0E-100	BE180609.1	EST_HUMAN	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1021	14067	27017	4.33	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1021	14067	27018	4.33	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1549	14582		1.23	1.0E-100	AW207555.1	EST_HUMAN	UI-H-B11-afk-c-07-4-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
							q62009.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COT1A P81061 CYSTATIN 1
1554	14586	27558	1.49	1.0E-100	AI200857.1	EST_HUMAN	Homo sapiens mRNA for KIAA1168 protein, partial cds
1881	14906	27808	0.98	1.0E-100	AB032994.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2254	15268		1.25	1.0E-100	D83349.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
2717	15711	28728	1.98	1.0E-100	11418976	NT	Homo sapiens RGH2 gene, retrovirus-like element
3031	16089		3.1	1.0E-100	D11078.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4238	17267	30154	1.46	1.0E-100	AF057354.1	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
4294	17293	30172	1.94	1.0E-100	4503792	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5127	18136	31012	3.58	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5127	18136	31013	3.58	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5362	18467	31338	1.71	1.0E-100	BF244218.1	EST_HUMAN	601863164F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4080969 5'
							xa8201.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN);
5586	18692	31650	0.66	1.0E-100	AW075983.1	EST_HUMAN	AI118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5785	18877	32059	1.5	1.0E-100	AU118182.1	EST_HUMAN	Homo sapiens NF-E2-related factor 3 gene, complete cds
5839	18929	32113	1.29	1.0E-100	AF135118.1	NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
5937	19023	32217	0.9	1.0E-100	X14690.1	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6287	18359	32595	0.89	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6287	18359	32596	0.89	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6576	19636		1.1	1.0E-100	5729867	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6645	19703	32979	4.85	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6704	19760	33039	0.61	1.0E-100	AU113690.1	EST_HUMAN	AU136800 PLACE1 Homo sapiens cDNA clone PLACE1005099 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6843	19898	33180	1.35	1.0E-100	R10887.1	EST_HUMAN	y38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
6834	20158	33478	1.08	1.0E-100	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7019	20145	33482	0.96	1.0E-100	AA496841.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
7019	20145	33463	0.96	1.0E-100	AA496841.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
7070	20092	33401	1.12	1.0E-100	BF376478.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
7070	20092	33402	1.12	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
7078	20099	33410	6.82	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-505 TN0048 Homo sapiens cDNA
7990	20929	34323	0.52	1.0E-100	U63139.1	NT	MR1-TN0046-060900-004-505 TN0048 Homo sapiens cDNA
7990	20929	34324	0.52	1.0E-100	U63139.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8877	21844	35286	11.88	1.0E-100	BF103853.1	EST_HUMAN	Homo sapiens Rad50 (Rad50) mRNA, complete cds
8914	21880		5.3	1.0E-100	AL163203.2	NT	Homo sapiens Rad50 (Rad50) mRNA, complete cds
9368	22333	35763	0.59	1.0E-100	AU116951.1	EST_HUMAN	6016473577.1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
9368	22333	35764	0.59	1.0E-100	AU116951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9588	22550	36001	3.34	1.0E-100	AB040918.1	NT	Homo sapiens HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9588	22550	36001	3.34	1.0E-100	AB040918.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9588	22550	36001	3.34	1.0E-100	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9665	22822		2.44	1.0E-100	A1872388.1	EST_HUMAN	wr37g09.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2489820 3' similar to contains element
9788	21111	34511	2.04	1.0E-100	AW998611.1	EST_HUMAN	MER22 repetitive element ;
9842	22778		1.06	1.0E-100	AU127720.1	EST_HUMAN	PMO-BN0085-100300-001-c06 BN0085 Homo sapiens cDNA
9842	22778		1.06	1.0E-100	AU127720.1	EST_HUMAN	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9942	22868	36331	2.29	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1628 protein, partial cds
9942	22868	36332	2.29	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1628 protein, partial cds
10203	23128	36614	1.47	1.0E-100	AW630487.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2969396 5'
10203	23128	36615	1.47	1.0E-100	AW630487.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2969396 5'
10364	23287	36764	0.46	1.0E-100	AV732101.1	EST_HUMAN	AV732101 HTF Homo sapiens cDNA clone HTFBIG01 5'
10366	23756	37256	1.94	1.0E-100	BF347619.1	EST_HUMAN	602020554F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156165 5'
10924	23844		1.56	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
11111	24071	37593	7.51	1.0E-100	BF327292.1	EST_HUMAN	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
11618	24556	38118	1.78	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
11618	24556	38119	1.78	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
11681	24647	38223	3.57	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11681	24647	38224	3.57	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11712	13123	26021	1.96	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11989	24866		2	1.0E-100	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12127	24998	38600	3.03	1.0E-100	AJ131034.1	NT	Homo sapiens case gene, exon 12
12128	24997	38601	1.65	1.0E-100	BE791491.1	EST_HUMAN	601586031F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940423 5'
12177	25025	38622	15.03	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12307	25851		2.32	1.0E-100	BF446549.1	EST_HUMAN	7488103.X1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to TR:Q21997 Q21997 COSMID R151. [2] TR:Q9UA08
12488	25293	31799	2.58	1.0E-100	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
13084	25815	31691	8.6	1.0E-100	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
78	13195	26118	1.19	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
78	13195	26119	1.19	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
687	13750	26876	2.63	1.0E-101	AB007815.2	NT	Homo sapiens mRNA for KIAA0448 protein, partial cds
705	13767	26702	6.85	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
705	13767	26703	6.85	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
772	13831	26776	1.48	1.0E-101	7657454	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
854	13910	26868	2.88	1.0E-101	4503914	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
924	13977	26929	1.22	1.0E-101	Z20653.1	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
987	14038	26994	7.23	1.0E-101	BF681218.1	EST_HUMAN	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
1055	14101	27051	0.78	1.0E-101	A1221678.1	EST_HUMAN	Homo sapiens of cardiac alpha-myosin heavy chain gene
1586	14619	27594	1.34	1.0E-101	5921460	NT	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287281 5'
1586	14619	27595	1.34	1.0E-101	5921460	NT	gg99a09.x1 Searles_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1761	14790	27776	1.12	1.0E-101	7662183	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1761	14790	27777	1.12	1.0E-101	7662183	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1982	14984	27987	1.58	1.0E-101	4502998	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
2072	15089	28107	1.07	1.0E-101	BE843070.1	EST_HUMAN	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
2367	15891	28387	1.17	1.0E-101	5729892	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2622	15821	28646	5.3	1.0E-101	X72993.1	NT	RC3-ST0281-160600-016-H09 ST0281 Homo sapiens cDNA
2753	15745	28763	2.07	1.0E-101	AJ237744.1	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2753	15745	28764	2.07	1.0E-101	AJ237744.1	NT	H sapiens EWS gene, exon 5
2967	16025		13.42	1.0E-101	AJ252312.1	NT	H sapiens RIBIR gene (partial), exon 12
3216	16271	29194	1.69	1.0E-101	4886270	NT	H sapiens RIBIR gene (partial), exon 12
3255	16309		2.48	1.0E-101	BF035327.1	EST_HUMAN	Homo sapiens genomic downstream Rhesus box
3392	16441	29367	1.73	1.0E-101	AW965556.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3411	15745	28763	2.03	1.0E-101	AJ237744.1	NT	601458531F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3862088 5'
							EST377629 MAGI Homo sapiens cDNA
							Homo sapiens RIBIR gene (partial), exon 12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3411	15745	28784	2.03	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3890	16930	29839	4.58	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5072	18082	30983	1.54	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5072	18082	30984	1.54	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5391	18494	31371	2.08	1.0E-101	AW965139.1	EST_HUMAN	EST377212 MAGC resequences, MAGI Homo sapiens cDNA
6118	19196	32420	3.59	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6118	19196	32421	3.59	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6853	19806	33202	1.16	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7488	20453		1.18	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7542	20505	33863	4.82	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7542	20505	33864	4.82	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7717	20674	34040	7.39	1.0E-101	AW008475.1	EST_HUMAN	ww5812.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7828	20774		1.76	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5'
7993	20932	34327	6.3	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-F12 BT0313 Homo sapiens cDNA
8245	21214	34621	1.07	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
8245	21214	34622	1.07	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
8390	21359	34766	5.11	1.0E-101	BF029174.1	EST_HUMAN	601764886F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3968837 5'
8665	21633	35053	0.83	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8665	21633	35054	0.83	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9364	22329	35758	0.93	1.0E-101	AA036800.1	EST_HUMAN	zk29g08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471998 5' similar to PIR:S54640 S54640 YD9335.03c protein - yeast ;
9855	22638	36094	0.82	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9855	22638	36095	0.82	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9817	21139	34544	19.42	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9817	21139	34545	19.42	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9830	22879	36135	18.13	1.0E-101	9845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
10115	23041	36520	13.91	1.0E-101	BE610667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10115	23041	36521	13.91	1.0E-101	BE610667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10254	23179	36866	0.61	1.0E-101	10853960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10773	23694	37192	1.68	1.0E-101	11429127	NT	Homo sapiens Janus Kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10807	23728	37229	0.56	1.0E-101	AJ570293.1	EST_HUMAN	kb77d11.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10807	23728	37230	0.56	1.0E-101	A1570293.1	EST_HUMAN	bø77d1.1.x1 NCI_QGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10914	23834	37349	0.64	1.0E-101	BE673648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10914	23834	37350	0.64	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
11225	24178	37705	2.38	1.0E-101	S38327.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 9]
12083	24955	38550	162.1	1.0E-101	AA321316.1	EST_HUMAN	EST23763 Bone marrow Homo sapiens cDNA 5' end similar to defensin 1
12735	28387		7.64	1.0E-101	AW939051.1	EST_HUMAN	QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
41	13161	26064	0.73	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pk4K230) mRNA, complete cds
341	19430	26351	5.2	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
776	13835	26781	1.07	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1119	14163	27114	1.9	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete proviral segment
1273	14308	27268	2.27	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1273	14308	27269	2.27	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1417	14450	27423	200.41	1.0E-102	BE408447.1	EST_HUMAN	601239982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629801 5'
2318	15329	28352	1.36	1.0E-102	A1124669.1	EST_HUMAN	sm60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95; ;
2318	15329	28353	1.36	1.0E-102	A1124669.1	EST_HUMAN	sm60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95; ;
3037	18095		0.73	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3078	16135	28047	1.48	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3150	16207	29120	3.24	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3150	16207	29121	3.24	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4260	17289	30170	1.83	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4441	17467	30368	1.95	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343982 5'
5157	18167	31045	1	1.0E-102	R68488.1	EST_HUMAN	y32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
5445	18547	31460	1.52	1.0E-102	AF087133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5842	18932		3.3	1.0E-102	AB034951.1	NT	Homo sapiens HSCS4 mRNA for heat shock cognate protein 54, complete cds
5882	18971	32163	3.45	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5882	18971	32164	3.45	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5889	18977	32169	0.98	1.0E-102	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6425	19492	32744	2.74	1.0E-102	A459825.1	EST_HUMAN	air82f09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52; ;
7293	20016	33310	0.5	1.0E-102	AW451643.1	EST_HUMAN	UHH-BI3-all-q-10-Q-UJ.s1 NCI_QGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736635 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7343	20314	33656	0.75	1.0E-102	BE789323.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7371	20341	33683	0.77	1.0E-102	BE386105.1	EST_HUMAN	601272721F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818243 5'
7494	20459	33818	0.54	1.0E-102	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7578	20540	33899	8.85	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7886	20830	34208	2.64	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5'
8168	21106	34505	0.58	1.0E-102	10947053	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8565	21533	34953	3.61	1.0E-102	BE763051.1	EST_HUMAN	QV2.NT0025-210600-236-H08 NT0025 Homo sapiens cDNA
8645	21613	35035	0.91	1.0E-102	BE910555.1	EST_HUMAN	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903145 5'
8839	21806	35223	1.22	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKO Homo sapiens cDNA clone GKCEEE11 5'
8839	21806	35224	1.22	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKO Homo sapiens cDNA clone GKCEEE11 5'
8950	21916	35340	0.74	1.0E-102	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9283	22249	35679	0.73	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9283	22249	35680	0.73	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9606	22610	36062	0.56	1.0E-102	AJ762859.1	EST_HUMAN	wf63b06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2397971 3' similar to contains MER4.1
9636	22580	36030	0.89	1.0E-102	AV755842.1	EST_HUMAN	MER4 MER4 repetitive element;
9676	22629	36082	2.15	1.0E-102	T70393.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD06 5'
9678	22629	36083	2.15	1.0E-102	T70393.1	EST_HUMAN	y413d07.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:67021 5'
9766	22707	36163	3.86	1.0E-102	AU124629.1	EST_HUMAN	y413d07.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:67021 5'
10748	23670		0.71	1.0E-102	AF153715.1	NT	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
10798	23719	37221	0.43	1.0E-102	11425430	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10798	23719	37222	0.43	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA
10835	23755	37254	3	1.0E-102	AJ905037.1	EST_HUMAN	Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA
10835	23755	37255	3	1.0E-102	AJ905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10896	23816	37323	1.15	1.0E-102	AA970786.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
11410	24354	37887	2.36	1.0E-102	4507822	NT	on57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1660823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2, [1];
11410	24354	37888	2.36	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11732	24618	38195	2.7	1.0E-102	BF359243.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
12019	24896	38494	4.74	1.0E-102	U41302.1	NT	RC8-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
12079	24951	38546	5.67	1.0E-102	U57053.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
12182	25030		2.49	1.0E-102	AL163280.2	NT	Human unconventional myosin-ID (MYO1F) gene, partial cds
12727	26380	31748	4.15	1.0E-102	AW300862.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13028	25576		1.59	1.0E-102	J05235.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
70	13188	26107	1.14	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
70	13188	26108	1.14	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
100	13216	26140	9.55	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
209	13310	26237	1.02	1.0E-103	5453793	NT	Homo sapiens nuclear protein (KKE/D repeat) (NOP56) mRNA
982	14033	26985	1.02	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1248	14284	27250	16.75	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1600	14632	27608	2.39	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1992	15013	28018	1.4	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1992	15013	28019	1.4	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2313	15925	28348	0.93	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE1 Homo sapiens cDNA clone PLAGE1000965 5'
2457	15461	28484	1.66	1.0E-103	AF060598.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2601	15601	28622	1.07	1.0E-103	BF529379.1	EST_HUMAN	602041882F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179429 5'
2601	15601	28623	1.07	1.0E-103	BF529379.1	EST_HUMAN	602041882F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179429 5'
2627	15626	28650	1.01	1.0E-103	N32770.1	EST_HUMAN	yw91d08.s1 Soares placenta_8bc9weeks_2NblHP8tc9W Homo sapiens cDNA clone IMAGE:259599 3'
3082	16139		2.5	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3391	16440	28366	4.42	1.0E-103	AW288245.1	EST_HUMAN	UI-H-BW0-ajh-h-11-0-UJ.s1 NCI_CGAP_Sub65 Homo sapiens cDNA clone IMAGE:2733165 3'
3453	16499	28416	1.29	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3767	16809		5.31	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3808	16848	28756	1.28	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element;
3841	16881	29785	3.18	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4029	17067	29668	2.9	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
4858	17875	30763	0.83	1.0E-103	BE900203.1	EST_HUMAN	601673135F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955953 5'
6044	19126	32332	0.98	1.0E-103	BF569527.1	EST_HUMAN	602180023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
6052	19133	32342	1.67	1.0E-103	AF179995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6398	19466	32712	0.73	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6398	19466	32713	0.73	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6602	19661	32933	0.79	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6602	19661	32934	0.79	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6847	19705	32981	0.53	1.0E-103	10947051	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 1, mRNA
6746	25667	33081	1.28	1.0E-103	AA781442.1	EST_HUMAN	q28603.s1 Soares testis_NHT Homo sapiens cDNA clone 1391452 3'
6787	19842	33125	0.98	1.0E-103	AF053460.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6879	19931	33229	1.47	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6879	19931	33230	1.47	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
7024	18356	31275	1.73	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS239, DXS288, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7024	18356	31276	1.73	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS239, DXS288, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7161	18393	31237	1.62	1.0E-103	11431100	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7234	20255	33589	1.06	1.0E-103	AJ269880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
7437	20404	33758	2.58	1.0E-103	AW665776.1	EST_HUMAN	EST377849 IMAGE:3888545 5'
7556	20519	33874	3.47	1.0E-103	BE748158.1	EST_HUMAN	601571637F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3888545 5'
8051	20988	34384	3.69	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
8051	20988	34385	3.69	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
8632	21600	35022	0.43	1.0E-103	T31080.1	EST_HUMAN	EST27193 Human Brain Homo sapiens cDNA 5' end similar to None
8668	21934	35359	0.92	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8668	21934	35360	0.82	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
9051	22017	35441	1.06	1.0E-103	BF109244.1	EST_HUMAN	716e03.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525984 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
9463	22427	35865	2.86	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9463	22427	35866	2.86	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9503	22467	35908	1.13	1.0E-103	AA581086.1	EST_HUMAN	nd13x02.st NCI_CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
9544	22507	35956	0.48	1.0E-103	AA774980.1	EST_HUMAN	ae84412.st Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970871 3' similar to gb:X03747 cds1 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);
10418	23340	36826	1.28	1.0E-103	Z37876.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10459	23381	36874	1.81	1.0E-103	AW563676.1	EST_HUMAN	EST376749 IMAGE:3888545 5'
10598	23520	37012	10.03	1.0E-103	AI876856.1	EST_HUMAN	au51q04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:O15046 KIAA0338 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11004	23970	37494	1.64	1.0E-103	BE549708.1	EST_HUMAN	7b4103.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
11085	24048	37568	3.99	1.0E-103	AT92759.1	EST_HUMAN	002a06.y6 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING;
11183	24139	37672	1.99	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11183	24139	37673	1.99	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11341	24291		1.48	1.0E-103	BE671418.1	EST_HUMAN	7e50708.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3285927 3' similar to gb:J05272 INOSINE-5-MONOPHOSPHATE DEHYDROGENASE 1 (HUMAN);
11570	24509	38068	6	1.0E-103	BE885279.1	EST_HUMAN	601506347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908147 5'
11702	24667	38244	2.59	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
11774	23929	37450	7.57	1.0E-103	IL43810.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11980	24857		1.47	1.0E-103	AB024759.1	NT	Homo sapiens TSA305 gene, exon 16
12047	24920	38516	2.25	1.0E-103	BE644611.1	EST_HUMAN	7e68a10.x1 Soares NSF_F8 gw OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.13 MER29 repetitive element;
12178	25026		1.88	1.0E-103	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12208	25049		1.95	1.0E-103	11526201	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12410	25183	31820	4.32	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
238	13336	26260	1.65	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 584 (synonym: hfb2) Homo sapiens cDNA clone DKFZp564H1072 5'
238	13336	26261	1.65	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZp564H1072 5'
1805	14929	27625	1.86	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2203	15218	28238	2.52	1.0E-104	AA132875.1	EST_HUMAN	za22c06.s1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14116.ma1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2214	15228	28251	2.87	1.0E-104	BE744628.1	EST_HUMAN	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928438 5'
2377	15385	28408	1.02	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-2144f12 CT0249 Homo sapiens cDNA
2377	15385	28409	1.02	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-2144f12 CT0249 Homo sapiens cDNA
2444	15450	28469	2.43	1.0E-104	6031670	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2882	15941	28858	7.18	1.0E-104	MS4671.1	NT	Human lymphocytic antigen CD59/MEI43 mRNA, complete cds
2927	15985		2.84	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3277	16331	29252	0.94	1.0E-104	AU133926.1	EST_HUMAN	AU133926 OVARC1 Homo sapiens cDNA clone OVARC1000936 5'
3402	16451		1.88	1.0E-104	AA319436.1	EST_HUMAN	EST12658 Adrenal gland tumor Homo sapiens cDNA 5' and
3615	16659	29577	0.9	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3615	16659	29578	0.9	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3963	17003	29917	0.94	1.0E-104	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4166	17187	30076	0.86	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4404	17432	30317	4.11	1.0E-104	X02781.1	NT	Human mRNA for fibronectin (FN precursor)
4639	17660	30547	1.44	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4639	17660	30548	1.44	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5255	18263	31132	1.02	1.0E-104	4835570	NT	Homo sapiens novel centrosomal protein RanBPM (RANBPM), mRNA
5292	18297	31158	0.93	1.0E-104	AF202314.1	NT	Homo sapiens erythropoietin (EPO) gene, exons 4 and 5 and complete cds
5292	18297	31159	0.93	1.0E-104	AF202314.1	NT	Homo sapiens erythropoietin (EPO) gene, exons 4 and 5 and complete cds
6050	19131	32338	1.44	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6050	19131	32339	1.44	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6100	19179	32398	0.89	1.0E-104	AB017332.1	NT	Homo sapiens alk3 mRNA for Aurora/p11-related kinase 3, complete cds
6611	19669	32945	24.48	1.0E-104	A1768797.1	EST_HUMAN	wj03b12.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
6611	19669	32946	24.48	1.0E-104	A1768797.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6805	19859	33146	0.92	1.0E-104	7706512	NT	wj03b12.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
6973	20196	33523	1.53	1.0E-104	BE314182.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6973	20196	33524	1.53	1.0E-104	BE314182.1	EST_HUMAN	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
7435	20402	33796	2.14	1.0E-104	11425572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
8944	21910	35335	0.74	1.0E-104	BF509244.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
9522	22485	35932	3.58	1.0E-104	BF448230.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9618	22562	36010	0.63	1.0E-104	AA882308.1	EST_HUMAN	U1-H-B14-80w-b-08-q-U1.s1 NCI CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3086178 3'
9639	22583		1.21	1.0E-104	T74219.1	EST_HUMAN	hnd16g11.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9669	22622	36073	4.58	1.0E-104	AF081395.1	NT	z198505.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9669	22622	36074	4.58	1.0E-104	AF091395.1	NT	yc83f02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22440 5'
9798	21119	34520	4.97	1.0E-104	BF352841.1	EST_HUMAN	Homo sapiens Trio isoform mRNA, complete cds
9798	21119	34521	4.97	1.0E-104	BF352841.1	EST_HUMAN	Homo sapiens Trio isoform mRNA, complete cds
10111	23037	36516	0.68	1.0E-104	AW103848.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
10111	23037	36517	0.68	1.0E-104	AW103848.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
10307	23231	36714	0.62	1.0E-104	AF113514.1	NT	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
10463	23375	36867	3.35	1.0E-104	BE791713.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
10463	23375	36868	3.35	1.0E-104	BE791713.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
10765	23686	37182	1.36	1.0E-104	AV728070.1	EST_HUMAN	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10808	23729	37231	5.11	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
10917	23837	37353	4.5	1.0E-104	U66535.1	NT	Human beta4-integrin (ITGB4) gene, exon 19,20,21,22,23,24 and 25
10931	23851		0.82	1.0E-104	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11629	24587	38129	3.09	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-509 HT0885 Homo sapiens cDNA
11629	24587	38130	3.09	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-509 HT0885 Homo sapiens cDNA
11656	24592	38165	3.48	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
12888	25548		1.43	1.0E-104	BE393802.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658678 5'
278	15810	26302	1.61	1.0E-105	4602168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
425	13120	26018	9.28	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
596	13663	26576	3.89	1.0E-105	AF032887.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
596	13663	26577	3.89	1.0E-105	AF032887.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1689	14720		2.33	1.0E-105	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1837	14864	27862	1.47	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1943	14987	27964	2.09	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2199	15214	28234	2	1.0E-105	AA318390.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit
2731	15725		1.07	1.0E-105	AA584808.1	EST_HUMAN	not0405.e1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
3018	16076		3.14	1.0E-105	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3362	16412	29336	1.11	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3362	16412	29337	1.11	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4125	17158	30046	3.14	1.0E-105	AW961688.1	EST_HUMAN	EST373761 MAGG Homo sapiens cDNA
4773	17793	30684	0.69	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3850156 5'
4773	17793	30685	0.69	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3850156 5'
4793	17810	30702	1.65	1.0E-105	AA699335.1	EST_HUMAN	z44g02.e1 Soares_fetal_liver_spleen_TNFRS_S1 Homo sapiens cDNA clone IMAGE:433682 3'
4976	17991		4.04	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5147	18156	31036	1.21	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
5403	18506	31383	0.7	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5471	18572		1.02	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7089	20023	33324	1.57	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7089	20023	33325	1.57	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7174	18405	31203	3.49	1.0E-105	11419198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7174	18405	31204	3.49	1.0E-105	11419198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7223	20245	33579	0.56	1.0E-105	AW951634.1	EST_HUMAN	EST363689 MAGG Homo sapiens cDNA
7501	20466	33827	0.89	1.0E-105	BE902616.1	EST_HUMAN	601677279F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980019 5'

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8192	21182	34572	1.09	1.0E-105	X12556.1	NT	Human mRNA for dcl proto-oncogene
8362	21331	34743	6.09	1.0E-105	T05097.1	EST_HUMAN	EST02975 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBGR32
8741	21709	35132	1.52	1.0E-105	AW007194.1	EST_HUMAN	ws60c10.x1 NCL_CGAP_Brim25 Homo sapiens cDNA clone IMAGE:2500626 3' similar to
9280	22246	35676	0.75	1.0E-105	AW840817.1	EST_HUMAN	SW/ACSA_PENCH_P86333 ACETYL-COENZYME A SYNTHETASE ;
9405	22370	35805	3.19	1.0E-105	AW016879.1	EST_HUMAN	RC1-CN0009-070100-011-e05 CN0008 Homo sapiens cDNA
9558	22520	35968	0.91	1.0E-105	AW882372.1	EST_HUMAN	UI-H-B10p-abb-b-12-UJI.s1 NCL_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9558	22520	35969	0.91	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d08 OT0062 Homo sapiens cDNA
9928	22810	36282	0.76	1.0E-105	BE867793.1	EST_HUMAN	QV2-OT0062-140300-083-d08 OT0062 Homo sapiens cDNA
9928	22810	36263	0.76	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11278	24229	37756	4.59	1.0E-105	AF254822.1	NT	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11564	24504	38081	1.61	1.0E-105	D63548.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11611	24549	38109	2.93	1.0E-105	7705936	NT	Homo sapiens COL4A6 gene for $\alpha 6$ (IV) collagen, exon 31
11914	24795	38386	2.81	1.0E-105	AW027554.1	EST_HUMAN	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11984	24861	38457	2.56	1.0E-105	BF430821.1	EST_HUMAN	ww7407.x1 Soares_thymus_NHFT Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
12104	24975	38572	1.5	1.0E-105	AB004924.1	NT	P87892 PROTEASE ;
12104	24975	38573	1.5	1.0E-105	AB004924.1	NT	7018c10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P97680 P97680
152	13255		1.76	1.0E-106	AW503208.1	EST_HUMAN	RIN1. ;
206	13307	26235	1.59	1.0E-106	AI565065.1	EST_HUMAN	Homo sapiens gene for Smad 3, exon 2 and 3
543	13614	26534	2.23	1.0E-106	AW985656.1	EST_HUMAN	Homo sapiens gene for Smad 3, exon 2 and 3
607	13674	26589	3.07	1.0E-106	J00146.1	NT	UI-HF-BND-ak-g-07-0-UJI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
608	13674	26589	1.71	1.0E-106	J00146.1	NT	ig79c01.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'
1712	14742	27726	4.6	1.0E-106	U48724.1	NT	EST377629 MAGC resequences, MAGI Homo sapiens cDNA
1732	14762	27746	1.01	1.0E-106	U04510.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1820	14847	27839	4.27	1.0E-106	AA527446.1	EST_HUMAN	Human dihydrofolate reductase pseudogene (psi-hd1)
1820	14847	27840	4.27	1.0E-106	AA527446.1	EST_HUMAN	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
2132	15149	28164	1.52	1.0E-106	BE144286.1	EST_HUMAN	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
2325	16336	28359	3.99	1.0E-106	4504184	NT	ng41c05.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937952 3' similar to contains element
2542	15545	28530	1.07	1.0E-106	AF003528.1	NT	LTR3 repetitive element ;
2542	15545	28530	1.07	1.0E-106	AF003528.1	NT	LTR3 repetitive element ;
2542	15545	28530	1.07	1.0E-106	AF003528.1	NT	ng41c05.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937952 3' similar to contains element
2542	15545	28530	1.07	1.0E-106	AF003528.1	NT	LTR3 repetitive element ;
2542	15545	28530	1.07	1.0E-106	AF003528.1	NT	LTR3 repetitive element ;
2542	15545	28530	1.07	1.0E-106	AF003528.1	NT	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2542	15545	28530	1.07	1.0E-106	AF003528.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2542	15545	28530	1.07	1.0E-106	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2610	15809	28633	1.79	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2768	15760	28782	4.05	1.0E-106	A1276526.1	EST_HUMAN	q16h10.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2836	14481	27437	1.13	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2836	14481	27438	1.13	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2886	15945	28860	0.99	1.0E-106	BE384266.1	EST_HUMAN	601272675F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2952	16009	28934	4.42	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2952	16009	28935	4.42	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3196	18250	29188	1.72	1.0E-106	8922865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3195	18250	29189	1.72	1.0E-106	8922865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3454	16500	29417	1	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3454	16500	29418	1	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4068	17104	29996	7.68	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4068	17104	29997	7.68	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4631	17652	30539	0.73	1.0E-106	BE144266.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
4634	17950	30841	0.92	1.0E-106	U31520.1	NT	Human alpha mannosidase II mRNA, complete cds
6289	18284		0.96	1.0E-106	L41644.1	NT	Homo sapiens dystrophin gene, exon 41
5443	18545	31457	2.52	1.0E-106	AA781155.1	EST_HUMAN	aj24b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN);
5954	19039	32236	0.82	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5954	19039	32237	0.82	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6009	19092	32282	0.56	1.0E-106	AA434168.1	EST_HUMAN	zw28d12.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:7706153'
6108	19187	32406	0.78	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6108	19187	32407	0.78	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6221	19295	32529	18	1.0E-106	BF076574.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295067 5'
6332	19402	32643	0.68	1.0E-106	BE897112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6536	19402	32643	0.62	1.0E-106	BE897112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6559	19618	32884	17.32	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6559	19619	32885	17.32	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
7598	20557	33917	5.25	1.0E-106	AA663779.1	EST_HUMAN	ae72607.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7655	20615	33979	5.04	1.0E-106	11429617	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
7746	20700	34066	1.17	1.0E-106	BE292722.1	EST_HUMAN	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
7869	20813	34190	8.48	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7869	20813	34191	8.48	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8119	21066	34463	0.63	1.0E-106	AU116850.1	EST_HUMAN	AU116850 HEMBA1 Homo sapiens cDNA clone HEMBA1000129 5'
8317	21286	34689	5.05	1.0E-106	BE741408.1	EST_HUMAN	6015949331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8317	21286	34700	5.05	1.0E-106	BE741408.1	EST_HUMAN	6015949331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8515	21483	34897	108.87	1.0E-106	AI523088.1	EST_HUMAN	ar68a07.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233
8976	21942	35366	0.76	1.0E-106	BE387950.1	EST_HUMAN	CALGRANULIN B (HUMAN);
8976	21942	35367	0.76	1.0E-106	BE387950.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9054	22020	35445	3.3	1.0E-106	AI654123.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9060	22026	35449	0.53	1.0E-106	AI991109.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9407	22372	35807	0.87	1.0E-106	AW838831.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9502	22466	35906	2.47	1.0E-106	AA825307.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9502	22466	35907	2.47	1.0E-106	AA825307.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9641	22585	36034	1.55	1.0E-106	AI750447.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9784	22725	36181	1.81	1.0E-106	AI479569.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9784	22725	36182	1.81	1.0E-106	AI479569.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10391	23284	36781	1.22	1.0E-106	BE389234.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10444	23366	36856	0.92	1.0E-106	BF027310.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10444	23366	36857	0.92	1.0E-106	BF027310.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10601	23523	37017	5.46	1.0E-106	AA604417.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10601	23523	37018	5.46	1.0E-106	AA604417.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10648	23570	37066	1.58	1.0E-106	AW383299.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10653	23575	37071	0.5	1.0E-106	11436432	NT	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10653	23575	37072	0.5	1.0E-106	11436432	NT	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10827	23748	37249	0.49	1.0E-106	AL039886.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10944	23864	37379	3.52	1.0E-106	AL163202.2	NT	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
11242	24195	37713	4.84	1.0E-106	BF032755.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
11242	24195	37714	4.84	1.0E-106	BF032755.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
11402	24346	37879	2.78	1.0E-106	J05200.1	NT	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
11402	24346	37880	2.78	1.0E-106	J05200.1	NT	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11736	24822	38200	3.21	1.0E-108	BE257385.1	EST_HUMAN	607108219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349987 5'
12250	25763		8.02	1.0E-106	AW410405.1	EST_HUMAN	fr05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961644 5'
12481	25229	31798	3.58	1.0E-106	BE894488.1	EST_HUMAN	6071433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12481	25229	31797	3.58	1.0E-106	BE894488.1	EST_HUMAN	6071433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12687	25354		4.46	1.0E-103	BE685905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
237	13337		4.26	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
264	13360		1.85	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
631	13696	26616	3.39	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
814	13872	26820	2.77	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
887	13842	26800	1.31	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
970	14022	26975	12.86	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1283	14318	27251	1.8	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1573	14606	27579	3.93	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1767	14706	27781	2.54	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1867	14883	27879	0.86	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1857	14883	27880	0.96	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2218	15232	28256	1.11	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2370	15378	28401	1.02	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2370	15378	28402	1.02	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2540	15542	28566	1.12	1.0E-107	BE732450.1	EST_HUMAN	6071567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2540	15542	28567	1.12	1.0E-107	BE732450.1	EST_HUMAN	6071567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
3019	16077	28997	3.8	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3019	16077	28998	3.8	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3116	16173	29083	3.16	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3839	16879	29782	4.78	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5706	18601	31978	0.56	1.0E-107	AW968038.1	EST_HUMAN	EST361116 MAGE resequences, MAGE Homo sapiens cDNA
5985	19050	32251	3.4	1.0E-107	BE867469.1	EST_HUMAN	607144258F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845494 5'
6975	20188	33527	0.56	1.0E-107	6005708	NT	Homo sapiens A kinase (PKA) anchor protein 10 (AKAP10), mRNA
7107	20041	33343	0.83	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1), mRNA
7107	20041	33344	0.83	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1), mRNA
7588	20549	33909	1.16	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BND-alf-c-08-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7588	20549	33910	1.16	1.0E-107	AW503913.1	EST_HUMAN	U1HF-BN0-ah-e-04-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7773	20726	34098	1.54	1.0E-107	AI765078.1	EST_HUMAN	wh56h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
8004	20943	34336	0.81	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
8004	20943	34337	0.81	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
8078	21015	34415	0.59	1.0E-107	AW410961.1	EST_HUMAN	fh09d11.x2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2964524 5'
9742	22770	36225	1	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
11061	24024	37548	2.92	1.0E-107	AI392850.1	EST_HUMAN	ig10d03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1 P05095 ALPHA-ACTININ 3, NON MUSCULAR
11293	24243	37770	1.92	1.0E-107	L49141.1	NT	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11308	24258	37784	2.09	1.0E-107	BF66511.1	EST_HUMAN	602123963F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11651	24588	38158	4.76	1.0E-107	BE540550.1	EST_HUMAN	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11721	23918	37435	2.44	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11721	23918	37436	2.44	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
12321	25902		5.18	1.0E-107	AA001415.1	EST_HUMAN	ze45601.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361844 3' similar to contains THR.b1 THR repetitive element;
12345	25759		1.48	1.0E-107	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
956	14009	26862	1.66	1.0E-108	BE296042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1270	14305	27265	4.69	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
2091	15108	28127	1.24	1.0E-108	BF026728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2435	15442	28460	9.44	1.0E-108	BE206694.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J06277 Mouse hexokinase mRNA, complete cds (MOUSE);
3360	16410	29332	0.79	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3360	16410	29333	0.79	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4184	17215	30102	1.13	1.0E-108	AW664438.1	EST_HUMAN	h112a11.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3BP-1;
4555	17578	30468	1.73	1.0E-108	U72951.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4555	17578	30469	1.73	1.0E-108	U72951.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4842	17859	30754	1.39	1.0E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4956	17971	30862	0.98	1.0E-108	AW504789.1	EST_HUMAN	U1HF-BN0-ah-e-04-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5'
4986	18001	30890	2.59	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5184	18193	31068	0.71	1.0E-108	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
6556	18653	31597	1.1	1.0E-108	AW384094.1	EST_HUMAN	RCO-HT0372-241199-031-d03 HT0372 Homo sapiens cDNA
5605	18701	31673	2.27	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5605	18701	31674	2.27	1.0E-108	BE69016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
6036	18119		0.8	1.0E-108	AF012623.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6117	19195	32419	0.92	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6262	19335	32567	6.27	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6262	19335	32568	6.27	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6392	19460	32706	1.22	1.0E-108	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6494	19195	32419	0.99	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6773	19828	33110	0.67	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6773	19828	33111	0.67	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7365	20335	33685	5.42	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR9B), mRNA
7673	20631	33995	1.98	1.0E-108	4758333	NT	Homo sapiens delta-8 fatty acid desaturase (FADS2) mRNA
7718	20875	34041	1.13	1.0E-108	BE252607.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3364094 5'
7749	20702	34069	0.68	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4181037 5'
7749	20702	34070	0.68	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4181037 5'
8149	21086	34485	0.57	1.0E-108	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8398	21368		1.8	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8452	21421	34835	5.44	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMO-ads-e-12-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8452	21421	34836	5.44	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMO-ads-e-12-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
9402	22367	35800	0.93	1.0E-108	AF203977.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
9441	22405	35842	0.48	1.0E-108	N44974.1	EST_HUMAN	yy35h10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773 A45773 kelch protein, long form - fruit fly;
10983	23903	37417	2.67	1.0E-108	11428155	NT	Homo sapiens similar to high-mobility group (nonthistone chromosomal) protein 4 (H4, sapiens) (LOC63446), mRNA
11027	21040	34439	2.14	1.0E-108	BE535227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
11177	18353	31298	1.64	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
11602	24540	38099	3.33	1.0E-108	AW566185.1	EST_HUMAN	EST378258 MAGE for Golgi-associated microtubule-binding protein (GMAP-210)
11653	24590	38160	1.75	1.0E-108	AV708780.1	EST_HUMAN	AV708780 ADC Homo sapiens cDNA clone ADCAEE03 5'
11653	24590	38161	1.75	1.0E-108	AV708780.1	EST_HUMAN	AV708780 ADC Homo sapiens cDNA clone ADCAEE03 5'
11698	24663		2.05	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11757	24695	38265	1.6	1.0E-108	D63539.1	NT	Homo sapiens COL4A6 gene for $\alpha 6(V)$ collagen, exon 23

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12493	25236	31800	5.14	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12864	25467		11.97	1.0E-108	BF346356.1	EST_HUMAN	602018571F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4164297 5'
44	13164	26067	2.17	1.0E-109	AW803116.1	EST_HUMAN	IL2-JM0077-260400-079-D08 UM0077 Homo sapiens cDNA
67	13185	26104	6.88	1.0E-109	D88974.1	NT	Human mRNA for KIAA0220 gene, partial cds
220	13320	26245	1.51	1.0E-108		NT	Homo sapiens hypohelical protein FLJ11316 (FLJ11316), mRNA
229	13328	26251	1.97	1.0E-109	11422486	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
467	13540	26465	2.2	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
600	13667	26581	13.45	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
600	13667	26582	13.46	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1014	14062	27203	0.98	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1207	14246	27204	23.68	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1208	14246	27204	21.33	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1644	14577	27549	1.2	1.0E-109	BE293673.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1544	14577	27550	1.2	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1891	14916	27911	1.63	1.0E-109	D13643.2	NT	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
2253	15267	28294	2.68	1.0E-109	AL163284.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2262	15276	28300	2.59	1.0E-109	Y11723.1	NT	Homo sapiens chromosome 21 segment HS21C084
2630	15629	28654	3.42	1.0E-109	A1022328.1	EST_HUMAN	Homo sapiens SNF5/INI1 gene, exon 6
2630	15629	28655	3.42	1.0E-109	A1022328.1	EST_HUMAN	ow95a01.x1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 O02197 CIRCULATING CATHODIC ANTIGEN.;
2631	15630	28656	1.84	1.0E-108	4504206	NT	ow95a01.x1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 O02197 CIRCULATING CATHODIC ANTIGEN.;
3071	16128	29040	1.81	1.0E-109	N86190.1	EST_HUMAN	Homo sapiens guanylate cyclase activator 1A (retina) (GUCY1A) mRNA
3399	18448	28374	1.33	1.0E-109	AW893192.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3399	18448	28375	1.33	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA
3530	16976	29499	1.66	1.0E-109	AF240598.1	NT	CM3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA
3572	16617	29538	0.92	1.0E-109	M37928.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3572	16617	29539	0.92	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3556	16996		2.3	1.0E-109	BE146144.1	EST_HUMAN	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
4171	17202	30089	4.97	1.0E-109	A1655417.1	EST_HUMAN	MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
4189	17220	30107	1.33	1.0E-109	AA662274.1	EST_HUMAN	ts8a06.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP.F53A2.8 CE18100;
							nu83c12.s1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218282 3' similar to SW.GTT2_HUMAN
							P30712 GLUTATHIONE S-TRANSFERASE THETA 2;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4189	17220	30108	1.33	1.0E-109	AA62274.1	EST_HUMAN	nu93c12.s1 NCI_CGAP_P222 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN
4432	17459	30350	2.38	1.0E-109	4504208	NT	P30712 GLUTATHIONE S-TRANSFERASE THETA 2;
4630	17651	30538	1.42	1.0E-109	7662083	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4968	17973	30864	0.94	1.0E-109	R15400.1	EST_HUMAN	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5318	18424	31227	0.5	1.0E-109	AU137282.1	EST_HUMAN	ya48e06.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:53057 5'
5332	18438	31190	0.86	1.0E-109	BF673718.1	EST_HUMAN	AU137282 PLACE1 Homo sapiens cDNA clone PLACE1006189 5'
5386	18489	31384	2.28	1.0E-109	5174822	NT	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272822 5'
5688	18783		1.49	1.0E-109	BE178356.1	EST_HUMAN	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6037	25651	32323	0.83	1.0E-109	BF379688.1	EST_HUMAN	RC1-HT0615-200400-022-404 HT0615 Homo sapiens cDNA
6111	18783		1.29	1.0E-109	BE178356.1	EST_HUMAN	CM1-UT0038-060900-390-107 UT0038 Homo sapiens cDNA
6485	19550	32798	0.57	1.0E-109	M23442.1	NT	RC1-HT0615-200400-022-404 HT0615 Homo sapiens cDNA
6485	19550	32800	0.57	1.0E-109	M23442.1	NT	Human Interleukin 4 (IL-4) gene, complete cds
6742	19797	33077	8.68	1.0E-109	A1221385.1	EST_HUMAN	Human Interleukin 4 (IL-4) gene, complete cds
6933	20157	33476	0.52	1.0E-109	11024711	NT	qg86f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
6933	20157	33477	0.52	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7145	18377	31285	0.49	1.0E-109	BE074988.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7451	20417	33772	0.93	1.0E-109	AB046811.1	NT	RC5-BT0580-170300-021-F08 BT0580 Homo sapiens cDNA
7815	20764	34140	3.31	1.0E-109	11432574	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7817	20766	34142	5.45	1.0E-109	BF182707.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8513	21481	34895	1.37	1.0E-109	AL049784.1	NT	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8628	21598	35017	1.08	1.0E-109	AW749130.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
9004	21970		3.59	1.0E-109	AA077498.1	EST_HUMAN	Novel human gene mapping to chromosome 13
9086	22052	35474	17.25	1.0E-109	BE787540.1	EST_HUMAN	PMO-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
9086	22052	35475	17.25	1.0E-109	BE787540.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
9583	22585	36005	1.78	1.0E-109	H84860.1	EST_HUMAN	601478417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9705	22658	36113	0.65	1.0E-109	BE397068.1	EST_HUMAN	601478417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9705	22658	36114	0.65	1.0E-109	BE397068.1	EST_HUMAN	ya90g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491
9839	22775	36230	2.5	1.0E-109	F06804.1	EST_HUMAN	A53491 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER - SP:INV;
11128	24088	37616	2.42	1.0E-109	BE540909.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
11128	24088	37617	2.42	1.0E-109	BE540909.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
11158	24116	37642	31.85	1.0E-109	BF694831.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
							601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
							602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11459	24402	37650	1.65	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
11697	24662	38240	2.82	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11735	24621	38199	5.45	1.0E-109	W16510.1	EST_HUMAN	z08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat; hh23f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2953969 3' similar to TR:Q9Z124 Q9Z124
11910	24781	38380	1.59	1.0E-109	BE045560.1	EST_HUMAN	YGR163W MRNA HOMOLOGUE, COMPLETE CDS. ;
12125	24994	38597	2.03	1.0E-109	BF339540.1	EST_HUMAN	602039003F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186753 5'
12125	24994	38598	2.03	1.0E-109	BF339540.1	EST_HUMAN	602039003F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186753 5'
12132	25001	38607	1.65	1.0E-109	AA490558.1	EST_HUMAN	aa4207.r1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:823621 5'
12395	15276	28300	2.1	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12613	15276	28300	2.24	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12720	25374	31774	1.85	1.0E-109	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3	13124	26022	0.89	1.0E-110	7549804	NT	Homo sapiens deiodinase, liothyronine, type II (DIO2), transcript variant 2, mRNA
39	13159	26061	4.69	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
39	13159	26062	4.69	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
109	13124	26022	1.73	1.0E-110	7549804	NT	Homo sapiens deiodinase, liothyronine, type II (DIO2), transcript variant 2, mRNA
294	13388	26316	1.6	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
528	13599	26517	13.41	1.0E-110	U94550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1184	14225	27181	1	1.0E-110	5031620	NT	Homo sapiens calcitriol receptor-like (CALCRL) mRNA
1284	14319	27282	0.72	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1837	14961	27658	1.35	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2073	15090		1.85	1.0E-110	BF508896.1	EST_HUMAN	UIH-B14-aos-b-05-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2853	15913		1.05	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3043	14319	27282	0.89	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3103	16160		1.01	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3209	16284	29185	1.65	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3209	16284	29186	1.55	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4231	17260	30145	0.93	1.0E-110	MT5918.1	NT	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene
4665	17686	30570	2.11	1.0E-110	AI017213.1	EST_HUMAN	ou32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827963 3' similar to SW:NI21 RAT P62591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4684	17705	30597	4.29	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5009	18023		1.94	1.0E-110	7562441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5367	18472	31343	2.23	1.0E-110	BE299408.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5814	18904	32087	0.78	1.0E-110	BE621069.1	EST_HUMAN	601493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'
5834	18924	32108	7.66	1.0E-110	11418323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5834	18924	32108	7.66	1.0E-110	11418323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6878	25670	33228	3.64	1.0E-110	M55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7235	20256	33590	0.59	1.0E-110	BE251496.1	EST_HUMAN	601109398F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
7309	20280	33619	0.71	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7309	20280	33620	0.71	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7545	20508	33867	0.69	1.0E-110	A160289.1	EST_HUMAN	tn12408.x1 NC1_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2187407 3' similar to SW:ETV1_HUMAN
7656	20616	33980	10.79	1.0E-110	AV714276.1	EST_HUMAN	P50549 ETS TRANSLOCATION VARIANT 1;
7656	20616	33981	10.79	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7688	20646	34010	2.84	1.0E-110	AB020675.1	NT	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7820	20769	34145	1.01	1.0E-110	AU137923.1	EST_HUMAN	Homo sapiens mRNA for KIAA0868 protein, partial cds
9690	22843	36101	0.79	1.0E-110	BE302594.1	EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
9936	22863	36324	3.25	1.0E-110	AW838394.1	EST_HUMAN	ba8870.1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905651 5' similar to TR:O77258 O77258
10886	23608	37102	3.4	1.0E-110	Y12337.1	NT	EG:114D9.2 PROTEIN.;
11099	24059	37583	2.78	1.0E-110	Y12337.1	NT	QV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
11314	24284	37791	3.18	1.0E-110	BE734357.1	EST_HUMAN	Homo sapiens galactokinase 2 (GALK2), mRNA
11314	24284	37792	3.18	1.0E-110	BE734357.1	EST_HUMAN	H. sapiens mRNA for myotonic dystrophy protein kinase like protein
11770	23925	37445	2.49	1.0E-110	AA448528.1	EST_HUMAN	601566804F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
12210	25051		5.81	1.0E-110	BE897218.1	EST_HUMAN	601566804F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
12339	25137		9.66	1.0E-110	AW062258.1	EST_HUMAN	zw67g02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781288 5' similar to TR:G1145816
12579	25288		1.72	1.0E-110	AB011399.1	NT	G1145816 FKBP54;
12706	25913		2.05	1.0E-110	BF364546.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12987	15090		1.34	1.0E-110	BF508896.1	EST_HUMAN	IL0-BT0163-040869-094-g10 BT0163 Homo sapiens cDNA
176	13277		12.39	1.0E-111	U43701.1	NT	Homo sapiens gene for AF-6, complete cds
736	13797		3.39	1.0E-111	BF036327.1	EST_HUMAN	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA
745	13808	26746	5.88	1.0E-111	8393092	NT	UI-H-B14-acc-b-05-0-J1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
927	13980	26934	3.63	1.0E-111	M25142.1	NT	Human ribosomal protein L23a mRNA, complete cds
2250	18264	28290	1.53	1.0E-111	AF036126.1	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
4357	17384	30266	4.65	1.0E-111	K02288.1	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
5293	18298	31160	0.72	1.0E-111	AB033356.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
							Homo sapiens collagen type IX alpha 1 chain (COL9A1) gene, exons 29, 30, 31, and 32
							Human enkephalin B (enkeB) gene, exon 4 and 3' flank end complete cds
							Homo sapiens mRNA for neuroxin I-alpha protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5553	18650	31593	0.66	1.0E-111	AA151017.1	EST_HUMAN	z47b07.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5553	18650	31594	0.66	1.0E-111	AA151017.1	EST_HUMAN	z47b07.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5714	18808	31986	0.89	1.0E-111	BE867909.1	EST_HUMAN	601443690F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847655 5'
5837	18927	32111	0.49	1.0E-111	U19969.1	NT	Human two-handed zinc finger protein ZEB mRNA, partial cds
6148	19223	32453	1.5	1.0E-111	A1344679.1	EST_HUMAN	qp09g12.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN);
6837	18690	33185	0.95	1.0E-111	AL040762.1	EST_HUMAN	DKFZp434C1815_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434C1815 5'
6978	20201	33531	1.3	1.0E-111	AW294648.1	EST_HUMAN	U1H.BW0-ail-4-03-0-J1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729525 3'
7405	20373	33724	0.52	1.0E-111	AW693165.1	EST_HUMAN	RC2-BN0033-160200-013-b05 BN0033 Homo sapiens cDNA
7690	20638	34000	2.57	1.0E-111	BF366228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
7772	20725	34097	0.51	1.0E-111	9981253	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant A, mRNA
7779	20732	34104	0.58	1.0E-111	A1761228.1	EST_HUMAN	w168d01.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIIA5 (HUMAN);
7873	20817	34195	0.8	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8067	21004	34402	1.52	1.0E-111	AA133914.1	EST_HUMAN	zn62c12.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:562774 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8431	21400	34812	0.82	1.0E-111	AA278898.1	EST_HUMAN	zs79g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. ;
8431	21400	34813	0.82	1.0E-111	AA278898.1	EST_HUMAN	zs79g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. ;
8630	21498	34914	0.55	1.0E-111	U66533.1	NT	Homo sapiens protein x0001 (LOC51185), mRNA
8593	21551	34969	3.24	1.0E-111	U66533.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
9027	21893	35413	0.77	1.0E-111	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
9128	22094	35522	0.83	1.0E-111	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9160	22126	35632	28.95	1.0E-111	BF214902.1	EST_HUMAN	601847132F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
9236	22202	35632	15.22	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9236	22202	35633	15.22	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9443	22407	35944	2.88	1.0E-111	AF091395.1	NT	Homo sapiens T10 isoform mRNA, complete cds
9672	22625	36079	0.48	1.0E-111	BF333210.1	EST_HUMAN	QV2-BT0817-270900-398-e06 BT0817 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10512	23434	36932	1.98	1.0E-111	AA504160.1	EST_HUMAN	aa5802.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235
10540	23482		1.69	1.0E-111	D10083.1	NT	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10635	23587	37057	6.39	1.0E-111	AA131248.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
11110	24070	37592	3.4	1.0E-111	AA296467.1	EST_HUMAN	z31601.r1 Scarses_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
11288	24238		2.64	1.0E-111	AW374340.1	EST_HUMAN	UI-H-BW0-aig-q-07-Q-UJ.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730276 3'
11383	24330	37859	2.98	1.0E-111	U68159.1	NT	IL0-CT0031-221099-113-406 CT0031 Homo sapiens cDNA
12168	25018	38618	4.77	1.0E-111	11417901	NT	Human thrombospondin receptor (MPL) gene, exons 1,2,3,4,5 and 6
12955	18298	31160	1.75	1.0E-111	AB035356.1	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
610	13875	26590	0.9	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
612	13877	26592	5.51	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (SAR) gene, exon 5
612	13877	26593	5.51	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (SAR) gene, exon 5
633	13698	26618	1.91	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-aot-g-04-Q-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
633	13698	26619	1.91	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-aot-g-04-Q-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1003	14034	27006	1.21	1.0E-112	AF157823.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1063	14109	27058	1.85	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1692	14722	27703	3.1	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1692	14722	27704	3.1	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2207	15222	28242	1.08	1.0E-112	A1766925.1	EST_HUMAN	w190f06.x1 NCL_CGAP_K12 Homo sapiens cDNA clone IMAGE:2400611 3'
2515	15518	28541	1.34	1.0E-112	BE868859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846888 5'
3094	16182		3.53	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
							wk45b12.x1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81650_rna1
3371	16421	28346	1.07	1.0E-112	A1826511.1	EST_HUMAN	SEMNOCGELIN 1 PROTEIN PRECURSOR (HUMAN);
3598	16938	29849	0.69	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-090300-113-409 BT0590 Homo sapiens cDNA
4634	17655	30542	0.79	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4784	17803	30694	5.01	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4784	17803	30695	5.01	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5750	18844	32027	38.43	1.0E-112	N46046.1	EST_HUMAN	y35407.r1 Scarses melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5'
6195	19289	32504	1.28	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6298	19341	32573	0.89	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajs-g-06-Q-UJ.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6298	19341	32574	0.89	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajs-g-06-Q-UJ.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6378	19446	32687	0.9	1.0E-112	BE741666.1	EST_HUMAN	601594717F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6603	19692	32835	0.83	1.0E-112	BF072815.1	EST_HUMAN	602162849F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293420 5'
6792	19846	33130	0.74	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'

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6792	19846	33131	0.74	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506608 5'
7018	20144	33491	1.23	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7362	20332	33682	0.66	1.0E-112	AL043289.1	EST_HUMAN	DKFZp34M0523_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M0523 5'
7659	20522	33879	1.62	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7659	20522	33880	1.62	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8535	21503	34921	1.93	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
9309	22274	35705	2.56	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9309	22274	35706	2.56	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
10253	23178	36665	2.18	1.0E-112	BF111413.1	EST_HUMAN	713097.x1 Soares NSF F8 9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW35 Q9VW35 CG8743 PROTEIN ;
11132	24092	37621	2.93	1.0E-112	AW863327.1	EST_HUMAN	MF3-SN0009-100400-108-b72 SN0009 Homo sapiens cDNA
11295	24245	37772	2.35	1.0E-112	AJ246900.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11433	24377	37917	1.7	1.0E-112	BE280479.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
11518	24459	38009	3.58	1.0E-112	AW377870.1	EST_HUMAN	PMO-CT0237-141099-001-h02 CT0237 Homo sapiens cDNA
12095	24968	38563	6.59	1.0E-112	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
744	13803	26744	5.37	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
744	13805	26745	5.37	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
941	13994	26946	5.76	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1543	14578	27648	3.01	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1956	15821	27980	1.29	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2105	15123	28143	0.99	1.0E-113	BF516218.1	EST_HUMAN	U1H-BW1-ant-f-03-o-U1.e1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
3147	18204	29118	1.16	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5316	25748		1.54	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5570	18667	31628	6.68	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
5918	19002	32193	0.54	1.0E-113	BE789172.1	EST_HUMAN	601476296F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879406 5'
5918	19002	32194	0.54	1.0E-113	BE789172.1	EST_HUMAN	601476296F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879406 5'
6031	19114	32317	4.18	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLAC2 Homo sapiens cDNA clone PLAC2000274 5'
6061	19142	32354	0.97	1.0E-113	AF016335.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
							Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8), mRNA
6188	19263	32499	2.42	1.0E-113	11525737	NT	

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6280	19352	32587	0.62	1.0E-113	8961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6280	19352	32588	0.62	1.0E-113	8961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6449	19514	32764	0.89	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6449	19514	32765	0.89	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7543	20506	33865	0.72	1.0E-113	BE262161.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7543	20506	33866	0.72	1.0E-113	BE262161.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
9450	22414	35850	2.93	1.0E-113	BE382842.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3508362 5'
9450	22414	35851	2.93	1.0E-113	BE382842.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3508362 5'
9756	22697		0.7	1.0E-113	BE772957.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3627554 5'
10180	23115	36599	1.3	1.0E-113	11429367	NT	RC1-F10134-280600-021-402 F10134 Homo sapiens cDNA
10290	23216	36599	0.73	1.0E-113	M21535.1	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10410	23332	36817	0.77	1.0E-113	5453997	NT	Human erg protein (ets-related gene) mRNA, complete cds
10410	23332	36818	0.77	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11457	24400	37948	1.51	1.0E-113	AW500519.1	EST_HUMAN	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11466	24409	37956	3	1.0E-113	AW630291.1	EST_HUMAN	UI-HF-BNO-ak1-b-12-0-UI-17 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:3077328 5'
11466	24409	37957	3	1.0E-113	AW630291.1	EST_HUMAN	h181a09.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN ;
11592	24530	38087	2.94	1.0E-113	BE292968.1	EST_HUMAN	h181a09.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN ;
11826	24709	38292	3.1	1.0E-113	AA580720.1	EST_HUMAN	KIAA0584 PROTEIN ;
11826	24709	38293	3.1	1.0E-113	AA580720.1	EST_HUMAN	KIAA0584 PROTEIN ;
60	13179	26092	0.65	1.0E-114	Y17151.2	NT	601105523FT NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5'
60	13179	26093	0.65	1.0E-114	Y17151.2	NT	nc80b03.r1 NCI CGAP GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1 ;
60	13179	26094	0.65	1.0E-114	Y17151.2	NT	nc80b03.r1 NCI CGAP GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1 ;
							Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
							Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
							Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
							yd15c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
646	13712	26634	5.97	1.0E-114	T70551.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1072	14117	27068	1.78	1.0E-114	8923087	NT	Homo sapiens thadoid tumor deletion region protein 1 (RTDR1), mRNA
1316	14351	27319	5	1.0E-114	7657629	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1648	14650	27653	1.79	1.0E-114	6631094	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1681	14713	27691	5.92	1.0E-114	8679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
3148	16205	29119	2.91	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3187	16242	29160	1.26	1.0E-114	BF206374.1	EST_HUMAN	601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4044	17082	28980	1.26	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4417	17444	30335	0.78	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
5228	18236	31110	0.99	1.0E-114	AA194468.1	EST_HUMAN	zq05e05.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:628832 5' similar to contains MER22.13 MER22 repetitive element;
5474	18575	31483	1.47	1.0E-114	4508880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5474	18575	31484	1.47	1.0E-114	4508880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5878	18771	31943	1	1.0E-114	9257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
8354	19423	32686	0.51	1.0E-114	Z26298.1	NT	H. sapiens isoform 1 gene for L-type calcium channel, exon 20
7191	18422	31224	0.54	1.0E-114	4759163	NT	Homo sapiens sparc/osteonectin, cwcx and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
7280	20014		1.01	1.0E-114	AB041533.1	NT	Homo sapiens HOMOGT-1 mRNA for sperm antigen, complete cds
7460	20416	33770	1.08	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7450	20416	33771	1.08	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7499	20464	33824	5.65	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7499	20464	33825	5.65	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
8223	21192	34600	1.87	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8507	21475	34888	1.65	1.0E-114	A1363139.1	EST_HUMAN	q68d06.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2017163 3'
8607	21475	34889	1.65	1.0E-114	A1363139.1	EST_HUMAN	q68d06.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2017163 3'
9049	22015	35439	3.38	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
9119	22085	35514	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9119	22085	35515	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9353	22318	35744	0.42	1.0E-114	AB046784.1	NT	Homo sapiens mRNA for KIAA1564 protein, partial cds
9537	22500	35948	0.61	1.0E-114	BF109832.1	EST_HUMAN	7169g12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR:Q9JHNG Q9JHNG TRANSMEMBRANE PROTEIN 2.:
9769	22710		14.09	1.0E-114	AW327455.1	EST_HUMAN	dq0305.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9818	22140	34546	3.34	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9906	22858		1.15	1.0E-114	M13536.1	NT	Human caruloplasmin mRNA
10498	23420	36919	0.95	1.0E-114	BE870004.1	EST_HUMAN	601449762F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10522	23444	36942	1.42	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10907	23827	37340	0.87	1.0E-114	BE171984.1	EST_HUMAN	MR0-HT0559-250200-002-407 HT0559 Homo sapiens cDNA
11140	24100						bat3g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20832 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
11524	24465	38018	15.04	1.0E-114	BE302666.1	EST_HUMAN	
11524	24465	38019	3.01	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cDNA Homo sapiens cDNA clone cdABA08 5'
12818	25974		2.9	1.0E-114	1141804.1	NT	AV733454 cDNA Homo sapiens cDNA clone cdABA08 5'
12859	25464	31725	3.55	1.0E-114	11034850	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12859	25464	31726	3.55	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
24	13144	26044	2.83	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
130	13235	26165	2.37	1.0E-115	4505638	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
134	13239		3.36	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
292	13386	26313	5.22	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-508 UM0094 Homo sapiens cDNA
537	13608	26528	1.12	1.0E-115	A1339206.1	EST_HUMAN	q106f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-1 INTERACTING PEPTIDE 5;
537	13608	26527	1.12	1.0E-115	A1339206.1	EST_HUMAN	q106f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-1 INTERACTING PEPTIDE 5;
787	13848	26792	0.78	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
787	13848	26793	0.78	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
789	13848	26795	58.69	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1561	14593	27566	1.46	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1561	14593	27567	1.46	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1858	14884	27891	1.24	1.0E-115	U76027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2883	15923		1.7	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-508 UM0094 Homo sapiens cDNA
3132	16189	29099	2.74	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3132	16189	29100	2.74	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3486	16532	29457	2.07	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4072	17108	30002	4.75	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4295	17324	30204	0.86	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4429	17456	30347	3.89	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4465	17491	30378	3.73	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4702	17723	30616	2.53	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4702	17723	30617	2.53	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4943	17859	30849	2.57	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4943	17859	30850	2.57	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
5420	18523	31401	0.81	1.0E-115	AW970335.1	EST_HUMAN	EST382416 MAGE resequences, MAGK Homo sapiens cDNA
5408	18588	31510	1.06	1.0E-115	BF665387.1	EST_HUMAN	602119346F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4276738 5'
5820	18716	31875	1.68	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5820	18716	31876	1.68	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5775	18867	32049	1.1	1.0E-115	AI928799.1	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
5775	18867	32050	1.1	1.0E-115	AI928799.1	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
6391	19459	32704	0.68	1.0E-115	11428786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6391	19459	32705	0.68	1.0E-115	11428786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6535	19598	32861	19.47	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
6678	19735	33010	1.82	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6678	19735	33011	1.82	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7120	20054	33368	0.57	1.0E-115	T88774.1	EST_HUMAN	yd8b08.r1 Scores fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:115095 5' similar to SP-DPOG_YEAST P15801 DNA POLYMERASE GAMMA ;
7493	20458	33816	1.22	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Scores_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7493	20458	33817	1.22	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Scores_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7638	20608	33962	7.12	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
8500	21468	34894	11.55	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8500	21468	34895	11.55	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8164	22130	35667	4.68	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
10133	23059	36536	0.64	1.0E-115	BF382029.1	EST_HUMAN	G01816352F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4050108 5'
10358	23282	36758	1.74	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10358	23282	36759	1.74	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10887	23807	37312	1.02	1.0E-115	AI221878.1	EST_HUMAN	qg9e09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10887	23807	37313	1.02	1.0E-115	AI221878.1	EST_HUMAN	qg9e09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10894	23814	37321	0.7	1.0E-115	AI524687.1	EST_HUMAN	th12a07.x1 NCI_CGAP_GIL1 Homo sapiens cDNA clone IMAGE:2118038 3' similar to TR:O16129 O16129 PHENYLALANYL TRNA SYNTHETASE ;
10920	23840	37356	0.73	1.0E-115	BE886295.1	EST_HUMAN	G01503879F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911610 5'
11072	24034	37558	3.4	1.0E-115	AW571644.1	EST_HUMAN	xx32f03.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA P10463 CALCYPHOSINE ;

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11589	24527	38083	2.1	1.0E-115	BE045890.1	EST_HUMAN	h54c10.x1 NCI_CGAP_Pan3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG ;
11589	24527	38084	2.1	1.0E-115	BE045890.1	EST_HUMAN	h54c10.x1 NCI_CGAP_Pan3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG ;
11726	24812	38189	2.06	1.0E-115	4502528	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
12191	25036		1.52	1.0E-115	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
574	13643	26557	1.02	1.0E-116	BE275902.1	EST_HUMAN	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988875 5'
801	13860	26807	2.44	1.0E-116	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
860	13916		0.68	1.0E-116	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
2013	15034	28044	2.89	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
2013	15034	28045	2.89	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
2316	15327	28350	1.86	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2348	15357		1.68	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo-olfr17-01 (OR17-01) pseudogene, complete cds
2462	15466	28489	2.69	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2744	15829	28754	3.32	1.0E-116	BE889256.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3180	16235		0.95	1.0E-116	T07515.1	EST_HUMAN	EST05405 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBK28 similar to EST containing L1 repeat
3189	16244	29161	5.44	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3189	16244	29162	5.44	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4405	17433	30318	2.36	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4892	17809	30798	2.03	1.0E-116	AI907096.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5230	18238	31111	0.92	1.0E-116	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5351	18456	31326	0.92	1.0E-116	AJ302062.1	EST_HUMAN	qm19404.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898695 3' similar to contains element MER25 repetitive element ;
6090	19169	32384	2.18	1.0E-116	W42822.1	EST_HUMAN	zc24007.t1 Scores_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
6336	19405	32845	1.8	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6336	19405	32846	1.8	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6408	19476	32723	0.95	1.0E-116	BE408097.1	EST_HUMAN	601302281F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636764 5'
6849	19707	32982	0.73	1.0E-116	5729867	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6849	19707	32983	0.73	1.0E-116	5729867	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6663	19720		2.08	1.0E-116	BE158133.1	EST_HUMAN	MR2-HT0379-210200-102-604 HT0379 Homo sapiens cDNA
7130	20106	33417	1.69	1.0E-116	C02944.1	EST_HUMAN	C02944 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC0567
7410	20377	33728	7.19	1.0E-116	AV716314.1	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCBCCG06 5'
8712	21680	35106	1.32	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8712	21680	35107	1.32	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8824	21791	35213	1.04	1.0E-116	AI904151.1	EST_HUMAN	CM-BT043-060299-075 BT043 Homo sapiens cDNA
9290	22256	35686	1.39	1.0E-116	BE565507.1	EST_HUMAN	601338268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680680 5'
9455	22419	35857	2.9	1.0E-116	AI216352.1	EST_HUMAN	qh09c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gb:53741_rnat1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
10033	22960	36428	1.49	1.0E-116	11418648	NT	Homo sapiens laminin, alpha 2 (mercsin, congenital muscular dystrophy) (LAMA2), mRNA
10633	23565	37055	0.71	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10633	23555	37056	0.71	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10713	23635	37128	0.91	1.0E-116	BE168013.1	EST_HUMAN	QV4-HT0401-281299-063-c09 HT0401 Homo sapiens cDNA
11046	24010	37536	2.44	1.0E-116	BF335849.1	EST_HUMAN	CM2-CT0482-300800-349-c06 CT0482 Homo sapiens cDNA
11470	24413	37962	2.63	1.0E-116	AI367140.1	EST_HUMAN	qq41e04.x1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:B0495.7
12904	25840		1.68	1.0E-116	AL134989.1	EST_HUMAN	CE01765 ;
560	13630	26547	1.04	1.0E-117	4826638	NT	DKFZp782L1110_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782L1110 5'
1079	15958	27076	0.86	1.0E-117	AF124393.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1228	14267	27224	2.2	1.0E-117	AF264750.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1848	14874	27870	2.04	1.0E-117	M19816.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2221	15235	28259	1.28	1.0E-117	AW957699.1	EST_HUMAN	Human apolipoprotein B-100 (apoB) gene, exon 10
3281	16335	29255	1.51	1.0E-117	AA978114.1	EST_HUMAN	EST369769 MAGe resequences, MAGe Homo sapiens cDNA
4016	17055	29958	5.89	1.0E-117	AA316723.1	EST_HUMAN	cp32c1.1.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
4371	17398	30278	2.1	1.0E-117	8559564	NT	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4608	17629	30521	1.95	1.0E-117	AL042120.1	EST_HUMAN	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4755	17775	30670	1.19	1.0E-117	X89670.1	NT	DKFZp434C1120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1120 5'
4755	17775	30671	1.18	1.0E-117	X89670.1	NT	H.sapiens mRNA for TPCR16 protein
4847	17864	30757	10.31	1.0E-117	AF134304.2	NT	H.sapiens mRNA for TPCR16 protein
4847	17864	30758	10.31	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4977	17892	30881	4.01	1.0E-117	AB020673.1	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5421	18524	31402	3.29	1.0E-117	BE730508.1	EST_HUMAN	Homo sapiens mRNA for KIAA0866 protein, complete cds
7148	18380	31269	0.53	1.0E-117	AA323348.1	EST_HUMAN	601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
							EST26111 Cerebellum II Homo sapiens cDNA 5' end similar to zinc finger domain

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7683	20641	34004	4.55	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7683	20641	34005	4.55	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7795	20747	34121	3.71	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
7795	20747	34122	3.71	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
8311	21280	34691	3.78	1.0E-117	AI950145.1	EST_HUMAN	wp86807.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75065
8654	21622	35042	1.01	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8654	21622	35043	1.01	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8754	21722	35144	0.63	1.0E-117	AI904151.1	EST_HUMAN	CM-BT043-080289-075 BT043 Homo sapiens cDNA
8754	21722	35145	0.63	1.0E-117	AI904151.1	EST_HUMAN	CM-BT043-080289-075 BT043 Homo sapiens cDNA
8654	22597	35046	1.61	1.0E-117	D16524.1	NT	Human gene for very low density lipoprotein receptor, exon 11
10145	23071	35546	1.71	1.0E-117	BE733922.1	EST_HUMAN	601569317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
10306	25701	36713	0.64	1.0E-117	AF09033.1	NT	Homo sapiens gamma-aminobutyric acid type B receptor 2 (GABABR2) mRNA, complete cds
10934	23854	37370	1.98	1.0E-117	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
11207	24161	37691	2.17	1.0E-117	D83776.1	NT	Human mRNA for KIAA0191 gene, partial cds
11375	24322	37850	1.96	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11375	24322	37851	1.96	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11604	24542	38101	2.72	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11604	24542	38102	2.72	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11722	24608		34.45	1.0E-117	BE269856.1	EST_HUMAN	601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544298 5'
11921	24602	38393	1.76	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11921	24602	38394	1.76	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
12429	25911		1.39	1.0E-117	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
71	13189	28109	2.9	1.0E-118	AF161600.1	NT	Homo sapiens HSPC151 mRNA, complete cds
95	13211	28135	1.27	1.0E-118	AL045854.1	EST_HUMAN	DKFZp434i056_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434i056 5'
518	13599	28509	4.46	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
915	15894	28923	1.66	1.0E-118	5174880	NT	Homo sapiens hypothetical protein (Drosophila) homolog 1 (SIX1) mRNA
2242	15256	28280	1.93	1.0E-118	BE399705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2242	15256	28281	1.93	1.0E-118	BE399705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2242	15256	28282	1.93	1.0E-118	BE399705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2337	15348		1.55	1.0E-118	AW951729.1	EST_HUMAN	EST363789 IMAGE resequences, MAGB Homo sapiens cDNA
2750	15743	28760	2.48	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2750	15743	28761	2.48	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3121	16178		3.87	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3210	16285	29187	4.61	1.0E-118	AI347694.1	EST_HUMAN	qp01105.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916789 3'
3210	16285	29188	4.61	1.0E-118	AI347694.1	EST_HUMAN	qp01105.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916789 3'
3970	17010	29924	0.98	1.0E-118	AB024489.1	NT	Pongo pygmaeus DNA, similar to pol gene of HERV-W and MSRV, isolate:ORW3-3
4116	17149	30041	5.07	1.0E-118	D23560.1	NT	Human mRNA for ribosomal protein, complete cds
5497	18597	31508	1.86	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5497	18597	31509	1.86	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5713	18807	31984	0.66	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5713	18807	31985	0.66	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5800	18892	32074	0.58	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5800	18892	32075	0.58	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5885	18984	32141	1.44	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
5962	19047	32247	0.95	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5962	19047	32248	0.95	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6083	19134	32343	1.81	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6849	19902	33196	1.79	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6849	19902	33197	1.79	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7304	20275	33611	1.07	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434O0127 5'
7304	20275	33612	1.07	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434O0127 5'
7858	20803	34179	5.13	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7872	20816	34194	0.72	1.0E-118	L46590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
8305	21274	34685	2.41	1.0E-118	BE781223.1	EST_HUMAN	601469159F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
8726	21684	35119	7.01	1.0E-118	BE082855.1	EST_HUMAN	QVQ-BT0263-090200-097-H03 BT0263 Homo sapiens cDNA
8726	21694	35120	7.01	1.0E-118	BE082855.1	EST_HUMAN	QVQ-BT0263-090200-097-H03 BT0263 Homo sapiens cDNA
8732	21700	35125	1.39	1.0E-118	AA443024.1	EST_HUMAN	z98807.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8732	21700	35126	1.39	1.0E-118	AA443024.1	EST_HUMAN	z98807.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
9021	21987	35408	1.02	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
9021	21987	35409	1.02	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
9071	22037	35460	1.32	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9071	22037	35461	1.32	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9390	22356	35786	5.12	1.0E-118	BE283194.1	EST_HUMAN	601144803F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
9421	22396	35925	0.53	1.0E-118	AL048474.2	EST_HUMAN	DKFZp586K1824_r1 586 (synonym: huler1) Homo sapiens cDNA clone DKFZp586K1824
9951	22878	36341	2.29	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
10598	23620	37115	0.46	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10698	23620	37116	0.46	1.0E-118	BE736213.1	EST_HUMAN	601307148F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10741	23663	37158	2.31	1.0E-118	BF185407.1	EST_HUMAN	7n17e09.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN
10899	23819	37328	0.54	1.0E-118	AW266351.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ;
11607	24545	38108	6.48	1.0E-118	AA315007.1	EST_HUMAN	UI-H-BW0-elo-a-07-0.U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729772 3'
11884	24765	38351	1.9	1.0E-118	BE908676.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' and similar to dynein, light chain 1, cytoplasmic
11884	24765	38352	1.9	1.0E-118	BE908676.1	EST_HUMAN	601489514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11887	24768	38355	1.51	1.0E-118	BF093687.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11887	24768	38356	1.51	1.0E-118	BF093687.1	EST_HUMAN	QVO-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
12036	24911		1.58	1.0E-118	6325465	NT	QVO-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
1038	15857	27034	1.75	1.0E-119	7708607	NT	Homo sapiens flap structure-specific endonuclease 1 (FEN1), mRNA
1050	14973	27972	2.88	1.0E-119	AB023147.1	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
3119	16176	28087	0.98	1.0E-119	8922208	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3254	16308		0.68	1.0E-119	AA918760.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3975	17015	29929	1.12	1.0E-119	4504118	NT	on10b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1566241 3' similar to WP:E04F6.2
5410	18513	31391	2.79	1.0E-119	AU133399.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5423	18528	31404	14.68	1.0E-119	M89914.1	NT	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5'
5428	18531	31411	2.88	1.0E-119	BE936121.1	EST_HUMAN	Human neurofibromin (NF1) gene, complete cds
5508	18608	31538	1.55	1.0E-119	AV693731.1	EST_HUMAN	RC1-NN0073-260800-018-g06 NN0073 Homo sapiens cDNA
5671	18766	31937	0.68	1.0E-119	AL134903.1	EST_HUMAN	AV693731 GKGC Homo sapiens cDNA clone GKCDHB03 5'
5671	18766	31938	0.68	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6250	19323	32553	7.38	1.0E-119	AI150703.1	EST_HUMAN	DKFZp762M0710_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6415	19483	32730	0.69	1.0E-119	AF315683.1	NT	qb77c08.x1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to
6415	19483	32731	0.69	1.0E-119	AF315683.1	NT	SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
6465	19530	32778	1	1.0E-119	AI476732.1	EST_HUMAN	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6504	19663	32936	2.67	1.0E-119	X06292.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6616	19674	32952	4.98	1.0E-119	AW974193.1	EST_HUMAN	im23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
7640	20600	33964	1.3	1.0E-119	BE786614.1	EST_HUMAN	Human c-fos proto-oncogene
9009	21975	35395	1.15	1.0E-119	BE616150.1	EST_HUMAN	EST1386296 MAGC resequences, MAGM Homo sapiens cDNA
10113	23039	36519	0.5	1.0E-119	11545921	NT	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'
10287	23192	36679	1.1	1.0E-119	11036643	NT	601280564F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622826 5'
							Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10608	23530	37025	5.31	1.0E-119	AA465124.1	EST_HUMAN	aa3205.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
10870	23790	37290	1.12	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10911	23831	37344	0.73	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10911	23831	37345	0.73	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10885	23905	37419	0.78	1.0E-119	AB032261.1	NT	Homo sapiens Scd mRNA for stearyl-CoA desaturase, complete cds
11394	24340	37870	1.86	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11394	24340	37871	1.86	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11535	24476		13.43	1.0E-119	BF569571.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
12486	25901		3.21	1.0E-119	AW847519.1	EST_HUMAN	RC3-CT0212-240999-011-403 CT0212 Homo sapiens cDNA
301	13395	26322	0.99	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
1042	14088	27040	1.6	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1042	14088	27041	1.8	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1422	14455	27429	2.56	1.0E-120	N44873.1	EST_HUMAN	y44g12.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:273766 5'
1605	14637	27614	2.5	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1823	14860	27844	1.4	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2534	15537	28558	1.08	1.0E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
3318	13395	28322	1.34	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4385	17413	30297	1.81	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4385	17413	30298	1.81	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4691	17712	30606	2.67	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4691	17712	30607	2.67	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5825	18915	32098	13.85	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5825	18915	32099	13.85	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6583	19643	32910	0.53	1.0E-120	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
6583	19643	32911	0.53	1.0E-120	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
7823	20771	34147	1.84	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
8228	21195	34602	1.76	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8228	21195	34603	1.76	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8675	21643	35068	2.82	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183333 5'
8747	21715	35138	0.75	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8747	21715	35139	0.75	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8761	21719	35141	2.6	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8761	21719	35142	2.5	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8798	21763	35185	1.13	1.0E-120	AB007934.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9859	22795	36247	4.14	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9859	22795	36248	4.14	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
10102	23028	36505	3.99	1.0E-120	BF306541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
10118	23044	36524	7.33	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
10135	23061	36539	0.67	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10252	23177		0.51	1.0E-120	AI804151.1	EST_HUMAN	CM-BT043-090298-075 B7043 Homo sapiens cDNA
10436	23358	36846	3.02	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11461	24404	37852	19.45	1.0E-120	BE296397.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
11672	24638	38216	2.5	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11672	24638	38217	2.5	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11963	24842	38436	2.23	1.0E-120	U94774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
12632	25318	31785	1.45	1.0E-120	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
74	13191	26113	0.97	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
378	13462	26392	1.92	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
725	15848	26721	1.83	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1983	15004	28007	1.17	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1983	15004	28008	1.17	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2112	15129	28149	1.36	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2980	16038	29961	1.69	1.0E-121	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
3097	16154	29067	3.41	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3097	16154	29068	3.41	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3547	16593	29518	0.84	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3547	16593	29519	0.84	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3690	16733	29846	8.63	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4368	17395	30267	1.39	1.0E-121	AI263294.1	EST_HUMAN	qx57501.x1 NC1_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2005417 3'
5012	18026	30911	3.4	1.0E-121	X91837.1	NT	H. sapiens ECE-1 gene (exon 17)
5182	18197	31067	0.93	1.0E-121	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
5340	18445	31198	0.86	1.0E-121	BE222250.1	EST_HUMAN	hu0908.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5641	18737	31901	0.58	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
7072	20094		0.7	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
7155	18387	31230	0.82	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
7155	18387	31231	0.82	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8269	21238	34649	1.57	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8273	21242	34653	2.22	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8273	21242	34654	2.22	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
10217	23142	36630	0.79	1.0E-121	AW593858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
10217	23142	36631	0.79	1.0E-121	AW593858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
11130	24090	37619	1.87	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
11136	24096	37625	1.52	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
11316	24265	37793	3.61	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11340	24290	37815	3.42	1.0E-121	N59624.1	EST_HUMAN	y74c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'
11664	24600	38175	4.22	1.0E-121	AU119320.1	EST_HUMAN	AU119320 HEMBA1 Homo sapiens cDNA clone HEMBA1005536 5'
267	13663	26287	2.23	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
336	13425	26347	3.36	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
358	13445	26372	2.1	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
883	13638	26887	3.29	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1224	14262	27219	16.68	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1702	14732	27714	1.02	1.0E-122	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1725	14755	27741	1.67	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1725	14755	27742	1.67	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1831	14858	27856	5.11	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899358 5'
2499	15502	28528	8.15	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2499	15502	28529	8.15	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2851	15911	28834	0.91	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4883	17900	30789	1.03	1.0E-122	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5025	18039	31904	1.4	1.0E-122	AW504645.1	EST_HUMAN	U1HF-BN0-all-a-03-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
5843	18739	31904	1.31	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6920	18739	31904	7.59	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7422	20389	33740	0.6	1.0E-122	AA888671.1	EST_HUMAN	ak49106.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8135	21072	34471	0.51	1.0E-122	AA224259.1	EST_HUMAN	zr15a03.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:663436 5' similar to TR:G940370 G940370 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;
8135	21072	34472	0.51	1.0E-122	AA224259.1	EST_HUMAN	zr15a03.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:663436 5' similar to TR:G940370 G940370 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;
9148	22114	35539	0.56	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
9383	22348	35780	1.17	1.0E-122	11424218	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9878	22631	36086	0.78	1.0E-122	AJ359618.1	EST_HUMAN	qy32h07.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1 ;
9878	22831	36087	0.78	1.0E-122	AJ359618.1	EST_HUMAN	qy32h07.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1 ;
10483	23415	36913	0.77	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dbf (proto-oncogene)
11714	24677	38255	6.11	1.0E-122	AB024088.1	NT	Homo sapiens gene for B120, exon 10
12102	24973	38570	1.5	1.0E-122	11434816	NT	Homo sapiens thyroid hormone receptor interactor 11 (TRIP11), mRNA
12228	25093		5.83	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
13107	14262	27219	3.03	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
769	13828	26772	1.18	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153670 5'
769	13828	26773	1.18	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1015	14063	27014	5.55	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1024	14070	27021	2.2	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1243	14278	27241	5.25	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1243	14279	27242	5.25	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1449	14482	27459	89.95	1.0E-123	AJ388641.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02
2109	15126	28145	2.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2109	15126	28146	2.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2109	15126	28147	2.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2323	15334		3.14	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3284	16318	29239	1.52	1.0E-123	6912617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPOT), mRNA
5522	18621	31553	1.58	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5522	18621	31558	1.58	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5631	18757	31925	1.31	1.0E-123	BE799746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6613	19671	32949	1.97	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7199	20223	33554	0.83	1.0E-123	H53198.1	EST_HUMAN	Yq84q03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14680 PROTEIN KINASE YAK1;
7212	20235	33569	1.24	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7400	20368	33721	0.57	1.0E-123	U55288.1	NT	Human HBRV0/Nr-CAM precursor (hBRV0/Nr-CAM) gene, complete cds
7632	20592	33955	0.9	1.0E-123	11528833	NT	Homo sapiens heparan sulfate (glucosaminide) 3-O-sulfotransferase 2 (HSSST2), mRNA
7904	20847	34232	1.29	1.0E-123	11436439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
7913	20856	34244	1.87	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
8083	21020	34419	0.71	1.0E-123	N36841.1	EST_HUMAN	yx89d11.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611
8083	21020	34420	0.71	1.0E-123	N36841.1	EST_HUMAN	S49611 protein kinase PkpA - Phycomyces blakesleeanus;
8248	21217	34826	0.5	1.0E-123	AU131881.1	EST_HUMAN	yx89d11.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611
8248	21217	34827	0.5	1.0E-123	AU131881.1	EST_HUMAN	S49611 protein kinase PkpA - Phycomyces blakesleeanus;
8880	21847	36205	1.43	1.0E-123	AW371924.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
9724	22752	36205	2.03	1.0E-123	AB007923.1	NT	RC4-BT0311-251199-012-a07 BT0311 Homo sapiens cDNA
9863	22799	36253	31.72	1.0E-123	U09823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10370	23293	38499	0.44	1.0E-123	4504808	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
12029	24905	38499	5.3	1.0E-123	BF677292.1	EST_HUMAN	Homo sapiens jerky (mouse) homolog-like (JRK), mRNA
12029	24905	38500	5.3	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
268	13364	26288	1.18	1.0E-124	4507500	NT	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
268	13364	26289	1.18	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
274	13370	28485	0.79	1.0E-124	D87675.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
486	13559	28485	2.11	1.0E-124	AL163246.2	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
692	13764	26983	8.04	1.0E-124	AA397551.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
692	13754	26984	8.04	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
758	13918	26763	6.06	1.0E-124	AF159654.1	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
809	13867	26816	1.34	1.0E-124	4507500	NT	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
905	13960	26816	4.34	1.0E-124	7705446	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
1349	14384	27352	12.68	1.0E-124	AF274892.1	NT	Human putative ribosomal protein S1 mRNA
1349	14384	27353	12.68	1.0E-124	AF274892.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
							Homo sapiens hypothetical protein (HSPC088), mRNA
							Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
							Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10230	23155	36845	1.75	1.0E-124	AW503755.1	EST_HUMAN	U1HF-BN0-akz-b-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'
11388	24333	37882	1.53	1.0E-124	U94776.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
11860	24596	38169	5.95	1.0E-124	AW665663.1	EST_HUMAN	h05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'
11801	23956	37479	2.06	1.0E-124	AI48455.1	EST_HUMAN	h19e03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
11801	23956	37480	2.06	1.0E-124	AI48455.1	EST_HUMAN	h19e03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
12305	13754	26683	4.06	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
12305	13754	26684	4.06	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
12730	25383	31749	1.36	1.0E-124	AB028016.1	NT	Homo sapiens mRNA for KIAA1083 protein, partial cds
12983	25852	31436	1.67	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12983	25852	31437	1.67	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
319	13411		10.43	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
426	13121	26019	5.43	1.0E-125	BE743922.1	EST_HUMAN	601677981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
645	13711	26632	1.26	1.0E-125	AI110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
645	13711	26633	1.26	1.0E-125	AI110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
728	13790	26725	2.34	1.0E-125	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
861	13917	26875	1.61	1.0E-125	AA042813.1	EST_HUMAN	z153c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1000	14051	27003	1.16	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1166	14188	27148	2.2	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1682	15874	27692	1.99	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1817	14844	27836	1.65	1.0E-125	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1828	14855	27852	2.84	1.0E-125	AF015450.1	NT	Homo sapiens Ueuprin-alpha mRNA, complete cds
1828	14855	27853	2.84	1.0E-125	AF015450.1	NT	Homo sapiens Ueuprin-alpha mRNA, complete cds
2366	15374	28395	1.78	1.0E-125	AA011278.1	EST_HUMAN	z101g08.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428568 5'
2604	15604	28628	1.19	1.0E-125	4504696	NT	Homo sapiens inhibitor, alpha (INH4) mRNA
2604	15604	28627	1.19	1.0E-125	4504696	NT	Homo sapiens inhibitor, alpha (INH4) mRNA
3022	18311	28001	1.19	1.0E-125	BE018009.1	EST_HUMAN	bb74f06.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:O95804 O95804 ZINC FINGER PROTEIN.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3872	16911	29821	1.11	1.0E-125	AA042813.1	EST_HUMAN	z53c07.t1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
4580	17602	30498	1.86	1.0E-125	11425114	NT	gbcX65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4580	17602	30499	1.86	1.0E-125	11425114	NT	Homo sapiens Zinc finger protein ZNF287 (ZNF287), mRNA
4848	17688	30556	1.66	1.0E-125	BE315412.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5973	19038	32259	1.47	1.0E-125	11436448	NT	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140786 5'
5984	19078	32275	1.01	1.0E-125	BE175169.1	EST_HUMAN	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6041	19123	32328	3.58	1.0E-125	BE892660.1	EST_HUMAN	QV2-HT0577-010500-165-b06 HT0577 Homo sapiens cDNA
6086	19166	32378	0.6	1.0E-125	A1679904.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6413	19481	32728	0.68	1.0E-125	BE736055.1	EST_HUMAN	tu87c07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2258108 3' similar to WP:C4639.2
6733	19789	33068	1.28	1.0E-125	BE562526.1	EST_HUMAN	CE01854;
6733	19789	33069	1.29	1.0E-125	BE562526.1	EST_HUMAN	601305870F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840087 5'
7263	19998	33296	5.05	1.0E-125	X03427.1	NT	601335828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7263	19998	33297	5.05	1.0E-125	X03427.1	NT	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7775	20728	34100	1.04	1.0E-125	BE278823.1	EST_HUMAN	Homo sapiens (GF-II) gene, exon 5
8032	20969	34363	0.54	1.0E-125	11425572	NT	Homo sapiens (GF-II) gene, exon 5
8891	21857	35278	0.99	1.0E-125	U90288.1	NT	Homo sapiens (GF-II) gene, exon 5
8891	21857	35279	0.99	1.0E-125	U90288.1	NT	601199076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
9473	22437	35875	12.5	1.0E-125	BE181640.1	EST_HUMAN	Homo sapiens adenylos-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9473	22437	35876	12.5	1.0E-125	BE181640.1	EST_HUMAN	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9736	22764	36219	0.93	1.0E-125	A1665986.1	EST_HUMAN	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
10819	23740	37242	0.65	1.0E-125	BE794576.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
10850	23780	37280	0.74	1.0E-125	AB002298.1	NT	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
11042	24006	37533	2.54	1.0E-125	AF043458.1	NT	in52b03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089
11124	24084	37610	1.97	1.0E-125	AW131202.1	EST_HUMAN	HYPOTHETICAL PROTEIN ;
11124	24084	37611	1.97	1.0E-125	AW131202.1	EST_HUMAN	601560345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944531 5'
11471	24414	37963	2.99	1.0E-125	AB014567.1	NT	Human mRNA for KIAA0300 gene, partial cds
11621	24559	38121	2.06	1.0E-125	7669505	NT	Homo sapiens LREL gene, exon 5
							x59f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284
							LAMBDA/OTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
							x59f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284
							LAMBDA/OTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
							Homo sapiens mRNA for KIAA0687 protein, partial cds
							Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
11626	24564	38128	5	1.0E-125	AF08029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11729	24615	38192	1.68	1.0E-125	AW81289.1	EST_HUMAN	RC3-3T0166-250200-076-c11 ST0186 Homo sapiens cDNA
11830	24713	38296	4.32	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
11830	24713	38297	4.32	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
12106	18942	32127	1.48	1.0E-125	BF683645.1	EST_HUMAN	602139874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'
775	13834	26780	6.16	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
920	13874	26926	0.8	1.0E-128	X68735.1	NT	H. sapiens gene for alpha1-antichymotrypsin, exon 3
2352	15361	28383	0.91	1.0E-126	8923058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2352	15361	28384	0.91	1.0E-126	8923058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2605	15605	28628	1.41	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3087	16145	29058	7.58	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pentreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
3087	16145	29059	7.58	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pentreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
3088	16146	29060	1.02	1.0E-126	BF510408.1	EST_HUMAN	UI-H-B14-acc-b-05-Q-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084608 3'
3088	16146	29061	1.02	1.0E-126	BF510408.1	EST_HUMAN	UI-H-B14-acc-b-05-Q-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084608 3'
3645	16888	29803	0.75	1.0E-126	X53941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3668	16711	29826	2.09	1.0E-126	7857038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4826	17843	30741	1.15	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4826	17843	30742	1.15	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4872	17869	30777	1.38	1.0E-126	N34078.1	EST_HUMAN	yx78c06.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:267850 5'
5787	18879	32061	0.71	1.0E-126	T66998.1	EST_HUMAN	ya52b12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:66527 3'
6360	19429	32672	3.23	1.0E-126	AA460075.1	EST_HUMAN	z66e03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:798444 5' similar to TR:G1145880 G1145880 TITIN ;
6422	19489	32739	3.5	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6422	19489	32740	3.5	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7742	20696	34061	0.98	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7742	20696	34062	0.98	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7869	20908	34296	0.64	1.0E-126	AU136463.1	EST_HUMAN	AU136463 PLACE1 Homo sapiens cDNA clone PLACE1004325 5'
8031	20988	34362	0.66	1.0E-126	A1806483.1	EST_HUMAN	wf0801.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350009 3' similar to SW:MPP2_HUMAN Q14168 MAGUK P55 SUBFAMILY MEMBER 2 ;
8210	21179	34587	0.92	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8210	21179	34588	0.92	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8320	21289	34703	4.9	1.0E-126	X16609.1	NT	Human mRNA for ankyrin (variant 2.1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8524	21492	34907	1.02	1.0E-126	AA483368.1	EST_HUMAN	ne74b12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:309983 similar to SW:TSG6_HUMAN
10155	23080	36555	0.44	1.0E-126	4505424	NT	P88066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR;
11208	24162	37692	4.45	1.0E-126	BF683176.1	EST_HUMAN	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
11846	24728	38315	2.96	1.0E-126	BE261660.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298240 5'
12765	18362	31297	7.78	1.0E-126	BE743922.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3302129 5'
173	13275	26201	1.37	1.0E-127	AB024597.1	NT	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
173	13275	26202	1.37	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
174	13275	26201	1.7	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
174	13275	26202	1.7	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
273	13369	26296	0.9	1.0E-127	D87675.1	NT	Homo sapiens DNA for anyfold precursor protein, complete cds
273	13369	26297	0.9	1.0E-127	D87675.1	NT	Homo sapiens DNA for anyfold precursor protein, complete cds
882	13937	26996	0.98	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
917	13971	26925	2.54	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1700	14730	27712	1.18	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2080	15097	28113	4.83	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2080	15097	28114	4.83	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2210	15225	28246	10.89	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2349	15358	28380	3.28	1.0E-127	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2617	15615	28840	2.23	1.0E-127	X12881.1	NT	Human mRNA for cyclokeratin 18
2628	15627	28651	1.15	1.0E-127	AA450131.1	EST_HUMAN	zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
2628	15627	28652	1.15	1.0E-127	AA450131.1	EST_HUMAN	zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
3702	16745	28658	0.98	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3824	16884	29768	0.81	1.0E-127	AW161297.1	EST_HUMAN	au80e08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN, contains element MER22 repetitive element;
4249	17278	30159	0.84	1.0E-127	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4282	17311	30189	20.15	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4282	17311	30189	20.15	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4523	17548	30436	1.42	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P-450 retinoid metabolizing protein P450RA-2 mRNA, complete cds
4533	17554	30541	5.27	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4663	17684		2.42	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4700	17721	30614	1.32	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							za01a10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291258 5' similar to SW:PIP6_RAT P10688 1-PHOSPHATIDYL INOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5791	18893	32065	1.46	1.0E-127	W03547.1	EST_HUMAN	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5826	18916	32100	2.07	1.0E-127	4826863	NT	H.sapiens NOS2 gene, exon 6
5900	18987	32178	4.51	1.0E-127	X85764.1	NT	H.sapiens TGF11 gene, exon 3-6
6286	19358	32594	1.95	1.0E-127	X84060.1	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
6454	19519	32769	5.46	1.0E-127	4504778	NT	Homo sapiens Immunoglobulin superfamily, member 3 (IGSF3), mRNA
6815	19689	33168	0.91	1.0E-127	11421695	NT	Homo sapiens reelin (RELN) mRNA
7264	19999	33298	1.05	1.0E-127	4826977	NT	Homo sapiens Pendred syndrome (PDS), mRNA
8066	21003	34400	1.34	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
8066	21003	34401	1.34	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
8076	21013	34413	0.98	1.0E-127	BF671355.1	EST_HUMAN	602161232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'
8079	21016	34416	0.6	1.0E-127	AW968292.1	EST_HUMAN	QV3-BN0046-150300-121-111 BN0046 Homo sapiens cDNA
9239	22205	35637	1.12	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9239	22205	35638	1.12	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9998	22925	36390	4.63	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9998	22925	36391	4.63	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10232	23157	36646	0.76	1.0E-127	AI296932.1	EST_HUMAN	qm94h09.x1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896449 3'
10708	23630	37125	1.88	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11492	24435	37983	5.12	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC83184), mRNA
11492	24435	37984	5.12	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC83184), mRNA
11949	24828	38423	2.78	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916917 5'
11949	24828	38424	2.78	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916917 5'
12089	21003	34400	2.11	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
12089	21003	34401	2.11	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
12532	13275	26201	1.39	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12532	13275	26202	1.39	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12721	26375	31776	2.4	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13082	25856		1.47	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
460	13533	26460	3.35	1.0E-128	BE365617.1	EST_HUMAN	601276127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1158	14200	27160	2.18	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1158	14200	27161	2.18	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2084	15101	28117	9.34	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2084	15101	28118	9.34	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2219	15233	28257	31.4	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2451	15456		1.49	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3405	16454	29377	1.23	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4893	17714	30609	5.95	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5824	18720	31879	0.84	1.0E-128	X69539.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6558	18618	32883	1.94	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (PDE1C), mRNA
7116	20050	33353	6.42	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3805764 5'
7661	20621	33986	0.69	1.0E-128	BE614105.1	EST_HUMAN	601503946F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3805764 5'
7983	20922	34313	0.53	1.0E-128	BF529931.1	EST_HUMAN	802042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'
7983	20922	34314	0.53	1.0E-128	BF529931.1	EST_HUMAN	802042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'
7983	20922	34315	0.53	1.0E-128	BF529931.1	EST_HUMAN	802042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'
8080	21017	34417	0.62	1.0E-128	11545923	NT	Homo sapiens putative ABC transporter (WHITE2), mRNA
8139	21076	34476	0.49	1.0E-128	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8139	21076	34477	0.49	1.0E-128	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8893	21859	35281	0.5	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8893	21859	35282	0.5	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10498	23418	36917	1.73	1.0E-128	AA639198.1	EST_HUMAN	ns04a11.1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338
11065	24028	37552	3.42	1.0E-128	11425254	NT	CHROMOSOME SEGREGATION GENE HOMOLOG CAS. ;
11073	24035	37559	3.94	1.0E-128	AA926959.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
11149	24108	37635	1.48	1.0E-128	AJ252060.1	NT	DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
11202	24156	37687	2.69	1.0E-128	BE384475.1	EST_HUMAN	Homo sapiens mRNA for TRABID protein (TRABID) gene
12400	25174		8.88	1.0E-128	AW955290.1	EST_HUMAN	601277826F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618750 5'
122	13486	26423	0.89	1.0E-128	S37722.1	NT	EST367360 MAGE resequences, MAGC Homo sapiens cDNA
413	13486	26423	1	1.0E-129	S37722.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1731	14761	27745	3.06	1.0E-129	AL096980.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1736	14766	27750	2.5	1.0E-129	AF240786.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1736	14766	27751	2.5	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1863	14888	27895	2.86	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3145	16202	28113	1.33	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3145	16202	28114	1.33	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3145	16202	28115	1.33	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4192	17223	30112	1.87	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4309	17338	30216	1.86	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
4309	17338	30217	1.86	1.0E-129	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
6210	19284	32516	4.28	1.0E-129	AJ006945.1	NT	Cardiomyopathy associated gene 5
6674	19731	33007	0.54	1.0E-129	BE88934.1	EST_HUMAN	Homo sapiens KVLQT1 gene
7334	20305	33849	4.07	1.0E-129	AJ006345.1	NT	601513961F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915350 5'
7396	20364	33716	6.8	1.0E-129	11420850	NT	Homo sapiens KVLQT1 gene
7771	20724	34095	0.78	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7771	20724	34096	0.78	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8661	21628		4.37	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10439	23361	36850	0.79	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10439	23361	36851	0.79	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10878	23798	37299	0.48	1.0E-129	AI199117.1	EST_HUMAN	q140d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840
10878	23798	37300	0.48	1.0E-129	AI199117.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIG-2;
11557	24497	38053	2.69	1.0E-129	AA025528.1	EST_HUMAN	q140d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1047569 5'
11630	20364	33716	6.2	1.0E-129	11420850	NT	MITOGEN INDUCIBLE GENE MIG-2;
12386	25164		4.21	1.0E-129	J883155.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
12758	25401		2.63	1.0E-129	AL120739.1	EST_HUMAN	y449c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199112 5' similar to SP:B48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN;
77	13194	26117	0.65	1.0E-130	7705530	NT	DKFZp762K171_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5'
1174	14215	27170	5.85	1.0E-130	AB037835.1	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1875	14707	27685	13.33	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens mRNA for KIAA1414 protein, partial cds
1675	14707	27686	13.33	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
2000	15021		3.15	1.0E-130	X04092.1	NT	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
							Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2781	15773		8.37	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2880	15949	28864	1.3	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885466 5'
2890	15949	28865	1.3	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885466 5'
3591	16638	29556	1.27	1.0E-130	AF240598.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3779	15949	28864	4.55	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885466 5'
3779	15949	28865	4.55	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885466 5'
3957	16937	29912	1.41	1.0E-130	AW503580.1	EST_HUMAN	U1-HF-BN0-aky-g-06-0-ULr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4059	17133	30027	1	1.0E-130	M97710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha RPM14265-variant, C alpha 1) mRNA
4569	17592	30485	8.22	1.0E-130	AW843993.1	EST_HUMAN	CM4-CN0045-180200-511-402 CN0045 Homo sapiens cDNA
5133	18142	31021	1.53	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
5133	18142	31022	1.53	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
6891	18943	33239	0.63	1.0E-130	X57825.1	NT	Human germline immunoglobulin lambda light chain pseudogene (VIL.1)
6994	20120	33433	0.89	1.0E-130	AW843875.1	EST_HUMAN	CMO-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6994	20120	33434	0.89	1.0E-130	AW843875.1	EST_HUMAN	CMO-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
7010	20136	33432	0.88	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7468	20432	33788	2.08	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7674	20536	33894	0.55	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7674	20536	33895	0.55	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
9030	21995		0.9	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
9171	22137	35563	2.81	1.0E-130	AW956242.1	EST_HUMAN	EST368312 MAGE resequences, MAGD Homo sapiens cDNA
9569	22531	35981	1.74	1.0E-130	AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
10293	23218		1.29	1.0E-130	AW103454.1	EST_HUMAN	xd36e06.x1 NCJ_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595874 3'
12015	24892	38489	1.71	1.0E-130	4504142	NT	Homo sapiens glutamate receptor, metabotropic 5 (GRM5) mRNA
13046	15773		1.44	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
4	13125	26023	2.64	0.0E+00	AA228126.1	EST_HUMAN	z58c04.r1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	13125	26024	2.64	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	13128	26028	2.59	0.0E+00	4885138	NT	z58c04.r1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
16	13136	26034	0.66	0.0E+00	8923349	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
16	13136	26035	0.66	0.0E+00	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
23	13143	26042	1.8	0.0E+00	D89327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13143	26043	1.8	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13143	26042	1.8	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
23	13143	26043	1.8	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
29	13149	26048	51.1	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
38	13158	26060	0.87	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
42	13162	26065	4.86	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
59	13178	26090	2.13	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	13178	26091	2.13	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	13180	26095	1.27	0.0E+00	D78804.1	EST_HUMAN	HUM1516H08B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'
61	13180	26096	1.27	0.0E+00	D78804.1	EST_HUMAN	HUM1516H08B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'
62	13181	26097	25.34	0.0E+00	L16568.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
64	13183	26100	11.49	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
64	13183	26101	11.49	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
68	13186		1.19	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
76	13193	26115	4.08	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
76	13193	26116	4.06	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
79	13193	26115	2.97	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
79	13193	26116	2.97	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
							Homo sapiens anion chloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
82	13198	26122	0.79	0.0E+00	4501850	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
83	13199		18.85	0.0E+00	4504444	NT	Homo sapiens actin, beta (ACTB) mRNA
91	13207	26131	80.78	0.0E+00	5016088	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
94	13210	26134	18.95	0.0E+00	U89277.1	NT	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
101	13217	26141	2.55	0.0E+00	A114743.1	EST_HUMAN	Homo sapiens mRNA for KIAA1363 protein, partial cds
102	13218	26142	1.19	0.0E+00	AB037784.1	NT	ts38b05.x1 NCJ CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
116	13227	26151	0.63	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCJ CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
117	13227	26151	0.78	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCJ CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
118	15909	26152	0.84	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270017 5'
118	15909	26153	0.84	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270017 5'
121	13230	26158	0.65	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
131	13236	26166	5.49	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
131	13236	26167	5.49	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
139	13474	26407	0.65	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
141	13244	26174	0.85	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
141	13244	26175	0.85	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
154	13267		64.2	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
158	13261	26188	4.4	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
160	13263		39.14	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
163	13268	26191	0.92	0.0E+00	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
165	13268	26192	0.74	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
166	13268	26192	1.17	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
167	13269	26193	2.37	0.0E+00	W73973.1	EST_HUMAN	z662b05.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to
168	13270	26194	0.85	0.0E+00	BE162832.1	EST_HUMAN	gb:XI6282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
168	13270	26195	0.85	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
168	13271	26196	1.59	0.0E+00	AF244088.1	NT	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
172	13274	26199	14.16	0.0E+00	AL163202.2	NT	Homo sapiens zinc finger protein mRNA, complete cds
172	13274	26200	14.16	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
182	13282	26207	4.87	0.0E+00	BE018970.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
182	13282	26208	4.87	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
187	13287	26211	4.35	0.0E+00	AB018327.1	NT	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
187	13287	26212	4.35	0.0E+00	AB018327.1	NT	CE22631.1
188	13288	26213	3.08	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
188	13288	26214	3.06	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
196	13297	26225	296.4	0.0E+00	D50659.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
200	13301	26229	4.35	0.0E+00	AF273045.1	NT	Human gamma-cytoplasmic actin (ACTG9) pseudogene
200	13301	26230	4.35	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set14-3 mRNA, complete cds
202	13303	26232	3.93	0.0E+00	AF167174.1	NT	Homo sapiens CTCL tumor antigen set14-3 mRNA, complete cds
202	13303	26233	3.93	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
211	15835	26239	51.32	0.0E+00	A1587308.1	EST_HUMAN	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
211	15835	26240	51.32	0.0E+00	A1587308.1	EST_HUMAN	tq0408.x1 NC1_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN1 (HUMAN);
213	13313	26242	1.57	0.0E+00	AF195658.1	NT	tq0408.x1 NC1_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN1 (HUMAN);
216	13316		43.74	0.0E+00	4506632	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
217	13317		6.46	0.0E+00	AF132000.1	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
223	13323	26248	1.5	0.0E+00	AB018264.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
							Homo sapiens mRNA for KIAA0721 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
224	13323	26248	1.81	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
225	13324	26249	3.11	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspy), mRNA
239	13338	26264	3.14	0.0E+00	5453806	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
240	13339		6.19	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
247	13344	26269	3.48	0.0E+00	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
249	13346	26272	2.06	0.0E+00	X89772.1	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
257	13354		6.67	0.0E+00	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
269	13365	26290	1.2	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
269	13365	26291	1.2	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
271	13367	26293	3.56	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
282	13377		1.55	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
283	13378	26306	1.75	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
283	13378	26307	1.75	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
284	13379		0.98	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
293	13387	26314	7.75	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
293	13387	26315	7.75	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
304	13398	26325	3.68	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
305	13399	26326	15.06	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
308	15838		12.15	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
307	13400	26327		0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
308	13401		1.85	0.0E+00	AA480002.1	EST_HUMAN	phosphoribosylaminimidazole synthetase (GART) mRNA
309	13402	26328	23.16	0.0E+00	4507152	NT	zvf18c06.r1 Sceres_Nh-MP_u_S1 Homo sapiens cDNA clone IMAGE:753894 5'
310	13402	26328	22.55	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
314	13408	26332	1.76	0.0E+00	AF114488.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
327	13418	26342	2.84	0.0E+00	O14867	SWISSPROT	Homo sapiens Intersectin short isoform (ITSN), complete cds
328	13419	26343	4.94	0.0E+00	7657213	NT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
329	13419	26343	1.14	0.0E+00	7657213	NT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
344	13433	26355	0.88	0.0E+00	5174574	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
345	13434	26356	2.48	0.0E+00	4505256	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
348	13437	26360	3.07	0.0E+00	4827057	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4
351	13440	26365	1.24	0.0E+00	U71600.1	NT	(MLLT4) mRNA
							Homo sapiens moesin (MSN), mRNA
							Homo sapiens X-box binding protein 1 (XBP1) mRNA
							Human zinc finger protein zfp31 (zfp31) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
356	13444	26369	2.64	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
356	13444	26370	2.54	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
357	15839	26371	2.87	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
359	13446	26373	0.97	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
361	13448	26376	0.9	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
362	13449	26377	1.91	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
363	13449	26377	1.41	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
365	13451	26379	0.63	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
376	13460	26390	2.41	0.0E+00	AU134983.1	EST_HUMAN	AU134983 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
387	13500	26433	7.69	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
388	13501	26434	2.78	0.0E+00	A1668014.1	EST_HUMAN	qy81h05.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE2018457 3' similar to gb:X54199
392	13467	26397	2.89	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);
395	13469	26400	1.3	0.0E+00	4503980	NT	RC3-CT0320-300100-076-e09 CT0320 Homo sapiens cDNA
396	13470	26401	2.24	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
396	13470	26402	2.24	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
397	13471	26403	1.22	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
398	13472	26404	1.27	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
398	13472	26405	1.27	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
399	13473	26406	3.09	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
400	13474	26407	0.67	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
401	13475	26408	2.69	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
401	13475	26409	2.69	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
402	13475	26408	2.37	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
402	13475	26409	2.37	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
406	13479		25.89	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
420	13115	26013	1.44	0.0E+00	R17795.1	EST_HUMAN	Y09a02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'
428	13502	26435	2.15	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
429	13503		15.71	0.0E+00	4506728	NT	phosphoribosylaminoimidazole synthetase (GART) mRNA
430	13504	26436	1.89	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
431	13505	26437	3.68	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
431	13505	26438	3.68	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
432	13506	26439	4.53	0.0E+00	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
							Mus musculus truncated SON protein (Son) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	13517		1.27	0.0E+00	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
446	13519	28452	8.45	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
451	13524		0.75	0.0E+00	AA324262.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
452	13525		1.25	0.0E+00	BE254447.1	EST_HUMAN	60111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
468	13541	28466	3.47	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
468	13541	28466	3.47	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
474	13546	28475	2.84	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
474	13546	28475	2.84	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
484	13557	28482	2.68	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
485	13558	28483	6.81	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
485	13558	28484	6.81	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
494	13566	28489	3.92	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
498	13568	28491	1.83	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
504	13576	28497	1.58	0.0E+00	BE385144.1	EST_HUMAN	60127495F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
505	13542	28498	1.88	0.0E+00	AW938825.1	EST_HUMAN	PM0-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
508	13579	28500	1.47	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
609	13580	28501	0.9	0.0E+00	8923855	NT	Homo sapiens PC326 protein (PC326), mRNA
613	13584		0.82	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
520	13591	28511	5.32	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
527	13643	28515	1.15	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
532	13603	28521	1.61	0.0E+00	BF028005.1	EST_HUMAN	60176485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996998 5'
538	13609	28528	2.23	0.0E+00	AB040609.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
541	13612	28531	10.84	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
542	13613	28532	4.48	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
542	13613	28533	4.46	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
544	13616	28535	0.99	0.0E+00	8923837	NT	Homo sapiens anillin (LOC54443), mRNA
545	13616	28536	1.2	0.0E+00	8923837	NT	Homo sapiens anillin (LOC54443), mRNA
545	13616	28537	1.2	0.0E+00	8923837	NT	Homo sapiens anillin (LOC54443), mRNA
							Homo sapiens X-linked antihidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
550	13620		5.14	0.0E+00	AF003528.1	NT	
558	13628	28546	1.55	0.0E+00	AW135324.1	EST_HUMAN	U1-H-B1-acb-h-04-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
568	13638		2.54	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
							Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
588	13658	28571	2.72	0.0E+00	5174742	NT	

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601	13668		15.19	0.0E+00	U04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
604	13671	26585	1.83	0.0E+00	BF104898.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
606	13673	26587	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
608	13673	26598	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
611	13678	26591	0.89	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
616	13681	26597	1.6	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
618	13681	26598	1.6	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
623	13688	26605	1.86	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
625	13690	26608	1.83	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
627	13692	26609	0.85	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
628	13693	26610	1.55	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
628	13693	26611	1.55	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
629	13694	26612	1.34	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
629	13694	26613	1.34	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
638	13702	26623	1.35	0.0E+00	AA399488.1	EST_HUMAN	z60007.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
640	13706	26627	4.81	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
644	13710	26630	1.86	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
644	13710	26631	1.86	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
647	13713	26631	5.61	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
664	13720	26643	2.78	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
658	13722	26646	2.3	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
659	13725	26650	3.11	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
663	13729	26653	0.99	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
663	13729	26654	0.99	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
669	13734	26659	4.94	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
669	13734	26660	4.94	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
675	15846		3.3	0.0E+00	X57147.1	NT	Human endogenous retrovirus phiE.1 (ERV9)
683	13746	26673	8.58	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
688	13751	26677	4.8	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
698	13760	26692	17.83	0.0E+00	7657488	NT	Homo sapiens similar to rat Integral membrane glycoprotein POM121 (POM121L1), mRNA
710	13772	26706	15.52	0.0E+00	AA814537.1	EST_HUMAN	np49d01.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
714	13778	26710	4.91	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
714	13776	26711	4.91	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
724	13786	26720	2.21	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
730	13791	26726	4.69	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
730	13781	26727	4.69	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
732	13793	26730	11.38	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
738	13789	26738	2.31	0.0E+00	BE241577.1	EST_HUMAN	TCAAP-1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) BAYOR-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
757	13817	26761	2.09	0.0E+00	AF226980.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
757	13817	26762	2.09	0.0E+00	AF226980.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
759	13819	26764	0.88	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
759	13819	26765	0.88	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
762	13822	26766	2.01	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
763	13823	26767	0.86	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
765	15850	26769	3.03	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
766	13825	26770	1.78	0.0E+00	BE969735.1	EST_HUMAN	601445647F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3849803 5'
770	13829	26774	3.68	0.0E+00	R48915.1	EST_HUMAN	y69g08.1 Soares breast 2NbtHst Homo sapiens cDNA clone IMAGE:154046 5'
771	13830	26775	2.14	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120KD (SF3A1), mRNA
779	13838	26783	1.88	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
782	13842	26787	2.77	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
793	13852	26799	2.38	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
793	13852	26800	2.38	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
798	13857	26804	2.72	0.0E+00	X89772.1	NT	H sapiens mRNA for interferon alpha/beta receptor (long form)
802	13861	26808	3.38	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
802	13861	26809	3.38	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
807	13865	26816	10.76	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
808	13866		9.93	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
825	13883	26836	1.58	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
826	13884	26837	2.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
828	13886	26839	1.82	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNK1) mRNA
834	13891	26845	3.12	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
834	13891	26846	3.12	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
835	13892	26847	1.34	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
840	13897	26852	2.18	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60KD) (GABPA), mRNA

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844	13900	26857	1.23	0.0E+00	4607500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
844	13900	26858	1.23	0.0E+00	4607500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
851	13907		1.78	0.0E+00	AF027453.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
855	13911	26869	4.48	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
855	13911	26870	4.48	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
856	13912	26871	10.69	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
857	13913	26872	4.54	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
858	13914	26873	14.11	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
862	13918	26876	1.18	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
862	13918	26877	1.18	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
863	13919	26878	1.8	0.0E+00	AA533272.1	EST_HUMAN	h66307.s1 NCL CGAP_P710 Homo sapiens cDNA clone IMAGE:987453
863	13919	26879	1.8	0.0E+00	AA533272.1	EST_HUMAN	h66307.s1 NCL CGAP_P710 Homo sapiens cDNA clone IMAGE:987453
864	13920		10.08	0.0E+00	BF67694.1	EST_HUMAN	602085579F1 NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:4248915 5'
868	13924	26880	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
868	13924	26881	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
869	13925	26882	1.95	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
869	13925	26883	1.95	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
892	13947	26906	0.86	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
899	13954	26911	1.72	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
899	13954	26912	1.72	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
909	13964	26921	1.69	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
919	13973		63.74	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
921	13973		24.73	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
922	13975	26927	0.71	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
923	13976	26928	2.39	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (Pl4) gene, exons 1-4, complete cds
925	13978	26930	0.64	0.0E+00	Z20856.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
925	13978	26931	0.84	0.0E+00	Z20856.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
926	13978	26932	0.63	0.0E+00	Z20856.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
926	13978	26933	0.63	0.0E+00	Z20856.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
946	13999	26950	2.86	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0994 protein, partial cds
946	13999	26951	2.66	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0994 protein, partial cds
952	14005	26957	0.88	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
953	14006	26958	8.74	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
954	14007	26959	0.72	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end

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955	14008	26980	0.83	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
955	14008	26981	0.83	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
963	15955	26988	2.24	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
963	15955	26989	2.24	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
965	14017	26971	10.17	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Mix2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA
976	14027	26981	2.04	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
984	14035	26987	1.86	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
984	14035	26988	1.86	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
984	14035	26989	1.86	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
986	14037	26992	3.55	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
986	14037	26993	3.55	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
995	14046	27000	2.25	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
1006	14056	27008	1.17	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1007	14057	27009	13.38	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1008	14057	27009	10.52	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1011	14060		2.58	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1012	14060		5.29	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1016	14064	27015	1.28	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1017	14084	27015	1.82	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1018	14064	27015	1.71	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1019	14065	27016	1.65	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1022	14068	27019	2.42	0.0E+00	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1026	14072	27023	1.21	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1027	14073		1.58	0.0E+00	AA458880.1	EST_HUMAN	aa8907.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW.PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;
1030	14076	27027	0.76	0.0E+00	N43182.1	EST_HUMAN	EST51124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1030	14076	27028	0.76	0.0E+00	N43182.1	EST_HUMAN	EST51124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1031	14077	27029	1.2	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1031	14077	27030	1.2	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1034	14080		3.19	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA
1049	14085	27046	2.4	0.0E+00	4759569	NT	Homo sapiens heat shock 70kD protein 98 (mortalin-2) (HSPA9B), mRNA

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1066	14111	27060	2.13	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1066	14111	27061	2.13	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1070	14115	27065	3.18	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1070	14115	27066	3.18	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1071	14116	27067	28.45	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1073	14118		0.82	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1075	14120	27071	3.85	0.0E+00	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1084	14128	27082	1.91	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1098	14142	27092	2.62	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-h08 BN0115 Homo sapiens cDNA
1121	14165	27116	5.54	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1121	14165	27117	5.54	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1134	14177	27127	0.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1134	14177	27128	0.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1135	14178	27129	33.54	0.0E+00	4508712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1137	14180	27131	2.34	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1140	14193	27134	8.07	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1142	14185	27135	20.89	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1143	14186	27136	5.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1143	14186	27137	5.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1147	14189	27140	1.84	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1148	14190	27141	0.76	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1148	14190	27142	0.76	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1149	14191	27143	1.25	0.0E+00	A1147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'
1151	14193	27145	1.68	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1160	14202	27154	3.19	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1160	14202	27155	3.19	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1161	14203	27156	0.89	0.0E+00	9966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1172	14213	27167	8.28	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1172	14213	27168	8.26	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1175	14216	27171	1.08	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1182	14223	27180	1.21	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1196	14236	27191	0.64	0.0E+00	AF073289.1	NT	Homo sapiens Na+/H+ exchanger isoform 2 (NHE2) mRNA, complete cds
1214	14252		1.24	0.0E+00	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1230	14268	27225	1.18	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

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1230	14288	27228	1.18	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1231	14289	27227	1.6	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1232	15881	27228	1.7	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1251	14287	27253	6.18	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1252	14288	27254	0.98	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1282	14297	27260	0.73	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PF4D4) mRNA
1271	14306		2.04	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1279	14314	27275	46.44	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1286	14321	27284	4.02	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSR9) mRNA, complete cds
1292	14327	27288	1.08	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1292	14327	27289	1.08	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1303	14339	27302	2	0.0E+00	5174748	NT	Homo sapiens Wolfgram syndrome (WFS) mRNA
1303	14339	27303	2	0.0E+00	5174748	NT	Homo sapiens Wolfgram syndrome (WFS) mRNA
1303	14339	27304	2	0.0E+00	5174748	NT	Homo sapiens Wolfgram syndrome (WFS) mRNA
1304	14340		3.46	0.0E+00	AF086156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1314	15863	27316	1.26	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1314	15863	27317	1.26	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1319	14354	27322	6.23	0.0E+00	5803148	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1320	14355	27323	0.81	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1322	14357	27324	6.68	0.0E+00	5803148	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1323	14358	27325	33.1	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1325	14360	27327	4.74	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1326	14361	27328	5.7	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1327	14362	27329	9.47	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1328	14363	27330	5.14	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1328	14363	27331	5.14	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1340	14374	27344	2.17	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1407	14440	27410	1.34	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyd gene
1415	14448	27421	1.79	0.0E+00	AI208756.1	EST_HUMAN	q38b06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP.T27A1.5 CE14213
1416	14449	27422	32.54	0.0E+00	6042208	NT	RAN, member RAS oncogene family-Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1423	14456	27430	1.31	0.0E+00	4505946	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1423	14456	27431	1.31	0.0E+00	4505946	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1425	14458	27434	2.29	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1425	14458	27435	2.29	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1427	14460	27436	6.81	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alt repeat elements
1434	14468	27445	2.91	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1447	14480	27456	1.01	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1447	14480	27457	1.01	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1457	14490	27464	3.14	0.0E+00	AL132998.1	NT	Novel human gene on chromosome 20
1459	14492	27465	2.5	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1463	14498	27470	1.59	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1466	14499	27473	5.38	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1468	14501	27475	1.7	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1468	14501	27476	1.7	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1469	14502		1.04	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1513	14545	27516	2.11	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51698), mRNA
1528	14561	27532	1.94	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE315118 5'
1534	14567	27536	29.54	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1534	14567	27537	29.54	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1536	14569	27540	1.37	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGC resequences, MAGN Homo sapiens cDNA
1536	14569	27541	1.37	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGC resequences, MAGN Homo sapiens cDNA
1538	14571		2.22	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1539	14572	27544	2.25	0.0E+00	M16769.1	NT	Human T-cell receptor gamma chain VJCI-CII region mRNA, complete cds
1540	14573	27545	2.04	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1540	14573	27546	2.04	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1541	14574	27547	3.31	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1542	14575		7.04	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1548	14581	27553	2.45	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1551	14584	27555	1.24	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1551	14584	27556	1.24	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1552	15871		19.78	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1553	14585	27557	26.31	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1553	14586	27571	0.94	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1553	14586	27572	0.94	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1555	14598	27573	10.15	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1583	14616	27589	9.8	0.0E+00	Z83738.1	NT	H. sapiens HH2B/e gene
1584	14617	27590	1.81	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1584	14617	27591	1.81	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1585	14618	27592	12.62	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKBOFO2 5'
1585	14618	27593	12.62	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKBOFO2 5'
1588	15872	27596	2.64	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1592	14624	27597	1.24	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1594	14626	27600	4.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1594	14626	27601	4.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1596	14628	27602	26.28	0.0E+00	5729878	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1596	14628	27603	26.28	0.0E+00	5729878	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1598	14630	27605	1.68	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1613	14845	27621	7.01	0.0E+00	H26973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b-4H55Y Homo sapiens cDNA clone IMAGE:183848 3'
1622	14655	27632	2.31	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1622	14655	27633	2.31	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1644	14676	27649	1.04	0.0E+00	AW444637.1	EST_HUMAN	UI-H-BJ3-ajw-c-04-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1673	14705	27682	1.19	0.0E+00	BE144394.1	EST_HUMAN	MRO-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1673	14705	27683	1.19	0.0E+00	BE144394.1	EST_HUMAN	MRO-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1677	14709	27687	1.84	0.0E+00	AI768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2HIS2 ZINC FINGER PROTEIN. ;
1678	14710	27688	1.44	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1679	14711	27689	3.61	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1683	14714	27693	1.72	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1683	14714	27694	1.72	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1685	14716	27696	1.53	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1686	14717	27697	2.12	0.0E+00	7657085	NT	Homo sapiens v-ba avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1690	14721	27700	1.27	0.0E+00	BE222374.1	EST_HUMAN	hu11405.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1690	14721	27701	1.27	0.0E+00	BE222374.1	EST_HUMAN	hu11405.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1693	14723	27705	5.17	0.0E+00	H30132.1	EST_HUMAN	yo59408.r1 Soares breast 3NbHbSt Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1693	14723	27706	5.17	0.0E+00	H30132.1	EST_HUMAN	yo59408.r1 Soares breast 3NbHbSt Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1695	14726		0.94	0.0E+00	AI149880.1	EST_HUMAN	q14309.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
1696	14726	27708	7.26	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
1696	14726	27709	7.26	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
1699	14729		28.3	0.0E+00	6031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1708	14739	27721	0.91	0.0E+00	AF169963.1	NT	Homo sapiens WNT16 protein (WNT16) mRNA, complete cds
1710	14740	27724	5.35	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1713	14743	27727	1.03	0.0E+00	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1716	14746	27731	0.96	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1716	14746	27732	0.96	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1720	14750	27736	1.37	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1), mRNA
1726	14756	27743	20.03	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1728	14758		2.59	0.0E+00	S84400.1	NT	TCR zeta [human, Genomic]mRNA, 365 nt, segment 1 of 8]
1737	14767	27752	0.97	0.0E+00	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
1744	15876	27759	1.21	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1760	14789	27775	2.63	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1800	15877		35.79	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1805	14833	27821	2.42	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1805	14833	27822	2.42	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1807	14835	27825	2.05	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1810	14838		1.32	0.0E+00	W76571.1	EST_HUMAN	z166g09.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345664 5'
1811	15878	27829	3.9	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1812	14839	27830	1.13	0.0E+00	AA113030.1	EST_HUMAN	z166g09.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563056 3'
1824	14851	27845	14.85	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1826	14853	27848	5.94	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1827	14864	27849	6.64	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1827	14854	27850	6.64	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1827	14854	27850	6.64	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1827	14854	27850	6.64	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1851	14877	27873	6.58	0.0E+00	6005855	NT	Homo sapiens Relina-derived POU-domain factor-1 (RPF-1), mRNA
1851	14877	27873	6.58	0.0E+00	6005855	NT	Homo sapiens Relina-derived POU-domain factor-1 (RPF-1), mRNA
1851	14877	27873	6.58	0.0E+00	6005855	NT	Homo sapiens Relina-derived POU-domain factor-1 (RPF-1), mRNA
1861	14887	27883	1.34	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1861	14887	27884	1.34	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1865	14890	27886	3.28	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1865	14890	27887	3.28	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1866	14891	27888	6.66	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1866	14891	27889	6.66	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1869	14884	27892	1.48	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B1-afn-f-07-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1869	14894	27893	1.48	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B1-afn-f-07-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1892	14917	27912	3.46	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1892	14917	27913	3.46	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1936	14960	27959	0.93	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1936	14960	27957	0.93	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1939	14963	27959	2.02	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1939	14963	27960	2.02	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1948	14972	27971	1.13	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1949	15881	27970	1.41	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1949	15881	27971	1.41	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1954	14977	27978	2.02	0.0E+00	4507494	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1954	14977	27979	2.02	0.0E+00	4507494	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1957	14979	27981	1.06	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1959	14981		5.63	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1964	14986		2.93	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1965	15892	27988	1.46	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1973	14994	27998	1.88	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1973	14994	27998	1.88	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1984	15005		0.9	0.0E+00	AL183252.2	NT	Homo sapiens chromosome 21 segment HS21C052
1986	15007	28010	1.81	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1986	15007	28011	1.81	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1987	15008	28012	2.97	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1987	15008	28013	2.97	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1997	15018	28025	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
1997	15018	28028	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2003	15024	28030	1.59	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2003	15024	28031	1.59	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2005	15026	28032	1.29	0.0E+00	AW193024.1	EST_HUMAN	xi69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879913 3'
2005	15026	28033	1.29	0.0E+00	AW193024.1	EST_HUMAN	xi69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879913 3'
2006	15027	28034	6.19	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2006	15027	28035	6.19	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2008	15028	28037	1.33	0.0E+00	AB011148.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2009	15030	28038	1.38	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2009	15030	28039	1.36	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2016	15037	28048	3.07	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2036	15055	28072	1.18	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2036	15055	28073	1.16	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2069	15086	28104	1.04	0.0E+00	7706742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2074	15091	28108	0.92	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2075	15092	28109	4.79	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2077	15094	28111	1.69	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2077	15094	28112	1.69	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2079	15098		3.79	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2081	15098		1.64	0.0E+00	4585963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2083	15100		1.7	0.0E+00	AJ244247.1	EST_HUMAN	qy60f08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element;
2088	15105	28123	3.3	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2089	15108	28124	1.88	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2089	15108	28125	1.88	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2093	15110	28129	2.38	0.0E+00	BE697125.1	EST_HUMAN	RC3-C70413-270700-022-d10 C70413 Homo sapiens cDNA
2093	15110	28130	2.38	0.0E+00	BE697125.1	EST_HUMAN	RC3-C70413-270700-022-d10 C70413 Homo sapiens cDNA
2098	15115	28136	2.35	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2098	15115	28137	2.35	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2103	15120	28147	2.29	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2122	15139		3.16	0.0E+00	BE767954.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2123	15140		1.29	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2125	15142	28159	3.87	0.0E+00	BF027582.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2126	15143	28160	1.42	0.0E+00	BE072624.1	EST_HUMAN	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2128	15145	28161	1.26	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2131	15148	28163	2.85	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2133	15150	28165	4.92	0.0E+00	AI804840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2133	15150	28166	4.92	0.0E+00	AI804840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2191	15206		1.37	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2198	15211	28229	0.93	0.0E+00	BE274698.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2198	15213	28232	16.22	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2198	15213	28233	16.22	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2200	15216	28235	1.16	0.0E+00	AA931691.1	EST_HUMAN	cc32a01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2204	15219	28239	32.02	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5'
2205	15220	28240	25.7	0.0E+00	BE748699.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2209	15224	28244	6.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2209	15224	28245	6.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2213	15887	28250	1.7	0.0E+00	BF313617.1	EST_HUMAN	bb84a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170
2216	15230	28253	1.26	0.0E+00	BE018750.1	EST_HUMAN	TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;
2217	15231	28254	1.59	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2217	15231	28255	1.59	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2225	15239	28263	3.38	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2225	15239	28264	3.38	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2230	15244		1.57	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2252	15266	28293	7.38	0.0E+00	4557568	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2258	15272	28297	1.33	0.0E+00	7662401	NT	Homo sapiens KIAA0052 protein (KIAA0052), mRNA
2264	15278	28303	2.29	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2266	15280	28305	1.56	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2266	15280	28306	1.56	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2269	15282	28308	1.54	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2308	15320	28340	1.32	0.0E+00	BF344756.1	EST_HUMAN	602014009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149770 5'
2308	15320	28341	1.32	0.0E+00	BF344756.1	EST_HUMAN	602014009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149770 5'
2309	15321	28342	4.01	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2309	15321	28343	4.01	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2310	15322	28344	2.11	0.0E+00	AI079404.1	EST_HUMAN	cd06c07.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2312	15324	28346	1.43	0.0E+00	AA428001.1	EST_HUMAN	zv78a11.1 Soares fetal_liver_9w Homo sapiens cDNA clone IMAGE:759740 5'
2312	15324	28347	1.43	0.0E+00	AA428001.1	EST_HUMAN	zv78a11.1 Soares fetal_liver_9w Homo sapiens cDNA clone IMAGE:759740 5'
2314	15328	28348	2.21	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4157339 5'
2315	14572	27544	1.36	0.0E+00	M16768.1	NT	Human T-cell receptor gamma chain VJCI-CII-CIII region mRNA, complete cds
2320	15331	28355	1.09	0.0E+00	L02840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2321	15332	28356	1.57	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2327	15338	28361	1.83	0.0E+00	BE676095.1	EST_HUMAN	7f22a02.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94939 O94939 KIAA0857 PROTEIN ;
2330	15341	28363	5.18	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHK42) gene, exon 32
2331	15342	28364	2.11	0.0E+00	AI625542.1	EST_HUMAN	iy57c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2336	15347	28368	1.76	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2336	15347	28369	1.76	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2342	15352	28372	1.44	0.0E+00	7862007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2342	15352	28373	1.44	0.0E+00	7862007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2346	15355	28377	0.97	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2346	15355	28378	0.97	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2356	15365	28386	3.77	0.0E+00	5174878	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1), mRNA
2360	15368	28390	1.86	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2361	15369		8.67	0.0E+00	BE794028.1	EST_HUMAN	601566843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2362	15370	28391	1.23	0.0E+00	AW567076.1	EST_HUMAN	MR1-SND033-120400-002-e04 SND033 Homo sapiens cDNA
2363	15371	28392	3.7	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2364	15372	28393	2.27	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2364	15372	28394	2.27	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2365	15373		6.34	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A6) gene, partial cds
2367	15375	28396	13.47	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2367	15375	28397	13.47	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2367	15375	28398	13.47	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2368	15376	28399	0.96	0.0E+00	8923089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2424	15431	28453	1.11	0.0E+00	AU118582.1	EST_HUMAN	AU118582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2428	15433		4.37	0.0E+00	AI042035.1	EST_HUMAN	ox60b02.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1660693 3' similar to TR:O08662 O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2429	15436		1.2	0.0E+00	BE959505.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2439	15446		1.83	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HeLa cDNA (T.Nome) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2443	15449	28468	5.37	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2446	15451	28471	2.23	0.0E+00	D85608.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2448	15451	28472	2.23	0.0E+00	D85608.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2454	15459	28481	3.38	0.0E+00	AF106276.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2459	15463	28486	1.08	0.0E+00	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153670 5'
2466	15470	28494	3.44	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2470	15474	28497	1.27	0.0E+00	BE831003.1	EST_HUMAN	CMD-MT0033-150600-428-111 MT0033 Homo sapiens cDNA
2470	15474	28498	1.27	0.0E+00	BE831003.1	EST_HUMAN	CMD-MT0033-150600-428-111 MT0033 Homo sapiens cDNA
2475	15478	28502	1.03	0.0E+00	U13668.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2475	15479	28503	1.03	0.0E+00	U13668.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2478	15480	28504	3.72	0.0E+00	BF569144.1	EST_HUMAN	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2486	15490	28514	2.12	0.0E+00	AW466922.1	EST_HUMAN	ha04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2488	15492	28515	3.03	0.0E+00	AW501010.1	EST_HUMAN	U1HF-BP0p-ais-c-07-0-U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2513	15516		2.64	0.0E+00	AW813853.1	EST_HUMAN	RC3-S T0197-300300-016-c04 ST0197 Homo sapiens cDNA
2517	15520	28543	11.9	0.0E+00	BE785942.1	EST_HUMAN	601692530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2518	15521	28544	1.43	0.0E+00	BF609482.1	EST_HUMAN	U1H-B14-aoz-b-08-0-U1.1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2521	15524	28546	2.26	0.0E+00	Z32884.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2523	15528		4.58	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
2526	15529	28550	3.56	0.0E+00	7857468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2527	15530	28551	2.51	0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2533	15536	28557	1.6	0.0E+00	BE886490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909863 5'
2538	15540	28563	6.2	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2538	15540	28564	6.2	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2539	15541	28565	1.07	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF6
2541	15543	28568	1.11	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2568	15560	28576	1.25	0.0E+00	BE536921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2563	15564	28583	3.18	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2563	15564	28584	3.18	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2564	15565	28585	1.51	0.0E+00	BE292898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2564	15565	28586	1.51	0.0E+00	BE292898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2565	15568	28587	1.4	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3' similar to TR:O00248 O00246 HYPOTHETICAL 8.3 KD PROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
2568	15509	28589	8.56	0.0E+00	AF245505.1	NT	Homo sapiens edlican mRNA, complete cds
2589	15580	28607	1.03	0.0E+00	BE296813.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
2606	15827	28629	2.16	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2606	15827	28630	2.16	0.0E+00	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2607	15608		2.35	0.0E+00	BF513835.1	EST_HUMAN	U1-H-BW1-amp-f-12-Q-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2611	15610	28634	1.01	0.0E+00	BF672818.1	EST_HUMAN	602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293612 5'
2620	15618	28642	1.11	0.0E+00	AI571737.1	EST_HUMAN	In19b08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gbl:20877 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN); Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF21)
2621	15619	28643	2.57	0.0E+00	5032160	NT	mRNA
2623	15622	28647	7.78	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2624	15623	28648	1.25	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2624	15623	28649	1.25	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2634	15633		8.15	0.0E+00	BE792472.1	EST_HUMAN	601594930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2642	15640	28664	2.66	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2653	15650		1.32	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2654	15651	28672	5.99	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2658	15655	28673	110.09	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2661	15658	28676	1.22	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2662	15659	28677	0.92	0.0E+00	M69225.1	NT	Human bulbus pemphigoid antigen (BPAG1) mRNA, complete cds
2664	15661	28679	1.26	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2664	15661	28680	1.26	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2667	15664	28683	2.07	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-d07 OT0086 Homo sapiens cDNA
2670	15667	28686	1.12	0.0E+00	BF000018.1	EST_HUMAN	7H15H05.x1 NCI_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:3316089 3'
2671	15668	28687	5.39	0.0E+00	BE383165.1	EST_HUMAN	601288714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2672	15669		3.03	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2709	15703	28719	0.92	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2732	15726		11.44	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2733	15727	28741	1.11	0.0E+00	BE794894.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2739	15733	28749	3.65	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2740	15734	28750	1.05	0.0E+00	7699517	NT	Homo sapiens neurogranin 1 (NRG1), transcript variant SMDF, mRNA
2741	15735	28751	1.6	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2748	15741	28758	9.77	0.0E+00	BE796376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2751	15903	28762	13.57	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2752	15744		1.22	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2754	15746	28765	2.9	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2754	15746	28766	2.9	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2755	15747	28767	0.98	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2755	15747	28768	0.98	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2756	15748	28769	3.23	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2757	15749		48.84	0.0E+00	AV651068.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2758	15750	28770	8.5	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2758	15750	28771	6.5	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2762	15754	28774	0.94	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2762	15754	28775	0.94	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2766	15758	28780	2.96	0.0E+00	BE747193.1	EST_HUMAN	601590903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2769	15771		1.71	0.0E+00	AL163201.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
2770	15772	28782	4.09	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-armw-e-07-QJLs1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2786	15778		1.02	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2792	15784	28800	1.56	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2792	15784	28801	1.56	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2793	15785	28802	4.03	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2793	15791	28810	1.58	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR), mRNA
2803	15795	28813	15.3	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2803	15795	28814	15.3	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2805	15797		13.6	0.0E+00	AI879183.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to
2806	15800	28819	2.83	0.0E+00	BF530681.1	EST_HUMAN	SW_R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2809	15801	28820	3.53	0.0E+00	BE872768.1	EST_HUMAN	602071957F1 NCI_CGAP_Bin87 Homo sapiens cDNA clone IMAGE:4214679 5'
2811	15803	28821	1.98	0.0E+00	AU131494.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854942 5'
2811	15803	28822	1.98	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2812	15804	28823	34.94	0.0E+00	BE300344.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2812	15804	28824	34.94	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960808 5'
2817	13290	26216	7.12	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2820	15811		0.75	0.0E+00	AB033281.1	NT	Homo sapiens BTROP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2826	13796	28735	1.8	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2826	13798	28736	1.8	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2830	14088	27037	3.41	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2830	14088	27038	3.41	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2847	15907	28832	2.28	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2848	15908		3.02	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
2850	15910		1.9	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2852	15912	28835	1.07	0.0E+00	4502568	NT	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10) mRNA
2852	15912	28836	1.07	0.0E+00	4502568	NT	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10) mRNA
2857	15917		0.98	0.0E+00	AJ238852.1	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2858	15918	28839	3.25	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2862	15922	28842	1.8	0.0E+00	M80802.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2865	15925	28844	0.98	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281299-003-602 HT0343 Homo sapiens cDNA
2865	15925	28845	0.98	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281299-003-602 HT0343 Homo sapiens cDNA
2867	15927		1.48	0.0E+00	X73428.1	NT	H. sapiens l33 gene for HLH type transcription factor
2868	15928		3.61	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2870	15930	28847	1	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2874	15933	28850	25.84	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2874	15933	28851	25.84	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2877	15936	28854	2.34	0.0E+00	AL068857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2878	15937		5.17	0.0E+00	Y10558.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2879	15938		1.17	0.0E+00	AF152303.1	NT	Homo sapiens probocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2880	15939	28855	61.62	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2880	15939	28856	61.62	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2891	15950	28866	2.45	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2894	15953	28870	0.91	0.0E+00	AL047599.1	EST_HUMAN	DKFZp586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621
2895	15954	28871	1.07	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2895	15954	28872	1.07	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2896	15955		2.07	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2898	15957	28874	5.43	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2898	15957	28875	5.43	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2903	15962	28883	0.53	0.0E+00	8806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2903	15962	28884	0.63	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2906	15965	28888	2.52	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2906	15965	28889	2.52	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2907	15966	28890	0.94	0.0E+00	AA215579.1	EST_HUMAN	z96b11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element
2915	15973		4.07	0.0E+00	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
2918	15976	28900	1.17	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2919	15977	28901	23.04	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2920	15978	28902	0.92	0.0E+00	AI581002.1	EST_HUMAN	ht18d07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2920	15978	28903	0.92	0.0E+00	AI581002.1	EST_HUMAN	O16247 F44E7.2 PROTEIN. ;
2922	15980	28905	0.97	0.0E+00	AF152338.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2931	15989	28910	1.26	0.0E+00	AI209084.1	EST_HUMAN	q94904.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838527 3' similar to SW:CB20_HUMAN P52298 20 KD NUCLEAR CAP BINDING PROTEIN ;
2939	15997	28918	2.92	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2939	15997	28919	2.92	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2940	15998	28920	4.91	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2940	15998	28921	4.91	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2943	16001	28924	2.56	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2943	16001	28925	2.56	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2944	16002	28926	2.73	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23) translocated to, 4 (MLLT4) mRNA
2944	16002	28927	2.73	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23) translocated to, 4 (MLLT4) mRNA
2956	16014	28941	2.36	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2956	16014	28942	2.36	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2965	16023	28948	1.71	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
2966	16024		1.03	0.0E+00	X98494.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2971	16028	28952	7.63	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2985	16043		1.1	0.0E+00	AI149880.1	EST_HUMAN	q43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2994	16052	28973	0.97	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
2995	16053	28974	2.71	0.0E+00	AB004894.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3007	16055	28984	1.51	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
3008	16066	28985	1.96	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3008	16066	28986	1.96	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3016	16074	28994	0.95	0.0E+00	AF114488.1	NT	Homo sapiens intercedin short isoform (ITSN) mRNA, complete cds
3016	16074	28995	0.95	0.0E+00	AF114488.1	NT	Homo sapiens intercedin short isoform (ITSN) mRNA, complete cds
3038	16096		0.74	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3040	16098	29014	1.28	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
3050	16107	29021	0.88	0.0E+00	4506882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3052	16109	29023	0.76	0.0E+00	AW976286.1	EST_HUMAN	EST388375 MAGE resequences, MAGN Homo sapiens cDNA
3057	16114		4.37	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3060	16117	29031	15.24	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3060	16117	29032	15.24	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3062	16119		6.14	0.0E+00	AL359403.1	NT	Isocform 2 of a novel human mRNA from chromosome 22
3066	16123	29036	2.48	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha
3069	16128		1.66	0.0E+00	AF198779.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
3084	16141	29052	0.73	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
3092	16150	29064	12.69	0.0E+00	X03529.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3098	16155		1.77	0.0E+00	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3102	16159	29071	1.71	0.0E+00	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3123	16180	29080	4.2	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3124	16181	29091	4.68	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3129	16186	29095	2.83	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3130	16187	29096	1.56	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3157	16213	29128	4.32	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3165	16220	29135	22.34	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3168	16223	29138	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3168	16223	29139	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3174	16229	29145	21.23	0.0E+00	T94870.1	EST_HUMAN	ye32103.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539
3190	16245	29163	1.13	0.0E+00	BF243336.1	EST_HUMAN	S29539 BASIC PROTEIN, 23K - ;
3192	16247	29164	1.11	0.0E+00	AI968086.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107493 5'
3197	16252	29171	4.28	0.0E+00	X98922.1	NT	wu12h10.xt NO1_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516803 3'
							H.sapiens mRNA for gamma-glutamyltransferase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3197	16252	29172	4.28	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3207	16262	29183	1.16	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3207	16262	29184	1.16	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3213	16268	29181	9.61	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3230	16285	29208	3.9	0.0E+00	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3234	16289	29211	1.55	0.0E+00	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3240	16295	29219	0.98	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3240	16295	29220	0.98	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3242	16297	29221	3.35	0.0E+00	AA774783.1	EST_HUMAN	aa87b11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3250	16305	29229	3.58	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3250	16305	29230	3.58	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3261	16315	29235	1.15	0.0E+00	4557560	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3267	16321	29243	1.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3275	16329	29250	1.04	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
3278	16332	29253	4.45	0.0E+00	AF050084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3288	16312	29261	2.4	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3288	16312	29262	2.4	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3303	16356	29275	2.89	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3304	16357	29276	0.86	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3335	16386	29307	2.87	0.0E+00	AI589294.1	EST_HUMAN	t58f08.x2 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:222635 3' similar to SW:RL11_RAT
3343	16394	29315	2.44	0.0E+00	AF128893.1	NT	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3343	16394	29316	2.44	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3344	16395	29317	0.85	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3344	16395	29318	0.85	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3346	16397	29319	1.11	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3346	16397	29320	1.11	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3349	16400	29322	10.77	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3351	16402	29324	1.09	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3358	16408	29330	0.85	0.0E+00	BE778039.1	EST_HUMAN	801464955F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3369	16419	29344	0.79	0.0E+00	AI632569.1	EST_HUMAN	wb10704.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91929
3407	16456	29379	4.18	0.0E+00	AU123664.1	EST_HUMAN	ZINC FINGER PROTEIN. ;
3414	16462	29382	1.15	0.0E+00	7363438	NT	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3414	16462	29383	1.15	0.0E+00	7363438	NT	Homo sapiens difactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3417	16465	29385	6.29	0.0E+00	7706239	NT	Homo sapiens difactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3418	16466	29386	1.51	0.0E+00	AF211189.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3436	16483	29401	1.13	0.0E+00	7662401	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
3436	16483	29402	1.13	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3437	16484	29403	1.05	0.0E+00	4502398	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3441	16488	29406	2.77	0.0E+00	5803067	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3450	15735	29751	1.38	0.0E+00	AF110763.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3455	16501	29419	2.15	0.0E+00	7657038	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3456	16502	29420	1.05	0.0E+00	5453965	NT	Homo sapiens death receptor 6 (DR6), mRNA
3456	16502	29421	1.05	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3459	16505	29425	1	0.0E+00	AJ277276.1	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3459	16505	29426	1	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
3460	16506	29427	5.55	0.0E+00	K02390.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
3463	16509	29430	1.31	0.0E+00	7427622	NT	Bacteriophage P1 replication region including repA, para, and parB genes and incA, incB, and incC incompatibility determinants
3469	16515	29435	5.12	0.0E+00	AI935159.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR), mRNA
3469	16515	29436	5.12	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3473	16519	29441	1.68	0.0E+00	AJ278120.1	NT	NEURAL CELL ADHESION MOLECULE. ;
3479	16525	29449	6.24	0.0E+00	6552332	NT	wp14d10.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3479	16525	29450	6.24	0.0E+00	6552332	NT	NEURAL CELL ADHESION MOLECULE. ;
3485	16531	29456	1.06	0.0E+00	M14123.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3490	16536	29461	6.79	0.0E+00	U43283.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3497	16544	29469	1.85	0.0E+00	AF045452.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3497	16544	29470	1.85	0.0E+00	AF045452.1	NT	Human endogenous retrovirus HERV-K10
3504	16551	29478	0.99	0.0E+00	AF231922.1	NT	Human MDS1A (AVL1MDS1 fusion) mRNA, partial cds
							Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
							Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
							Homo sapiens chromosome 21 unknown mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3516	16562	29486	2.29	0.0E+00	BE304791.1	EST_HUMAN	601143953F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3516	16562	29487	2.28	0.0E+00	BE304791.1	EST_HUMAN	601143953F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3519	16565	29490	1.07	0.0E+00	4826785	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3521	16567	29491	1.24	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3526	16572	29495	0.88	0.0E+00	A1384007.1	EST_HUMAN	le35g12.x1 Soares NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:2086742 3' similar to TR:000498
3529	16575	29498	1.08	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
3543	16589	29513	0.92	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3543	16589	29514	0.92	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3551	16597	29522	1.38	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ADBDAH08 5'
3552	16598	29523	0.92	0.0E+00	4506884	NT	Homo sapiens semogelin II (SEM/G2) mRNA
3554	16600		1.03	0.0E+00	AF078668.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3563	16609	29531	0.82	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3567	16612	29534	1.21	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3578	16623	29544	1.33	0.0E+00	8623087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3588	16633	29551	1.16	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3588	16633	29552	1.16	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3590	16635	29555	1.06	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3595	16640		4.69	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3602	16647		1.35	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCCL) gene, partial cds
3603	16648	29564	10.61	0.0E+00	BF676393.1	EST_HUMAN	602084563F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3617	16661	29579	1.04	0.0E+00	AW937977.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3629	16672	29585	1.46	0.0E+00	BF672054.1	EST_HUMAN	602182486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3629	16672	29586	1.46	0.0E+00	BF672054.1	EST_HUMAN	602182486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3630	16673		0.84	0.0E+00	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3632	16675	29588	0.84	0.0E+00	AW684693.1	EST_HUMAN	hB4g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3632	16675	29589	0.84	0.0E+00	AW684693.1	EST_HUMAN	hB4g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3636	16679	29593	0.83	0.0E+00	4826763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3638	16681	29596	1.03	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3646	16689	29604	0.67	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3646	16689	29605	0.67	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3661	16704	29618	3.11	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3664	16707		10.78	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3681	16724	29637	16.15	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds

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3685	16728	29839	4.02	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3685	16728	29840	4.02	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3692	16735	29847	1.6	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3692	16735	29848	1.8	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3695	16738	29851	1.34	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281098-005-e05 CT0222 Homo sapiens cDNA
3697	16740	29853	2.88	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3699	16742	29855	1.37	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
3701	16744	29857	0.72	0.0E+00	Q14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3703	16746	29859	1.45	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3703	16748	29860	1.45	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3705	16748	29862	1	0.0E+00	7662237	NT	Homo sapiens KIAA0670 protein/actin (KIAA0670), mRNA
3705	16748	29863	1	0.0E+00	7662237	NT	Homo sapiens KIAA0670 protein/actin (KIAA0670), mRNA
3719	16762	29872	4.6	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-O-UI st NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3719	16762	29873	4.6	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-O-UI st NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3742	16784	29896	1.47	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 8
3743	16785	29897	1.06	0.0E+00	AA463659.1	EST_HUMAN	aa06g01.r1 Soares, NHMMPu S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB4, [1];
3747	16789	29701	0.76	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3750	16792	29703	3.92	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3760	16801	29713	0.77	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3772	16814	29723	5.64	0.0E+00	7652183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3775	16817	29726	19.76	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3781	16822	29729	0.97	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3781	16822	29730	0.97	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3784	16825	29733	0.92	0.0E+00	4505594	NT	Homo sapiens plasminogen activator inhibitor, type II (arginine-serpin) (PAI2) mRNA
3834	16874	29776	3.15	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3837	16877	29778	2.76	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3837	16877	29780	2.76	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3843	16883	29787	0.91	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3843	16883	29788	0.91	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3844	16884	29789	1.01	0.0E+00	AI377699.1	EST_HUMAN	ta62f10.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3845	16885		1.81	0.0E+00	AF152496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3846	16886	29780	0.97	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3850	16890	28794	16.29	0.0E+00	578595.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/IR1) gene, complete cds
3852	16892	28786	2.25	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3853	16893	28797	1.54	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3857	16897	28800	1.1	0.0E+00	4504534	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D), mRNA
3862	16901	29805	1.15	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3862	16901	29806	1.15	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3863	16902	29807	0.77	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3868	16907	29816	7.17	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5), mRNA
3868	16907	29816	7.17	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5), mRNA
3870	16909	28819	4.34	0.0E+00	U08412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3871	16910	29820	1.13	0.0E+00	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
3874	16913	29822	1.29	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3877	16916	29825	1.3	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3878	16917	29826	2.38	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3880	16919	29828	0.73	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3889	16929	29838	2.34	0.0E+00	AI864727.1	EST_HUMAN	wk01f01.x1 NCL CGAP_Lyn12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340
3892	16932	29842	13.72	0.0E+00	4506742	NT	O43340 R28830_2; contains element PTR7 repetitive element;
3897	16937	29848	1.39	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3903	16943	29855	1.34	0.0E+00	6005887	NT	DKFZp434N0413_r1 434 (synonym: hess3) Homo sapiens cDNA clone DKFZp434N0413 5'
3903	16943	29856	1.34	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3904	16944	29857	1.78	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3906	16946		1.75	0.0E+00	4505078	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3910	16950	29861	1.06	0.0E+00	AF149412.1	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3924	16964	29877	1.17	0.0E+00	4506758	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3928	16968	29881	1.3	0.0E+00	4585842	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3936	16978	29890	1.64	0.0E+00	BF356295.1	EST_HUMAN	Homo sapiens zinc finger protein (KIAA0412) mRNA
3937	16977	29891	1.05	0.0E+00	AW888221.1	EST_HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
3937	16977	29892	1.05	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5
3947	16987	29902	1.85	0.0E+00	AF129533.1	NT	Matrix remodeling associated gene 5
							MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5
							Matrix remodeling associated gene 5
							Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds

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3952	16992	29908	3.36	0.0E+00	BE378602.1	EST_HUMAN	601236966F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
3961	17001	29916	1.06	0.0E+00	AW590740.1	EST_HUMAN	PM3-L T0031-100100-003-p09 L T0031 Homo sapiens cDNA
4000	17039	29945	5.21	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4000	17039	29946	5.21	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4010	17049		3.56	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4013	17052		6.54	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4022	17060	29961	3.12	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4031	17069	29970	1.59	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4036	17074	29974	0.99	0.0E+00	S78653.1	NT	mtg=mas-related [human, Genomic, 2416 nt]
4047	17085		56.15	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4054	17091		1.47	0.0E+00	AI657076.1	EST_HUMAN	H59g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:O60309 O60309
4057	17093	29988	1.13	0.0E+00	7662183	NT	KIAA0563 PROTEIN ;
4058	17094	29989	1.67	0.0E+00	U09366.1	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4076	17111	30007	5.87	0.0E+00	AB015610.1	NT	Human zinc finger protein ZNF133
4085	17119		3.81	0.0E+00	AJ238617.1	NT	Chlorococcus eathlops mRNA for ribosomal protein S4X, complete cds
4093	17127	30020	1.14	0.0E+00	AL163203.2	NT	Homo sapiens mRNA for UGA suppressor (RNA-associated antigenic protein (RNA48) gene)
4094	17128	30021	2.67	0.0E+00	AJ277276.1	NT	Homo sapiens chromosome 21 segment HS21C003
4094	17128	30022	2.67	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for repa-2 (repa gene)
4100	17134	30028	7.81	0.0E+00	5032026	NT	Homo sapiens mRNA for repa-2 (repa gene)
4100	17134	30029	7.81	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4111	17145	30039	1.27	0.0E+00	4503914	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4117	17150	30042	4.98	0.0E+00	4855306	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
4118	17151	30043	1.32	0.0E+00	AB006825.1	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4121	17154	30044	7.49	0.0E+00	11419297	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4122	17155	30045	2.95	0.0E+00	AL096957.1	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4123	17156		1.21	0.0E+00	AA018975.1	EST_HUMAN	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4129	17162	30051	3.26	0.0E+00	AF165527.1	NT	ze55009.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element
4138	14177	27127	1.62	0.0E+00	4826947	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4138	14177	27128	1.62	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4143	17175	30063	1.28	0.0E+00	5901905	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4144	17176	30064	1.09	0.0E+00	4503854	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
							Homo sapiens GA-binding protein transcription factor, alpha subunit (GBPA), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4144	17176	30085	1.09	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4146	16598	29523	0.86	0.0E+00	4506884	NT	Homo sapiens semaphorin II (SEMG2), mRNA
4148	17179	30067	0.8	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4148	17179	30068	0.8	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4153	17184	30071	0.66	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4159	17190	30078	4.7	0.0E+00	A1982597.1	EST_HUMAN	wu04404.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4159	17190	30079	4.7	0.0E+00	A1982597.1	EST_HUMAN	wu04404.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4161	17192	30081	1.2	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4161	17192	30082	1.2	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4165	17196		3.98	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867600 5'
4170	17201	30087	0.93	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4170	17201	30088	0.93	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4172	17203						Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
4172	17203	30090	1.02	0.0E+00	4507478	NT	
4173	17204	30091	2.64	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4174	17205					NT	Novel human gene on chromosome 20
4183	17214						ba51104.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW.TH12_BOVIN
4188	17219	30106	1.12	0.0E+00	AW675599.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4190	17221	30109	1.23	0.0E+00	AW408788.1	EST_HUMAN	U1-HF-BM0-adv-c-02-Q-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4190	17221	30110	1.23	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
					8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4200	17231						Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
			4.37	0.0E+00	5174632	NT	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4220	17249	30133			AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4220	17249	30134			AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4235	17264	30149	1.04	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4235	17264	30160	1.04	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4258	17287				AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4286	17315	30194	1.28	0.0E+00	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4302	17331	30211	2.19	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4317	17346	30230	0.87	0.0E+00	AW939689.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4322	17351	30236	0.74	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4322	17351	30237	0.74	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4324	17353	30239	3.59	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
4332	17360		2.53	0.0E+00	AI189844.1	EST_HUMAN	q23f06.x1 Soares, placenta 8to9weeks 2NBHP8169W Homo sapiens cDNA clone IMAGE:1724579 3'
4336	17363		5.62	0.0E+00	U14520.1	NT	similar to contains MER20.b2 MER20 repetitive element;
4347	17374	30254	0.92	0.0E+00	4505846	NT	Human CBFA3 (Cbfa3) gene, partial cds
4353	17380	30261	0.77	0.0E+00	6563384	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
4353	17380	30262	0.77	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4359	17386	30268	1.15	0.0E+00	U10991.1	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4359	17386	30269	1.15	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4369	17396	30275	8.53	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4387	17415		1.12	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4392	17420	30303	11.19	0.0E+00	U03801.1	NT	Human Ig light chain VL1 region germline (humivlc2c) gene, partial cds
4398	17428	30310	4.52	0.0E+00	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4402	17430	30315	6.75	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4402	17430	30316	6.75	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4408	17436	30322	1.31	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4408	17436	30323	1.31	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4413	17440	30329	9.47	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4413	17440	30330	9.47	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4423	17450	30341	1.22	0.0E+00	X82338.1	NT	Homo sapiens Menkes disease gene, exon 4
4428	17453	30345	15	0.0E+00	4885128	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4427	17454	30346	1.23	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4430	17457	30348	1.01	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4463	17489	30376	1.2	0.0E+00	7019458	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4471	17497		6.71	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4476	17502	30386	1.53	0.0E+00	AJ248765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4476	17502	30387	1.53	0.0E+00	AJ248765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4480	17505	30393	0.88	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4480	17505	30394	0.88	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4495	17520		2.47	0.0E+00	AF200628.1	NT	Homo sapiens HPS1 gene, intron 6
4514	17539	30424	0.63	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Col8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft205 5'
4514	17539	30426	0.63	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Col8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft205 5'

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4517	17542		0.9	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4529	17553	30441	3.45	0.0E+00	AW084984.1	EST_HUMAN	xs88e08.x1 NCL CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2889446 3' similar to SW:AHNK_HUMAN
4531	18318		1.85	0.0E+00	8051819	NT	Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4533	17556	30444	1.09	0.0E+00	AI896898.1	EST_HUMAN	ws65b02.x1 NCL CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2322803 3' similar to contains MER22.b2
4537	17560		8.59	0.0E+00	AL163207.2	NT	PTR5 repetitive element ; Homo sapiens chromosome 21 segment HS21C007
4539	17562	30449	1.96	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-101199-002-d03 HT0305 Homo sapiens cDNA
4545	17568	30456	1.2	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4546	17568	30457	1.2	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4547	17570	30459	1.73	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4548	17571	30460	2.8	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4553	17576	30466	0.94	0.0E+00	Z65626.1	NT	H. sapiens pancreatic polypeptide receptor PP1 gene
4554	17577	30467	0.96	0.0E+00	4506892	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminidase: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4559	17582	30473	0.93	0.0E+00	S76884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K _v -channel subunit (KCNJ6/BIR1) gene, exon
4560	17583	30474	1.91	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4560	17583	30475	1.91	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4570	18319	30486	2.31	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4575	17587	30491	6.31	0.0E+00	AF208161.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
4582	17604	30501	1.32	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4595	17616	30510	30.53	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4605	17626	30518	1.62	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4610	17631	30524	1.4	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4614	17635		2.89	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4616	17637	30526	13.95	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4616	17637	30527	13.95	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4632	17653	30540	1.97	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4635	17656	30543	10.93	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4635	17656	30544	10.93	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4637	17658	30545	1.21	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0795 protein, partial cds
4645	17666		46.99	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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4654	17675		1.51	0.0E+00	AA174072.1	EST_HUMAN	zp18g03.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4656	17677		1.62	0.0E+00	7657410	NT	Homo sapiens cdz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4658	17679		2.05	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4659	17680	30565	0.95	0.0E+00	H92741.1	EST_HUMAN	y92b01.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4659	17680	30566	0.95	0.0E+00	H92741.1	EST_HUMAN	y92b01.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4660	17681	30567	1.42	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4661	17682	30568	5.53	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4662	17683		1.84	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4664	17685	30569	0.66	0.0E+00	AF195558.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4669	17690	30576	1.04	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4672	17693	30579	1.89	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4672	17693	30580	1.89	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4673	17694	30581	1.26	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4682	17703	30592	1	0.0E+00	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4682	17703	30593	1	0.0E+00	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4682	17703	30594	1	0.0E+00	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4683	17704	30595	2.03	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4683	17704	30596	2.03	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4688	17709	30602	6.02	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4689	17720		2.24	0.0E+00	AF066941.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4704	17725	30619	2.92	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4704	17725	30620	2.92	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4705	17726	30621	3.31	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4709	17730	30624	2.42	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4709	17730	30625	2.42	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4711	13244	29174	2.02	0.0E+00	T56945.1	EST_HUMAN	y83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:66310 5'
4711	13244	29175	2.02	0.0E+00	T56945.1	EST_HUMAN	y83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:66310 5'
4713	17733		1.22	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'
4737	17757	30651	4.85	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4737	17757	30652	4.85	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4743	17763	30657	5.55	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4748	17766	30660	6.62	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4746	17766	30661	6.62	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds

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4750	17770	30686	2.21	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4752	17772	30688	24.63	0.0E+00	7662479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4754	17774	30689	2.9	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4760	17780	30675	0.96	0.0E+00	S71446.1	NT	SCN1A-brain type I sodium channel alpha-subunit (IIIS5 transmembrane region) (human, placenta, Genomic, 1556 nt)
4760	17780	30676	0.96	0.0E+00	S71446.1	NT	SCN1A-brain type I sodium channel alpha-subunit (IIIS5 transmembrane region) (human, placenta, Genomic, 1556 nt)
4765	17785	30681	0.96	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4770	17790	30681	1.25	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4781	17801	30692	0.81	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4792	17809	30701	1.58	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL3A3) gene, promoter region, and exons 1-26
4795	17812	30704	1.12	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4785	17812	30705	1.12	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4797	17814	30707	1.12	0.0E+00	7019320	NT	Homo sapiens protein0008 (AD013), mRNA
4797	17814	30708	1.12	0.0E+00	7019320	NT	Homo sapiens protein0008 (AD013), mRNA
4826	17842	30740	1.49	0.0E+00	AW444637.1	EST HUMAN	UI-H-B3-gly-c-04-Q-UI-s1 NCL CGAP_Sus5 Homo sapiens cDNA clone IMAGE:2733294.3'
4831	17848	30749	0.99	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4832	17849		1.83	0.0E+00	AF063242.1	NT	Homo sapiens HSPC024-Iso mRNA, complete cds
4873	17890	30778	0.68	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4873	17890	30779	0.68	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4879	17896		4.64	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4882	17899	30788	1.6	0.0E+00	X87205.1	NT	MI.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4884	17901	30790	0.93	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4885	17902	30791	1.29	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4886	17903	30792	3.04	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4888	17905	30794	13.14	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4889	17906	30795	1.37	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4891	17908	30797	1.65	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZb762E1312 (DKFZp762E1312), mRNA
4894	17911	30801	4.6	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4898	17915	30805	1.75	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4898	17915	30806	1.75	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1-J61 segments; and Tor-C-alpha gene, exons 1-4
4900	17917	30808	1.49	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4900	17917	30809	1.49	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4903	17920	30812	2.38	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4912	17929	30820	1.16	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF21) mRNA
4921	17938	30830	1.69	0.0E+00	X92841.1	NT	H. sapiens MICA gene
4923	17940	30832	1.34	0.0E+00	4585842	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4924	17941	30833	0.69	0.0E+00	AB037884.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4925	17942	30834	1.25	0.0E+00	Y09232.1	NT	H. sapiens fertilin alpha pseudogene
4928	17943	30835	1.17	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4927	17944	30836	2.3	0.0E+00	6677848	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zfk1), mRNA
4929	17946	30838	1.49	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP) mRNA
4930	17947	30839	0.97	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4931	17948	30840	1.15	0.0E+00	7705546	NT	Homo sapiens zinc finger DNA-binding protein (HUMHOXY1), mRNA
4932	17949		25.08	0.0E+00	AJ010442.1	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, therad 7
4936	17952	30844	25.15	0.0E+00	AF055086.1	NT	Homo sapiens MHC class 1 region
4938	17954		1.97	0.0E+00	4505508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA
4939	17955	30847	2.01	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4941	17957		0.91	0.0E+00	U39955.1	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3) gene, exon 7
4952	17957	30857	0.99	0.0E+00	D63562.1	NT	Homo sapiens COL4A9 gene for a(V) collagen, exon 44 and partial cds
4954	17969	30859	1.62	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPS) mRNA
4981	17976		0.96	0.0E+00	A1291129.1	EST_HUMAN	qm15105.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:061832 Q61832
4972	17987	30878	0.93	0.0E+00	4504082	NT	EN-2/LACZ FUSION PROTEIN :
4972	17987	30879	0.93	0.0E+00	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4990	18005	30893	1.88	0.0E+00	AL163284.2	NT	Homo sapiens glypican 4 (GPC4) mRNA
4995	18010	30897	1.24	0.0E+00	7862319	NT	Homo sapiens chromosome 21 segment HS21C084
5008	18022		5.04	0.0E+00	U14967.1	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
5018	18032	30918	1.06	0.0E+00	M10976.1	NT	Human ribosomal protein L21 mRNA, complete cds
5020	18034		2.79	0.0E+00	BE408983.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
5023	18037	30922	3.2	0.0E+00	4758199	NT	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5030	18044	30926	1.24	0.0E+00	AB028968.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5044	18057	30935	1.97	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5044	18057	30936	1.97	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5057	18068	30947	0.75	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;
5057	18068	30948	0.75	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;
5057	18068	30949	0.75	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;
5074	18084	30974	1.34	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5088	18098	30974	0.8	0.0E+00	U53588.1	NT	Homo sapiens MHC class 1 region
5094	18104		1.27	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5097	18107		24.84	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5122	18132	31009	3.45	0.0E+00	X52988.1	NT	Bacillus amyloqueliciens sacB gene for levansucrase (EC 2.4.1.10)
5141	18150	31029	0.98	0.0E+00	AF240835.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5141	18150	31030	0.98	0.0E+00	AF240835.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5142	18151	31031	0.95	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5171	18180	31057	1.07	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5171	18180	31058	1.07	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5176	18185	31082	1.31	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5208	18217	31092	0.84	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5208	18217	31093	0.84	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5218	18227	31101	1.13	0.0E+00	U26555.1	NT	Human versican V2 core protein precursor splice-variant mRNA, complete cds
5221	18229	31103	1.01	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
5221	18229	31104	1.01	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
5236	18244	31116	1.11	0.0E+00	4826777	NT	Homo sapiens jumonji (mouse) homolog (JMJ) mRNA
							Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ectopic viral integration site 25 (EV12B) exons 1-2; ecotropic viral integration site 2A (EV12A) exons 1-2; adenylate kinase (AK3) exons 1-2
5257	18265		1.35	0.0E+00	L05367.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
5264	18272		1.08	0.0E+00	AF057177.1	NT	Homo sapiens mRNA for neuraxin I-alpha protein, complete cds
5266	18301	31161	0.63	0.0E+00	AB035358.1	NT	DKFZp434i0713_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434i0713 5'
5305	18308		2.09	0.0E+00	AL040249.1	EST_HUMAN	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5313	18329		3.2	0.0E+00	AF093093.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5324	18430	31181	2.03	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5324	18430	31182	2.03	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5346	18451	31322	1.19	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
5349	18454	31325	1.2	0.0E+00	9256579	NT	Homo sapiens protobactherin alpha 13 (PCDH13) mRNA
5364	18469	31340	4.04	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-b03 GN0076 Homo sapiens cDNA
5368	18473	31344	2.83	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5368	18473	31345	2.93	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5376	18480	31354	32.34	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5376	18480	31355	32.34	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5457	18559	31470	8.37	0.0E+00	BE675498.1	EST_HUMAN	710c06.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5458	18560	31471	1.72	0.0E+00	BE220753.1	EST_HUMAN	h99a02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN
5459	18561	31472	1.69	0.0E+00	BE794412.1	EST_HUMAN	P42894 HYPOTHETICAL PROTEIN KIAA0054.1
5459	18561	31473	1.69	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
							601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5460	18562	31474	0.63	0.0E+00	AI189142.1	EST_HUMAN	qd04a04.x1 Soares_placenta_8to9weeks_2NbpP8to9W Homo sapiens cDNA clone IMAGE:1722702 3' similar to SW:T2D3_DROME P49846 TRANSCRIPTION INITIATION FACTOR TFIIID 86 KD SUBUNIT ;
5464	18566	31477	18.78	0.0E+00	M29908.1	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5468	18570	31480	0.56	0.0E+00	AI791363.1	EST_HUMAN	ch6Ba09.y5 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512 IG
5478	25639	31488	4.25	0.0E+00	11421038	NT	HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);
5488	18588	31498	1.72	0.0E+00	BF65592.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4), mRNA
5489	18589	31499	0.77	0.0E+00	AU134406.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276254 5'
5489	18589	31500	0.77	0.0E+00	AU134406.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5495	18595	31507	0.64	0.0E+00	BE538957.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5504	18604	31533	1.22	0.0E+00	BE292784.1	EST_HUMAN	601081489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5509	18609	31539	2.05	0.0E+00	BF626328.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5'
5509	18609	31540	2.05	0.0E+00	BF626328.1	EST_HUMAN	602071372F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272 5'
5529	20048	33350	2.31	0.0E+00	4557364	NT	602071372F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4214272 5'
5532	18630	31567	1.03	0.0E+00	AB007935.1	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5532	18630	31568	1.03	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
5536	18633	31572	4.25	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5536	18633	31573	4.25	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5550	18647	31589	1.18	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
5550	18647	31590	1.18	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5566	18663	31623	1.8	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5572	18668	31629	1.55	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin
5591	18687	31655	0.87	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5591	18687	31656	0.87	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5594	18680	31660	3.21	0.0E+00	BF529931.1	EST_HUMAN	602042322F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179888 5'
5594	18690	31661	3.21	0.0E+00	BF529931.1	EST_HUMAN	602042322F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179888 5'
5599	18695	31665	2.24	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5610	18706	31863	3.88	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5626	18722	31881	0.57	0.0E+00	AJ928181.1	EST_HUMAN	w085602.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054
5626	18722	31882	0.57	0.0E+00	AJ928181.1	EST_HUMAN	O75054 KIAA0466 PROTEIN ;
5644	18740	31905	1.24	0.0E+00	BE260777.1	EST_HUMAN	w085602.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054
5653	18749	31905	7.42	0.0E+00	AW567316.1	EST_HUMAN	O75054 KIAA0466 PROTEIN ;
5668	18763	31932	2.41	0.0E+00	BE292889.1	EST_HUMAN	601150262F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502909 5'
5668	18763	31933	2.41	0.0E+00	BE292889.1	EST_HUMAN	MRO-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5689	18784	31955	1.79	0.0E+00	11420819	NT	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5689	18784	31956	1.79	0.0E+00	11420819	NT	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5697	18792	31964	4.3	0.0E+00	AF094254.1	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5697	18792	31965	4.3	0.0E+00	AF094254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5704	18799	31975	2.98	0.0E+00	AJ224639.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5704	18799	31976	2.98	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5735	18829	32007	0.7	0.0E+00	A1198515.1	EST_HUMAN	Homo sapiens Surf-5 and Surf-6 genes
5739	18833	32013	7.46	0.0E+00	M85719.1	EST_HUMAN	q84g10.x1 Soares_placenta_8cd9weeks_2NBHP869W Homo sapiens cDNA clone IMAGE:1757730 3' similar to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR ;
5748	18840	32022	5.85	0.0E+00	AW405472.1	EST_HUMAN	EST02238 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBGM48
5759	18852	32032	1.19	0.0E+00	Z26269.1	NT	U1HF-BL0-adj-d-02-0-UL1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3051658 5'
5771	18863	32042	1.87	0.0E+00	AW361877.1	EST_HUMAN	H. sapiens isoform 1 gene for L-type calcium channel, exon 14 cdnd 15
5771	18863	32043	1.87	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5771	18863	32044	1.87	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5774	18866	32047	0.94	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds
5774	18866	32048	0.94	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5776	18968	32081	2.24	0.0E+00	U36281.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5811	18901	32084	1.13	0.0E+00	AB046861.1	NT	Homo sapiens mRNA for KIAA1641 protein, partial cds
5833	18923	32107	0.53	0.0E+00	AI114826.1	EST_HUMAN	HA1495 Human fetal liver cDNA library Homo sapiens cDNA
5873	18982	32151	2.4	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740
5874	18983	32162	1.22	0.0E+00	AJ006345.1	NT	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); Homo sapiens KVLQT1 gene
5874	18983	32163	1.22	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5883	18972	32165	1.32	0.0E+00	AI207616.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5905	18991	32182	5.12	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
5910	18998	32185	1.25	0.0E+00	BE791173.1	EST_HUMAN	601684032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938551 5'
5920	19006	32198	1.09	0.0E+00	5938943	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
5921	19007	32199	7.69	0.0E+00	BE560082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5922	19008	32200	1.33	0.0E+00	10048478	NT	Mus musculus ezonin (Ac2), mRNA
5923	19009	32201	3.08	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5923	19009	32202	3.06	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5942	19028	32222	1.81	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCI_CGAP_Bin64 Homo sapiens cDNA clone IMAGE:4184321 5'
5946	19032	32225	0.97	0.0E+00	AF142821.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
5947	19033	32226	2.82	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5959	19044	32243	1.14	0.0E+00	BE503096.1	EST_HUMAN	h283d11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q62084 Q62084
5963	19048	32249	1.79	0.0E+00	BF569005.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING
5968	19053	32263	1.11	0.0E+00	AA454642.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310078 5'
6004	19087	32287	2.27	0.0E+00	AF217289.1	NT	z89d06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811983 3'
6008	19089	32289	2.43	0.0E+00	BE828144.1	EST_HUMAN	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6011	19094	32294	0.91	0.0E+00	BE95836.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
6017	19100	32302	0.53	0.0E+00	AJ289980.1	NT	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
6030	19113	32315	0.61	0.0E+00	BE673986.1	EST_HUMAN	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
6030	19113	32316	0.61	0.0E+00	BE673986.1	EST_HUMAN	7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN
6035	19118	32322	0.8	0.0E+00	AW278760.1	EST_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1. [1]; 7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN P51843 ORPHAN NUCLEAR RECEPTOR DAX-1. [1]; xp65f03.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335 GUANYLATE KINASE ASSOCIATED PROTEIN. ;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6047	19128	32336	0.67	0.0E+00	BF031742.1	EST_HUMAN	601558080F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6047	19128	32337	0.67	0.0E+00	BF031742.1	EST_HUMAN	601558080F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6059	19140	32352	1.27	0.0E+00	AW470848.1	EST_HUMAN	ha34d06.x1 NCI_QGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875895 3' similar to TR:Q9Z1N3
6072	19153	32364	0.95	0.0E+00	BF155670.1	EST_HUMAN	Q8Z1N3 MYOSIN-RHO GAP PROTEIN, MYR 7. ;
6072	19163	32365	0.95	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-290900-399-a10 HT0894 Homo sapiens cDNA
6080	19160	32371	1.38	0.0E+00	W33069.1	EST_HUMAN	z008h06.r1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6080	19160	32372	1.38	0.0E+00	W33069.1	EST_HUMAN	z008h06.r1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6081	19161		2.28	0.0E+00	AF012818.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
6084	19164	32376	2.82	0.0E+00	BE280197.1	EST_HUMAN	601156515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
6091	19170	32385	2.31	0.0E+00	BE88910.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
6093	19172	32388	0.53	0.0E+00	BE388673.1	EST_HUMAN	601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613085 5'
6109	19188	32408	0.63	0.0E+00	AW752848.1	EST_HUMAN	IL3-C70220-11196-028-E04 C70220 Homo sapiens cDNA
6112	19190	32410	1.46	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6112	19190	32411	1.46	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6113	19191	32412	1.12	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6113	19191	32413	1.12	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6113	19191	32414	1.12	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6129	25654	32431	9.98	0.0E+00	9789986	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6132	19209	32434	1.43	0.0E+00	AA183506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6132	19209	32435	1.43	0.0E+00	AA183506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6155	19230	32460	11.54	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-8 mRNA, complete cds
6155	19230	32461	11.54	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-8 mRNA, complete cds
6157	19232	32463	0.54	0.0E+00	AW853983.1	EST_HUMAN	RC3-C70254-110300-027-a09 C70254 Homo sapiens cDNA
6157	19232	32464	0.54	0.0E+00	AW853983.1	EST_HUMAN	RC3-C70254-110300-027-a09 C70254 Homo sapiens cDNA
6197	19271	32506	1.14	0.0E+00	BE268330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355565 5'
6207	19281	32514	1.24	0.0E+00	BE166561.1	EST_HUMAN	QV0-HT0368-090200-099-e09 HT0368 Homo sapiens cDNA
6217	19291	32524	0.53	0.0E+00	M38107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6254	19327	32558	1.71	0.0E+00	BE378007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6260	19333	32584	1.19	0.0E+00	AU197772.1	EST_HUMAN	AU197772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6282	19354	32590	3.66	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-8 gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6311	18382	32822	4.53	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.t1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6312	19383	32623	4.05	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6312	19383	32624	4.05	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6331	19401	32842	0.56	0.0E+00	U07223.1	NT	Human beta2-chimerin mRNA, complete cds
6349	19418	32659	8.33	0.0E+00	11426367	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6353	19422	32664	3.68	0.0E+00	BE257173.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6369	19437		0.97	0.0E+00	AI688048.1	EST_HUMAN	#91f10.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2249939 3' similar to TR:Q14839 Q14839
6373	19441	32683	1.28	0.0E+00	L35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6382	19450	32691	1.28	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942328 5'
6382	19450	32692	1.28	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6393	19461	32707	0.65	0.0E+00	AI198025.1	EST_HUMAN	q150b11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838
6393	19461	32708	0.65	0.0E+00	AI198025.1	EST_HUMAN	q150b11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838
6396	19484	32710	1	0.0E+00	BF357123.1	EST_HUMAN	MRO-HT0923-220800-102-b05 HT0923 Homo sapiens cDNA
6404	19472	32720	1.77	0.0E+00	11435830	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA
6414	19482	32729	0.79	0.0E+00	D55649.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6432	19498	32751	1	0.0E+00	AW178142.1	EST_HUMAN	IL3-HT0062-010999-014-A04 HT0062 Homo sapiens cDNA
6453	19518	32768	0.74	0.0E+00	BE674544.1	EST_HUMAN	7e02c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302 3' similar to SW:Y176_HUMAN
6458	19523	32774	0.88	0.0E+00	7662039	NT	Q14881 HYPOTHETICAL PROTEIN KIAA0176 ;
6472	19537		8.48	0.0E+00	AV650020.1	EST_HUMAN	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6491	19546	32795	3.68	0.0E+00	AW573598.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'
6494	19549	32708	5.02	0.0E+00	H01255.1	EST_HUMAN	UI-HF-BL0-acc-g-12-O-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
6493	19558	32809	1.16	0.0E+00	11426293	NT	y27b03.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149833 5'
6498	19562	32814	8.09	0.0E+00	X15377.1	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
6500	19564	32816	0.72	0.0E+00	AA456375.1	EST_HUMAN	Human gene for the light and heavy chains of myeloperoxidase
6501	19565	32817	1.23	0.0E+00	AI612841.1	EST_HUMAN	aa14e07.r1 Soares, NihMPu_S1 Homo sapiens cDNA clone IMAGE:813252 5'
6507	19571	32823	3.93	0.0E+00	BE735989.1	EST_HUMAN	1257d08.x1 NCL CGAP_Ov36 Homo sapiens cDNA clone IMAGE:2292887 3' similar to SW:NTCS_HUMAN
6507	19571	32824	3.93	0.0E+00	BE735989.1	EST_HUMAN	P53798 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
6511	19575	32830	0.78	0.0E+00	AW748596.1	EST_HUMAN	601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
							601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
							MRO-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
6511	19575	32831	0.78	0.0E+00	AW748598.1	EST_HUMAN	MF0-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6512	19576		0.67	0.0E+00	U77629.1	NT	Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
6514	19578	32833	28.27	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6514	19578	32834	28.27	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6519	19582	32840	0.86	0.0E+00	BE780453.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
6520	19583	32841	1.02	0.0E+00	X92217.1	NT	H. sapiens germine immunoglobulin heavy chain, variable region, (13-2)
6537	19589	32862	1.64	0.0E+00	A1989483.1	EST_HUMAN	ws26c07.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2498220 3'
6551	19612	32873	1.76	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
6551	19612	32874	1.76	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
6584	19644	32912	0.71	0.0E+00	BE867657.1	EST_HUMAN	601443175F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847291 5'
6626	19684	32962	1.2	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-aco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
6626	19684	32963	1.2	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-aco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
6660	19717	32994	0.89	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone G1CEHC06 5'
6669	19726	33001	1.27	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6669	19726	33002	1.27	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6672	19729	33005	2.18	0.0E+00	AF190880.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
6675	19732	33008	0.84	0.0E+00	L48546.1	NT	Homo sapiens tuberin (TSC2) gene, exons 38, 39, 40 and 41
6677	19734	33009	1.11	0.0E+00	11420658	NT	Homo sapiens transformation/transcription domain-associated protein (TTRAP), mRNA
6684	19741	33016	3.24	0.0E+00	AW163640.1	EST_HUMAN	au89h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206;
6684	19741	33017	3.24	0.0E+00	AW163640.1	EST_HUMAN	au89h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206;
6688	19746	33020	0.85	0.0E+00	W37163.1	EST_HUMAN	SW:ZNA45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6688	19746	33021	0.85	0.0E+00	W37163.1	EST_HUMAN	SW:ZNA45_HUMAN Q02386 ZINC FINGER PROTEIN 45;
6706	19762	33041	1.19	0.0E+00	BE794853.1	EST_HUMAN	601588371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6713	19769	33048	4.81	0.0E+00	BE798873.1	EST_HUMAN	601587661F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6714	19770	33049	3.07	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0085-140800-318-h02 GN0085 Homo sapiens cDNA
6714	19770	33050	3.07	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0085-140800-318-h02 GN0085 Homo sapiens cDNA
6718	19774	33053	7.15	0.0E+00	BE869813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6718	19774	33054	7.15	0.0E+00	BE869813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6727	19783	33082	5.42	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6732	19788	33068	2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6732	19788	33067	2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6738	19784	33074	3.67	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6741	19786	33076	3.87	0.0E+00	AI639412.1	EST_HUMAN	t311f1.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR. ;
6743	19798	33078	1.41	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
6755	19809	33080	0.79	0.0E+00	AW505430.1	EST_HUMAN	U1-HF-BN0-ama-c-01-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6757	19811	33091	3.98	0.0E+00	AA434584.1	EST_HUMAN	zw52c03.r1 Soares, fetal, fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773668 5'
6771	19828		1.13	0.0E+00	BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
6775	19830	33113	1.68	0.0E+00	BE925875.1	EST_HUMAN	QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA
6808	19862	33149	0.75	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6808	19862	33150	0.76	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6826	19880	33171	2.04	0.0E+00	AU125828.1	EST_HUMAN	AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6828	19882	33173	0.84	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-H10 NN0174 Homo sapiens cDNA
6828	19882	33174	0.84	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-H10 NN0174 Homo sapiens cDNA
6851	19904	33199	1.46	0.0E+00	BE142363.1	EST_HUMAN	CM0-HT0143-270999-062-d08 HT0143 Homo sapiens cDNA
6873	19926	33222	1.01	0.0E+00	BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6873	19926	33223	1.01	0.0E+00	BE006012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6901	19953	33250	7.7	0.0E+00	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6903	19955	33252	3.49	0.0E+00	BF085687.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6943	20167	33480	3.27	0.0E+00	AA190755.1	EST_HUMAN	zp88e03.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:827292 5'
6954	20179	33504	1.04	0.0E+00	U39573.1	NT	Human salivary peroxidase mRNA, complete cds
6958	20183	33506	0.7	0.0E+00	BE671987.1	EST_HUMAN	7a49b07.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285 TEKTIN. ;
6970	20193	33520	6.96	0.0E+00	AI840621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6970	20193	33521	6.96	0.0E+00	AI840621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6984	20207	33537	1.98	0.0E+00	11435628	NT	Homo sapiens CD6 antigen (CD6), mRNA
6988	20224	33438	1.01	0.0E+00	AL042443.1	EST_HUMAN	DKFZp434D2021_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2021 5'
6999	20225	33440	47.69	0.0E+00	X56163.1	NT	H.sapiens Immunoglobulin heavy chain gene, variable region
7002	20228	33443	0.84	0.0E+00	AI168270.1	EST_HUMAN	oo10d01.x1 Soares, NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1665761 3' similar to TR:Q26623 Q26623 TEKTIN C1. ;
7007	20133	33448	0.92	0.0E+00	BE734087.1	EST_HUMAN	601667307F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7030	18362	31249	1.17	0.0E+00	BE66381.1	EST_HUMAN	601339877F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682267 5'
7040	18372	31259	12.91	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
7040	18372	31260	12.91	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
7048	20070	33376	1.94	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCL_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08378 GOLGIN-95. ;
7048	20070	33377	1.94	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCL_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
7074	20096	33406	2.29	0.0E+00	BF088376.1	EST_HUMAN	CMT1-HT0877-080900-397-q11 HT0877 Homo sapiens cDNA
7081	20102	33413	1.41	0.0E+00	AA195108.1	EST_HUMAN	z34g03.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:065332 5'
7088	20022		11.47	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
7090	20024	33328	0.91	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7092	20026	33329	0.78	0.0E+00	BE313075.1	EST_HUMAN	601150662F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503391 5'
7092	20026	33330	0.78	0.0E+00	BE313075.1	EST_HUMAN	601150662F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503391 5'
7106	20040	33342	3.08	0.0E+00	BF569905.1	EST_HUMAN	602185652F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7114	20048	33350	0.61	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
7122	20056		2.02	0.0E+00	J03069.1	NT	Human MYCL2 gene, complete cds
7132	20108	33419	3.33	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7132	20108	33420	3.33	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7133	20109	33421	1.77	0.0E+00	M38143.1	NT	Human neurofibromatosis type 1 gene, exon x6
7146	18378	31266	3.02	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7147	18379	31267	0.57	0.0E+00	AI419969.1	EST_HUMAN	Ig53c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN. ;
7147	18379	31268	0.57	0.0E+00	AI419969.1	EST_HUMAN	Ig53c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN. ;
7152	18384	31272	0.66	0.0E+00	BE256708.1	EST_HUMAN	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 5'
7173	18404	31202	1.21	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003676 5'
7176	18407	31208	5.02	0.0E+00	BE262941.1	EST_HUMAN	601148564F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'
7177	18408	31207	2.25	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7177	18408	31208	2.25	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7178	18409	31209	3.32	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 8 (DNAH9) mRNA, complete cds
7178	18409	31210	3.32	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7185	18416	31217	1.33	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7187	18418	31219	0.59	0.0E+00	BF130916.1	EST_HUMAN	601819722F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4051709 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7192	20216	33546	0.57	0.0E+00	BE762770.1	EST_HUMAN	QV3-NT0022-140600-223-f01 NT0022 Homo sapiens cDNA
7198	20222	33553	2.39	0.0E+00	BF669603.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7200	20224	33555	0.68	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7200	20224	33556	0.68	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7204	20228	33561	4.32	0.0E+00	LO1978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7209	20232	33565	1.49	0.0E+00	AW502362.1	EST_HUMAN	UI-HF-BR0p-aka-d-10-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7209	20232	33566	1.49	0.0E+00	AW502362.1	EST_HUMAN	UI-HF-BR0p-aka-d-10-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7218	20240	33574	0.93	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7218	20240	33575	0.93	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7227	20249	33583	5.15	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7233	20254	33588	2.16	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7275	20010	33312	1.21	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7315	20286	33627	0.69	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7315	20286	33628	0.69	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7320	20291	33634	0.68	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7320	20291	33635	0.68	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7326	20297	33641	1.23	0.0E+00	AW954806.1	EST_HUMAN	EST366878 IMAGE resequences, MAGC Homo sapiens cDNA
7327	20298	33642	1.14	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354566 5'
7340	20311	33654	1.23	0.0E+00	LO1973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7348	20318	33664	0.68	0.0E+00	AB007535.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7348	20318	33665	0.68	0.0E+00	AB007535.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7354	20324	33672	1.38	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001566 5'
7370	20340	33692	1	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7376	20346	33697	2.24	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
7376	20346	33697	0.96	0.0E+00	4758839	NT	Homo sapiens neitin 1 (NTN1), mRNA
7385	20355	33706	1.34	0.0E+00	BE991286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7385	20355	33707	1.34	0.0E+00	BE991286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7407	18430	31181	2.28	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7407	18430	31182	2.28	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7419	20386	33736	0.7	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7419	20386	33737	0.7	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7432	20399	33751	4.41	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7432	20399	33752	4.41	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7447	20413	33766	0.65	0.0E+00	AF227744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform aa (CACNA1G) mRNA, complete cds
7469	20435	33791	36.24	0.0E+00	AI128344.1	EST_HUMAN	qc87a07.x1 Soares_placenta_8t09weeks_2N5HP8t09W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ;contains element HGR repetitive element ;
7469	20435	33792	36.24	0.0E+00	AI128344.1	EST_HUMAN	qc87a07.x1 Soares_placenta_8t09weeks_2N5HP8t09W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ;contains element HGR repetitive element ;
7472	20438	33795	0.82	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7472	20438	33796	0.82	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7475	20441	33799	5.42	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7475	20441	33800	5.42	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7478	20444	33835	13.74	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4182839 5'
7480	20446	33802	2.75	0.0E+00	AA128453.1	EST_HUMAN	zn60f09.r1 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:562801 5' similar to TR:G806862
7485	20450	33808	0.75	0.0E+00	AL079497.1	EST_HUMAN	Q806562 NEBULIN ;
7485	20450	33809	0.75	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7486	20461	33821	0.57	0.0E+00	AJ270996.1	NT	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7530	20493	33855	1.12	0.0E+00	BE295499.1	EST_HUMAN	Homo sapiens partial mRNA for LTRPC5 protein (LTRPC5 gene)
7532	20495	33856	0.9	0.0E+00	11427865	NT	601174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794 5'
7535	20498	33859	1.48	0.0E+00	AU118607.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20261), mRNA
7538	20499	33859	2.02	0.0E+00	AF005213.1	NT	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
7538	20499	33860	2.02	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7547	20510	33868	0.85	0.0E+00	AF245505.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7555	20518	33873	7.23	0.0E+00	X70172.1	NT	Homo sapiens adican mRNA, complete cds
7557	20520	33875	6.84	0.0E+00	U45448.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7557	20520	33876	6.84	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7570	20533	33891	0.81	0.0E+00	AW956503.1	EST_HUMAN	Human P2x1 receptor mRNA, complete cds
7572	20535	33893	2.85	0.0E+00	AW950516.1	EST_HUMAN	EST388573 MAGC resequences, MAGD Homo sapiens cDNA
7599	20560	33920	0.79	0.0E+00	AF001543.1	EST_HUMAN	EST382588 MAGC resequences, MAGA Homo sapiens cDNA
7599	20560	33921	0.79	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7599	20560	33922	0.79	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7623	20583	33947	0.62	0.0E+00	IM90394.1	NT	Human BTIF3 protein homologue gene, complete cds
7624	20584	33947	0.72	0.0E+00	BE408293.1	EST_HUMAN	601302870F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7635	20595	33958	0.5	0.0E+00	AW402542.1	EST_HUMAN	UI-HF-BK0-aaa-g-07-Q-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054924 5'
7653	20613		1.3	0.0E+00	R87430.1	EST_HUMAN	ym8bh10.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:166051 5'
7654	20614	33978	2.42	0.0E+00	AW299326.1	EST_HUMAN	x639a05.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050
7676	20634		1.21	0.0E+00	AU117553.1	EST_HUMAN	HNF3/FH TRANSCRIPTION FACTOR GENESIS ;
7678	20636	33998	3.92	0.0E+00	11427135	NT	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'
7697	20655	34019	1.76	0.0E+00	AA211663.1	EST_HUMAN	Homo sapiens glucagon-like peptide 2 receptor (GLP2R). mRNA
7703	20660	34024	0.68	0.0E+00	BF229235.1	EST_HUMAN	zn56f02.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740
7710	20667	34034	0.62	0.0E+00	AW996499.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7713	20670	34037	0.81	0.0E+00	L32832.1	NT	MRO-AN0083-270900-004-07 AN0083 Homo sapiens cDNA
7740	20694	34058	1.17	0.0E+00	BF306998.1	EST_HUMAN	QV3-BN0046-220300-129-e04 BN0046 Homo sapiens cDNA
7740	20694	34059	1.17	0.0E+00	BF306996.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7750	20703	34071	1.24	0.0E+00	AU118767.1	EST_HUMAN	60188923F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7782	20735	34107	0.49	0.0E+00	AW499551.1	EST_HUMAN	60188923F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7809	20758	34132	0.64	0.0E+00	AB002355.1	NT	AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
7810	20759	34133	4.06	0.0E+00	A1762561.1	EST_HUMAN	UI-HF-BR0p-aj-e-10-Q-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074778 5'
7810	20759	34134	4.06	0.0E+00	A1762561.1	EST_HUMAN	Human mRNA for KIAA0357 gene, partial cds
7879	20823	34200	0.53	0.0E+00	AA399959.1	EST_HUMAN	en17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7879	20823	34201	0.53	0.0E+00	AA399959.1	EST_HUMAN	en17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7880	20824	34202	0.53	0.0E+00	AL046347.2	EST_HUMAN	zu68b07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743125 5'
7897	20840	34221	1.22	0.0E+00	AF064205.1	NT	zu68b07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743125 5'
7897	20840	34222	1.22	0.0E+00	AF064205.1	NT	DKFZp434J087_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J087 5'
7905	20848	34233	1.06	0.0E+00	U74315.1	EST_HUMAN	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7919	20862	34250	0.59	0.0E+00	BE430545.1	EST_HUMAN	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7920	20863	34251	1.03	0.0E+00	11417342	NT	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7939	20881	34271	0.5	0.0E+00	BF569005.1	EST_HUMAN	HTM1-183F1 HTM1 Homo sapiens cDNA
7950	20891	34282	0.73	0.0E+00	A1825504.1	EST_HUMAN	Homo sapiens serine domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
							602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
							wb17q05.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363
							AIBC1.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7950	20891	34283	0.73	0.0E+00	A1825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O75363 O75363
7958	20899	34292	3.09	0.0E+00	6912735	NT	A1BC1.1
7965	20904	34286	0.96	0.0E+00	N76126.1	EST_HUMAN	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7971	20910	34300	5.4	0.0E+00	BF217905.1	EST_HUMAN	zab6a05.e1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299456 3'
7976	20915	34306	0.53	0.0E+00	BF56982.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
7981	20920	34311	3.8	0.0E+00	AU129622.1	EST_HUMAN	602185808F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310286 5'
8006	25693	34338	0.97	0.0E+00	AW099274.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
8006	25693	34339	0.97	0.0E+00	AW099274.1	EST_HUMAN	cr42e09.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
8010	20948	34341	6.56	0.0E+00	4501848	NT	cr42e09.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
8017	20955	34348	1.05	0.0E+00	AV758467.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8020	20957	34350	5.84	0.0E+00	BE739870.1	EST_HUMAN	AV758467 BM Homo sapiens cDNA clone BMFBGG05 5'
8020	20957	34351	5.84	0.0E+00	BE739870.1	EST_HUMAN	601563156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8021	20958	34352	0.88	0.0E+00	6912461	NT	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8021	20958	34353	0.88	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8022	20959	34354	3.3	0.0E+00	AU120424.1	EST_HUMAN	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8022	20959	34355	3.3	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
8048	20985	34381	2.13	0.0E+00	BF590267.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
8060	20997	34393	1.52	0.0E+00	BE787610.1	EST_HUMAN	nab22c04.x1 Soares_NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3263214 3' similar to contains element TAR1 repetitive element;
8060	20997	34384	1.52	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
8101	21037	34437	0.54	0.0E+00	AW956307.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
8123	21050	34458	0.52	0.0E+00	Y16795.1	NT	EST396377 MAGE resequences, MAGD Homo sapiens cDNA
8129	21058	34466	0.49	0.0E+00	11425128	NT	Homo sapiens psithaA pseudogene
8130	21067	34467	0.69	0.0E+00	AU117333.1	EST_HUMAN	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
8131	21068		0.52	0.0E+00	BE613963.1	EST_HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001175 5'
8146	21053	34482	4.38	0.0E+00	AW968044.1	EST_HUMAN	601504084F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905733 5'
8147	21054	34483	0.75	0.0E+00	AU133435.1	EST_HUMAN	EST390119 MAGE resequences, MAGJ Homo sapiens cDNA
8186	21156	34555	0.64	0.0E+00	AU133435.1	EST_HUMAN	HA2043 Homo sapiens fetal liver cDNA library Homo sapiens cDNA
8231	21200		0.65	0.0E+00	BF217200.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
8244	21213	34620	0.87	0.0E+00	BE313013.1	EST_HUMAN	601865317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
8256	21225	34635	1.09	0.0E+00	AA149791.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8268	21237	34648	0.88	0.0E+00	BF026628.1	EST_HUMAN	601872310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
8281	21250	34662	0.52	0.0E+00	AA017021.1	EST_HUMAN	z633h08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360831 5'
8299	21288	34680	2.26	0.0E+00	BE736046.1	EST_HUMAN	601306558F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639803 5'
8314	21283	34685	2.42	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8314	21283	34686	2.42	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8344	21313	34727	0.74	0.0E+00	AW674581.1	EST_HUMAN	b634d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652
8344	21313	34728	0.74	0.0E+00	AW674581.1	EST_HUMAN	F17K2.26 PROTEIN.; b634d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652
8351	21320	34734	2.47	0.0E+00	AA397551.1	EST_HUMAN	z81b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
8353	21322	34735	0.92	0.0E+00	AW387131.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT); MRO-ST0031-061099-003-a11 ST0031 Homo sapiens cDNA
8356	21325		0.62	0.0E+00	AB020691.1	NT	Homo sapiens mRNA for KIAA0884 protein, partial cds
8357	21326	34737	7.99	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
8361	21330	34741	1.12	0.0E+00	BE588421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8361	21330	34742	1.12	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8376	21345	34756	0.48	0.0E+00	7957278	NT	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
8378	21347	34758	0.92	0.0E+00	W95278.1	EST_HUMAN	z605d01.r1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8378	21347	34759	0.92	0.0E+00	W95278.1	EST_HUMAN	z605d01.r1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8380	21349		17.98	0.0E+00	BF673086.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
8384	21353		0.95	0.0E+00	AU134114.1	EST_HUMAN	AU134114 OVARG1 Homo sapiens cDNA clone OVARG1001296 5'
8398	21367	34776	1.71	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8398	21367	34777	1.71	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8430	21399	34810	1.65	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8430	21399	34811	1.65	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8473	21442		1.24	0.0E+00	BE877663.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3867773 5'
8497	21465	34881	1.91	0.0E+00	AW500549.1	EST_HUMAN	U1HF-BN0-ak4-01-0-JL.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5'
8505	21473	34887	10.07	0.0E+00	AW157233.1	EST_HUMAN	au93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783798 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1]; xa07d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2507639 3' similar to contains element OFR repetitive element;
8523	21491	34906	0.67	0.0E+00	AW072395.1	EST_HUMAN	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8541	21508	34926	1.08	0.0E+00	11421722	NT	z63gd05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294633 5'
8544	21512	34929	0.83	0.0E+00	W01616.1	EST_HUMAN	

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8546	21514	34931	1.26	0.0E+00	BE745597.1	EST_HUMAN	601678195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8546	21514	34932	1.26	0.0E+00	BE745597.1	EST_HUMAN	601678195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8559	21527	34946	1.2	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8578	21548	34985	0.44	0.0E+00	D45032.1	NT	Human DNA for ceruloplasmin, exon 5
8599	21567	34983	1.08	0.0E+00	AI387350.1	EST_HUMAN	q195c12.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIA00164 PROTEIN. ;
8610	21578	34994	2.6	0.0E+00	BE674157.1	EST_HUMAN	7d76a04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:Q95793 Q95793 STAUJEN PROTEIN. ;
8612	21580	34996	1.22	0.0E+00	AI885671.1	EST_HUMAN	w60b10.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN_P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR. ;
8625	21593	35012	1.29	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8625	21593	35013	1.29	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8633	21601	35023	1.93	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8633	21601	35024	1.93	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8635	21603	35026	1.35	0.0E+00	AA403192.1	EST_HUMAN	z166f02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD. ;
8635	21603	35027	1.35	0.0E+00	AA403192.1	EST_HUMAN	z166f02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD. ;
8676	21644		3.69	0.0E+00	AA398511.1	EST_HUMAN	z173a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727988 3' similar to gb:S85855 PROHIBITIN (HUMAN);
8685	21653	35076	0.53	0.0E+00	BE837593.1	EST_HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sapiens cDNA
8686	21654	35077	1.25	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8686	21654	35078	1.25	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8705	21673	35097	1.26	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8705	21673	35098	1.28	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8720	21688	35115	1.65	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8720	21688	35116	1.65	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8730	21698	35123	0.7	0.0E+00	AI884477.1	EST_HUMAN	nm33a11.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
8737	21705	35129	0.85	0.0E+00	AA502294.1	EST_HUMAN	ne25d10.s1 NCL_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1136434
8742	21710		0.57	0.0E+00	11416789	NT	G1136434 KIAA0187 PROTEIN. ;
8749	21717	35140	0.99	0.0E+00	AI580780.1	EST_HUMAN	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
8752	21720		1.97	0.0E+00	BE880797.1	EST_HUMAN	ta04f11.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3'
							601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8778	21745	35168	0.55	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8778	21745	35167	0.55	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8779	21746	35168	2.62	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
8779	21746	35169	2.62	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
8783	21750	35172	0.52	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8783	21750	35173	0.52	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8851	21818	35238	1.02	0.0E+00	AJ251760.1	NT	Homo sapiens NESP55, GNAS1 antisense (partial) and XLaiphas (partial) genes
8856	21823	35244	3	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8856	21823	35245	3	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8856	21823	35246	3	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8871	21838	35260	1.82	0.0E+00	U82978.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8913	21879	35305	1.16	0.0E+00	AF022655.1	NT	Homo sapiens cap260 centrosome associated protein mRNA, complete cds
8913	21879	35306	1.16	0.0E+00	AF022655.1	NT	Homo sapiens cap260 centrosome associated protein mRNA, complete cds
8916	21882	35308	0.68	0.0E+00	AU131671.1	EST_HUMAN	AU131671 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
8931	21887	35325	0.81	0.0E+00	11426572	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8935	21901		1.53	0.0E+00	AW513513.1	EST_HUMAN	xc46e01.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4
8937	21903		0.55	0.0E+00	BE783232.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
							HOMO84C02B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-084C02
8938	21904	35328	11.32	0.0E+00	DS2650.1	EST_HUMAN	5'
8969	21935	35361	3.89	0.0E+00	BE378495.1	EST_HUMAN	601236486F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8975	21941	35365	3.98	0.0E+00	AA410545.1	EST_HUMAN	Z32604.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5'
8977	21943		3.27	0.0E+00	BF313946.1	EST_HUMAN	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128744 5'
							Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
8984	21950	35374	1.37	0.0E+00	11424387	NT	
8989	21955	35379	1.38	0.0E+00	AW139673.1	EST_HUMAN	U1-H-B11-adr-e-12-O-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8989	21955	35380	1.38	0.0E+00	AW139673.1	EST_HUMAN	U1-H-B11-adr-e-12-O-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8994	21960		0.61	0.0E+00	A1640190.1	EST_HUMAN	wa30b10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299579 3' similar to TR:O15044
9013	21979	35398	3.23	0.0E+00	BF377897.1	EST_HUMAN	O15044 KIAA0335 ;
9022	21988	35410	0.45	0.0E+00	AL163301.2	NT	CMH-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
9028	21994	35414	2.33	0.0E+00	BE260272.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
9033	21999	35418	2.98	0.0E+00	BF700165.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'
9033	21999	35419	2.98	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
9033	21999	35419	2.98	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'

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9033	21989	35420	2.98	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
9047	22013	35438	0.63	0.0E+00	AI458722.1	EST_HUMAN	IK1311.1.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150949 3'
9076	22042	35465	0.7	0.0E+00	AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
9084	22050	35472	12.96	0.0E+00	AA962527.1	EST_HUMAN	or60g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 80S
9080	22058	35480	4.79	0.0E+00	10947037	NT	RIBOSOMAL PROTEIN L7A (HUMAN);
9090	22056	35481	4.79	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
9114	22080	35508	1.23	0.0E+00	Y11107.3	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
9116	22082	35510	2.41	0.0E+00	BE278917.1	EST_HUMAN	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
9126	22092		3.32	0.0E+00	AV718377.1	EST_HUMAN	601156330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
9132	22098	35525	3.36	0.0E+00	AW337277.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'
9138	22104	35550	1.56	0.0E+00	AU124051.1	EST_HUMAN	xw73c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X63587
9214	22180	35611	0.86	0.0E+00	AU140704.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
9224	22180	35620	0.55	0.0E+00	AB007923.1	NT	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
9229	22195	35624	0.61	0.0E+00	R17132.1	EST_HUMAN	AU140704 PLCE4 Homo sapiens cDNA clone PLACE4000089 5'
9229	22195	35625	0.61	0.0E+00	R17132.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
9233	22199	35627	5.11	0.0E+00	AW592233.1	EST_HUMAN	yg09e09.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:31674 5'
9233	22199	35628	5.11	0.0E+00	AW592233.1	EST_HUMAN	yg09e09.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:31674 5'
9269	22235	35664	0.46	0.0E+00	AU128804.1	EST_HUMAN	nf48a09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
9281	22247	35676	0.89	0.0E+00	AV714764.1	EST_HUMAN	nf48a09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
9296	22262	35690	3.01	0.0E+00	AL040428.1	EST_HUMAN	AU128804 NT2RP2 Homo sapiens cDNA clone NT2RP2004245 5'
9296	22262	35691	3.01	0.0E+00	AL040428.1	EST_HUMAN	AV714764 DGB Homo sapiens cDNA clone DCBAUA06 5'
9302	22267	35697	1.27	0.0E+00	AF133901.1	NT	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9304	22269	35700	1.89	0.0E+00	AB040945.1	NT	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9310	22275	35707	2.24	0.0E+00	BF675505.1	EST_HUMAN	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
9312	22277		0.92	0.0E+00	BF059289.1	EST_HUMAN	Homo sapiens mRNA for KIAA1512 protein, partial cds
9342	22307	35733	4.84	0.0E+00	11422857	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9352	22317	35743	1.44	0.0E+00	K01241.1	NT	602138483F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274708 6'
9361	22328	35754	4.23	0.0E+00	AB020630.1	NT	Homo sapiens tumor protein p73 (TP73), mRNA
9361	22326	35755	4.23	0.0E+00	AB020630.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
9366	22331	35761	1.71	0.0E+00	AV660739.1	EST_HUMAN	Homo sapiens mRNA for KIAA0823 protein, partial cds
							Homo sapiens mRNA for KIAA0823 protein, partial cds
							AV660739 GLC Homo sapiens cDNA clone GLOGK12 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9372	22337	35787	3.07	0.0E+00	7706638	NT	Homo sapiens polycystin-L (PKDL), mRNA
9377	22342	35772	2.22	0.0E+00	BE793328.1	EST_HUMAN	601588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
9378	22343	35773	0.46	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
9378	22343	35774	0.46	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
9391	22356		0.98	0.0E+00	H73937.1	EST_HUMAN	yu03h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232767 5'
9401	22366	35798	4.19	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9401	22366	35798	4.19	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9411	22376	35814	0.59	0.0E+00	BE612721.1	EST_HUMAN	601452882F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859100 5'
9411	22376	35815	0.59	0.0E+00	BE612721.1	EST_HUMAN	601452882F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859100 5'
9414	22379		0.52	0.0E+00	M89986.1	NT	Human polymorphic loci in Xq28
9416	22381	35819	1.74	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9433	22397	35835	0.5	0.0E+00	AU127098.1	EST_HUMAN	AU127098 NT2RP2 Homo sapiens cDNA clone NT2RP2000579 5'
9437	22401	35839	1.29	0.0E+00	AJ061395.1	EST_HUMAN	an29e04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
9442	22406	35843	1.98	0.0E+00	AJ954607.1	EST_HUMAN	wq34e12.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MBG3_HUMAN
9447	22411	35848	4.1	0.0E+00	9256595	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
9458	22422	35860	1.18	0.0E+00	AW956311.1	EST_HUMAN	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
9468	22432	35870	4.72	0.0E+00	9635487	NT	EST370381 MAGe resequences, MAGe Homo sapiens cDNA
9484	22448	35888	1.44	0.0E+00	AU142662.1	EST_HUMAN	Human endogenous retrovirus, complete genome
9499	22463	35904	1.46	0.0E+00	11436895	NT	AU142662 Y79AA1 Homo sapiens cDNA clone Y79AA1000678 5'
9500	22464		0.8	0.0E+00	BE410768.1	EST_HUMAN	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
9513	22476	35921	1.29	0.0E+00	BF002024.1	EST_HUMAN	601301676F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9527	22490	35937	1.25	0.0E+00	AB011150.1	NT	7697h12.x1 NC1_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q9UJH62
9528	22491	35938	4.85	0.0E+00	BE794823.1	EST_HUMAN	Q9UJH62 HYPOTHETICAL 42.5 KD PROTEIN ;
9534	22497	35945	1.04	0.0E+00	AU136229.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9539	22502	35950	1.36	0.0E+00	BE883943.1	EST_HUMAN	601889294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943483 5'
9539	22502	35951	1.36	0.0E+00	BE883943.1	EST_HUMAN	AU136229 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
9557	22519	35967	0.77	0.0E+00	AB011166.1	NT	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9591	22523	35971	3.53	0.0E+00	AA344601.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9591	22523	35971	3.53	0.0E+00	AA344601.1	EST_HUMAN	Homo sapiens mRNA for KIAA0594 protein, partial cds
9591	22523	35971	3.53	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
9591	22523	35971	3.53	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
9591	22523	35971	3.53	0.0E+00	AA344601.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275
9619	22553	36011	1.02	0.0E+00	AW673469.1	EST_HUMAN	KIAA0522 PROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9619	22563	36012	1.02	0.0E+00	AW673469.1	EST_HUMAN	ba54408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN;
9653	22598	36044	4.71	0.0E+00	BE207083.1	EST_HUMAN	Bcl-xL mRNA, complete cds (MOUSE);
9653	22598	36045	4.71	0.0E+00	BE207083.1	EST_HUMAN	Bcl-xL mRNA, complete cds (MOUSE);
9664	22821	36275	1.77	0.0E+00	BF348013.1	EST_HUMAN	602023150F1 NCL CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158300 5'
9700	22663	36107	2.8	0.0E+00	BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-508 HT0698 Homo sapiens cDNA
9732	22760	36213	0.86	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9732	22760	36214	0.86	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9738	22766	36221	0.53	0.0E+00	AI906351.1	EST_HUMAN	RC-BT108-040399-032 BT108 Homo sapiens cDNA
9741	22769	36223	3.69	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9741	22769	36224	3.68	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9761	22692	36149	2.54	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
9786	22727	36183	2.35	0.0E+00	AI088043.1	EST_HUMAN	ow60101.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 Q14677 KIAA0171 PROTEIN;
9783	21118	34515	0.85	0.0E+00	BF309982.1	EST_HUMAN	601892245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138066 5'
9795	21118	34518	2.84	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9795	21118	34519	2.84	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9797	21120	34522	20.82	0.0E+00	AI290909.1	EST_HUMAN	qm09a06.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A;
9797	21120	34523	20.82	0.0E+00	AI290909.1	EST_HUMAN	qm09a06.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A;
9798	21121	34524	3.57	0.0E+00	AW953836.1	EST_HUMAN	EST366028 MAGE resequences, MAGE Homo sapiens cDNA
9825	22674	36129	3.43	0.0E+00	AF163486.1	NT	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
9828	22677	36133	0.66	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9828	22677	36134	0.66	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9837	22773	36231	22.2	0.0E+00	BE255829.1	EST_HUMAN	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
9840	22776	36231	1.35	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9840	22776	36232	1.35	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9843	22779	36234	30.94	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9854	22790	36242	0.44	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9867	22803	36257	3.12	0.0E+00	BE263191.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9885	22838	36283	4.11	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5805
9885	22838	36284	4.11	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5805
9887	22840	36297	2.92	0.0E+00	BE746215.1	EST_HUMAN	601578883F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9897	22850	36307	1.81	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9897	22850	36308	1.81	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9897	22850	36309	1.81	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9917	22738	36191	1.49	0.0E+00	BE600549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
9935	22862	36323	0.61	0.0E+00	AV701829.1	EST_HUMAN	AV701829 ADB Homo sapiens cDNA clone ADBBYH01 5'
9947	22874	36335	2.59	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9947	22874	36336	2.59	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9980	22907	36372	1.86	0.0E+00	BE082877.1	EST_HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA
9999	22926	36392	2.65	0.0E+00	AW500293.1	EST_HUMAN	U1-HF-BN0-akg-b-12-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9999	22926	36393	2.65	0.0E+00	AW500293.1	EST_HUMAN	U1-HF-BN0-akg-b-12-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
10008	22935	36399	1.45	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10008	22935	36400	1.45	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10010	22937	36401	0.76	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
10010	22937	36402	0.76	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
10019	22948	36413	0.52	0.0E+00	W56629.1	EST_HUMAN	z016e11.r1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:340844 5'
10019	22948	36414	0.52	0.0E+00	W56629.1	EST_HUMAN	z016e11.r1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:340844 5'
10032	22959	36427	1.05	0.0E+00	AB035358.1	NT	Homo sapiens mRNA for neurexin I-alpha protein, complete cds
10036	22963	36432	0.58	0.0E+00	AI124780.1	EST_HUMAN	am56a11.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'
10038	22965	36432	2.73	0.0E+00	AW500526.1	EST_HUMAN	U1-HF-BN0-akg-e-07-Q-U1.r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077364 5'
10082	23009	36481	1.51	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (p0) mRNA, partial cds
10108	23035	36512	2.37	0.0E+00	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
10109	23035	36513	2.37	0.0E+00	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
10112	23038	36518	3.13	0.0E+00	BE66320.1	EST_HUMAN	601334803F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688890 5'
10132	23058	36535	1.42	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Homo sapiens cDNA
10152	23077	36553	0.61	0.0E+00	11436432	NT	Homo sapiens multimetric (MMRN), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10153	23078	36554	1.71	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
10162	23087	36564	0.82	0.0E+00	BE206710.1	EST_HUMAN	5526601.X1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2964000 3'
10178	23103	36583	2.6	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10178	23103	36584	2.6	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10187	23112	36598	1.82	0.0E+00	AW500936.1	EST_HUMAN	UIHF-BP0p-af-f05-q-U1.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
10193	23118	36602	16.11	0.0E+00	BE740480.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10193	23118	36603	16.11	0.0E+00	BE740480.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10194	23119	36604	0.45	0.0E+00	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
10194	23119	36605	0.45	0.0E+00	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
10206	23131	36618	1.76	0.0E+00	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
10224	23149	36638	3.6	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
10229	23154	36644	0.71	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2416_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2416 5'
10238	23164	36651	2.57	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10240	23168	36652	2.44	0.0E+00	AF182308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
10268	23193	36680	5.52	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
10268	23193	36681	5.52	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
10284	23209	36694	2.5	0.0E+00	BF032898.1	EST_HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
10314	23236	36720	2.73	0.0E+00	BE280793.1	EST_HUMAN	601135227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
10323	23247	36728	1.2	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
10323	23247	36727	1.2	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
10332	23256	36733	3.64	0.0E+00	AW236269.1	EST_HUMAN	3x72b01.x1 NC1_CGAP_CML1 Homo sapiens cDNA clone IMAGE:269977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10333	23257	36734	0.75	0.0E+00	AA341305.1	EST_HUMAN	EST46740 Fetal kidney II Homo sapiens cDNA 5' end
10342	23266	36745	0.63	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
10363	23286	36763	0.75	0.0E+00	AW964113.1	EST_HUMAN	EST376186 MAGe resequences, MAGH Homo sapiens cDNA
10376	23299	36774	7.08	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10376	23299	36775	7.08	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10379	23302	36778	13.11	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10382	23304	36780	2.8	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10382	23304	36781	2.8	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10416	23338	36824	3.43	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10416	23338	36825	3.43	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10432	23354	36839	2.24	0.0E+00	AJ25844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10432	23354	36840	2.24	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
10437	23359	36847	0.75	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'
10437	23359	36848	0.75	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'
10443	23365	36855	0.76	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIR2C gene, exons 2, 3, and 4
10445	23367	36858	2.64	0.0E+00	AA196387.1	EST_HUMAN	z397h1.1 r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
10470	23392	36887	1.78	0.0E+00	AA131248.1	EST_HUMAN	z31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10470	23392	36888	1.78	0.0E+00	AA131248.1	EST_HUMAN	z31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10517	23439	36937	1.79	0.0E+00	AF179308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10591	23493	36978	0.88	0.0E+00	BE880588.1	EST_HUMAN	601491565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893657 5'
10573	23496	36987	11.49	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10573	23496	36988	11.49	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10578	23500	36992	0.62	0.0E+00	AU127403.1	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10588	23510	37003	0.86	0.0E+00	BE968511.1	EST_HUMAN	601645134F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930177 5'
10598	23510	37004	0.86	0.0E+00	BE968511.1	EST_HUMAN	601645134F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930177 5'
10605	23527	37023	0.98	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10616	23538	37037	0.68	0.0E+00	AA311624.1	EST_HUMAN	EST182363 Jurkat T-cells V1 Homo sapiens cDNA 5' end
10617	23539	37038	0.56	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
10629	23551	37051	0.78	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917898 5'
10632	23564	37054	1.19	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10642	23584	37060	1.39	0.0E+00	AB028280.1	NT	Homo sapiens mRNA for actin binding protein ABP820, complete cds
10643	23585	37061	0.6	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887918 5'
10643	23586	37062	0.6	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887918 5'
10650	23572	37067	4.13	0.0E+00	AB006580.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10650	23572	37068	4.13	0.0E+00	AB006580.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10658	23580	37077	1.27	0.0E+00	AA704457.1	EST_HUMAN	z1f8b06.e1 Soares_fetal_liver_spleen_1NFLS_51 Homo sapiens cDNA clone IMAGE:460707 3' similar to gb:M141423_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10660	23582	37078	1.19	0.0E+00	M22921.1	NT	Human beta 1,4-galactosyl-transferase mRNA, complete cds
10662	23584	37081	4.52	0.0E+00	BF340931.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184939 5'
10662	23584	37082	4.52	0.0E+00	BF340931.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184939 5'
10687	23609	37103	5.24	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10687	23609	37104	5.24	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10719	23641	37134	0.48	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DC8 Homo sapiens cDNA clone DC8BDC09 5'
10719	23641	37135	0.48	0.0E+00	AV716271.1	EST_HUMAN	AV716271 DC8 Homo sapiens cDNA clone DC8BDC09 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10750	23672	37167	1.13	0.0E+00	AI631818.1	EST_HUMAN	wa36603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE ;
10750	23672	37168	1.13	0.0E+00	AI631818.1	EST_HUMAN	wa36603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE ;
10764	23685	37181	2	0.0E+00	TO3078.1	EST_HUMAN	FB23A4 Fetal brain, Stratagene Homo sapiens cDNA clone FB23A4 3' end
10789	23710	37212	0.67	0.0E+00	AU122429.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002368 5'
10795	23716	37218	0.43	0.0E+00	6006921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10817	23738	37241	2.63	0.0E+00	BF436218.1	EST_HUMAN	hab45e12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10818	23739		1.3	0.0E+00	AV654765.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLC2C007 3'
10837	23757	37257	5.03	0.0E+00	AW517860.1	EST_HUMAN	xu74501.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M69066 MOESIN (HUMAN);
10841	23761	37261	18.38	0.0E+00	BE549213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10858	23778	37278	0.64	0.0E+00	11436005	NT	Homo sapiens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
10863	23803	37307	0.44	0.0E+00	X89893.1	NT	H sapiens mRNA for NK receptor (183 Act)
10884	23804	37308	4.15	0.0E+00	BE781742.1	EST_HUMAN	601467418F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
10903	23823	37334	3.07	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0842-150200-012-403 BT0842 Homo sapiens cDNA
10903	23823	37335	3.07	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0842-150200-012-403 BT0842 Homo sapiens cDNA
10910	23830	37343	0.56	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10915	23835	37351	0.7	0.0E+00	AI658890.1	EST_HUMAN	tt64e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2244812 3'
10922	23842	37358	1.6	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10922	23842	37359	1.6	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10925	23845	37360	0.97	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10925	23845	37361	0.97	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10946	23866	37380	0.55	0.0E+00	H39805.1	EST_HUMAN	yp01a10.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:186138 5'
10960	23880	37393	0.48	0.0E+00	AW748117.1	EST_HUMAN	QV0-BT0107-230789-007-c06 BT0107 Homo sapiens cDNA
10972	23892	37408	1.16	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10973	23893	37407	0.48	0.0E+00	AF081304.1	NT	Synthetic construct CD30 ligand-exon3 A fusion protein (CD30L-ETA fusion) mRNA, partial cds
10994	23914	37430	0.46	0.0E+00	AW342141.1	EST_HUMAN	EST 00007 Human differential display products Homo sapiens cDNA clone UNCCDD7
10994	23914	37431	0.46	0.0E+00	AW342141.1	EST_HUMAN	EST 00007 Human differential display products Homo sapiens cDNA clone UNCCDD7
10999	23965	37489	1.72	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAG05 5'
10999	23965	37490	1.72	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAG05 5'
11001	23967		3.29	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
11007	23972	37498	0.07	0.0E+00	AW695563.1	EST_HUMAN	EST376638 IMAGE resequences, MAGH Homo sapiens cDNA
11019	23984	37510	1.81	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11019	23984	37511	1.81	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11023	23988	37515	1.76	0.0E+00	AW057621.1	EST_HUMAN	wy61109.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60566 Q60566 VDX;
11029	23993	37520	1.98	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M4) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
11030	23984	37521	2.54	0.0E+00	AI652239.1	EST_HUMAN	w528a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
11030	23984	37522	2.54	0.0E+00	AI652239.1	EST_HUMAN	w528a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
11034	23998	37525	2.13	0.0E+00	BF306642.1	EST_HUMAN	601888704F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122849 5'
11041	24005	37531	3.83	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
11041	24005	37532	3.83	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
11055	24018	37541	5.31	0.0E+00	AW404795.1	EST_HUMAN	UHF-BLO-acm-d-04-0-UJ.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
11058	24021	37544	2.69	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
11059	24022	37546	7.34	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
11059	24022	37546	7.34	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
11080	24023	37547	2.71	0.0E+00	AI991827.1	EST_HUMAN	w32b06.x1 Soares_Dickgraefe_color_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
11083	24026	37551	1.64	0.0E+00	BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
11086	24026	37553	21.37	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'
11088	24031	37554	4.59	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11088	24031	37555	4.59	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11083	18982	32151	5.57	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.1 Stratiens muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
11103	24083	37586	100.2	0.0E+00	AA809080.1	EST_HUMAN	hw17c08.s1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:1240718 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);
11104	24084	37587	4.22	0.0E+00	BE793498.1	EST_HUMAN	601588829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
11113	24073	37595	15.77	0.0E+00	AV727382.1	EST_HUMAN	AV727382 HTC Homo sapiens cDNA clone HTCAHQ06 5'
11113	24073	37598	15.77	0.0E+00	AV727382.1	EST_HUMAN	AV727382 HTC Homo sapiens cDNA clone HTCAHQ06 5'
11126	24086	37613	14.2	0.0E+00	AA46413.1	EST_HUMAN	z178c12.1 Soares ovary tumor N6H0T Homo sapiens cDNA clone IMAGE:609878 5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-J REGION (HUMAN);
11129	24089	37618	24.26	0.0E+00	AW516055.1	EST_HUMAN	xx04g10.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S18 (HUMAN);
11134	24094	37623	1.88	0.0E+00	AU135741.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11139	24099	37626	3.36	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11139	24099	37627	3.36	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11139	24099	37628	3.36	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11141	24101	37629	1.68	0.0E+00	Z34897.1	NT	H sapiens mRNA for H1 histamine receptor
11142	24102	37630	2.84	0.0E+00	F13089.1	EST_HUMAN	HSC3IC031 normalized infant brain cDNA Homo sapiens cDNA clone o-3ic03
11159	24117	37643	2.4	0.0E+00	M27751.1	NT	Homo sapiens immunoglobulin kappa-chain A14 V-region precursor (IGKV) gene, partial cds
11159	24117	37644	2.4	0.0E+00	M27751.1	NT	Homo sapiens immunoglobulin kappa-chain A14 V-region precursor (IGKV) gene, partial cds
11167	24125	37654	40.1	0.0E+00	AW338094.1	EST_HUMAN	xw66f01.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);
11168	24126	37655	3.54	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-ah-e-01-0-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11168	24126	37656	3.54	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-ah-e-01-0-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11170	19316		8.04	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
11184	24140	37674	2.07	0.0E+00	BE288449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
11196	24151	37682	2.13	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
11199	24154	37686	1.69	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
11206	24160	37690	1.68	0.0E+00	BE264695.1	EST_HUMAN	60118388 HEMBA1 Homo sapiens cDNA clone IMAGE:3538012 5'
11214	24167	37696	1.62	0.0E+00	BE782155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936639 5'
11215	24168		70.33	0.0E+00	BF684061.1	EST_HUMAN	602141405F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302432 5'
11217	24170	37698	7.66	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone IMAGE:1003486 5'
11218	24171					EST_HUMAN	xn72b01.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699877 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
11223	24176	37702	4.92	0.0E+00	AW236269.1	EST_HUMAN	gf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
11223	24176	37703	4.92	0.0E+00	A1149809.1	EST_HUMAN	gf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
11224	24177	37704	2.09	0.0E+00	AW331937.1	EST_HUMAN	QV4-ST0234-121199-032-b08 ST0234 Homo sapiens cDNA
11234	24187		1.54	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone IMAGE:1000255 5'
11238	24191	37710	9.23	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
11244	24197	37716	145.89	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-408 UM0093 Homo sapiens cDNA
11245	24197	37717	145.89	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-408 UM0093 Homo sapiens cDNA
11245	24198	37718	3.26	0.0E+00	BF340308.1	EST_HUMAN	Q02037014F1 NCL CGAP_Bm54 Homo sapiens cDNA clone IMAGE:4184979 5'
11247	24200	37721	49.67	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
11251	24204	37726	1.74	0.0E+00	AB029040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11256	24208	37731	6.12	0.0E+00	U50328.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
11257	24209	37732	1.72	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
11260	24212	37735	6	0.0E+00	BE773036.1	EST_HUMAN	RC1-F10134-170700-012-07 FT0134 Homo sapiens cDNA
11260	24212	37736	6	0.0E+00	BE773036.1	EST_HUMAN	RC1-F10134-170700-012-07 FT0134 Homo sapiens cDNA
11283	24233	37759	89.91	0.0E+00	AA740782.1	EST_HUMAN	ob32207.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element
11285	24235	37762	38.54	0.0E+00	AW466922.1	EST_HUMAN	ha04h04.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
11291	24241	37768	2.85	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
11304	24254	37780	1.84	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536887 5'
11304	24254	37781	1.84	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536887 5'
11307	24257	37783	7.6	0.0E+00	C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHG4817
11313	24263	37789	1.91	0.0E+00	AA746375.1	EST_HUMAN	aa56h01.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11313	24263	37790	1.91	0.0E+00	AA746375.1	EST_HUMAN	aa56h01.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11321	24271	37798	1.66	0.0E+00	BF353625.1	EST_HUMAN	QV2-HT0698-020800-295-07 HT0698 Homo sapiens cDNA
11322	24272	37799	5.79	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
11333	24283	37807	6.83	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
11347	24297	37825	1.54	0.0E+00	AU132437.1	EST_HUMAN	AU132437 NT2RP3 Homo sapiens cDNA clone NT2RP3004422 5'
11367	18866	32047	2.84	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds
11367	18866	32048	2.84	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neurexin II, complete cds
11371	24318	37848	2.4	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0645-080500-002-E05 HT0645 Homo sapiens cDNA
11371	24318	37847	2.4	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0645-080500-002-E05 HT0645 Homo sapiens cDNA
11372	24319		1.48	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAD06 5'
11387	24334	37863	75.44	0.0E+00	AW406380.1	EST_HUMAN	UHF-BL0-acc-c-08-0-U1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060088 5'
11390	24336	37865	2.81	0.0E+00	BE896423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
11397	24342	37874	2.26	0.0E+00	AW500307.1	EST_HUMAN	UHF-BN0-akg-d-02-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
11397	24342	37875	2.26	0.0E+00	AW500307.1	EST_HUMAN	UHF-BN0-akg-d-02-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							bb78c-04.v1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb:Y00345_cds1
							POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding protein (MOUSE);
11398	24343	37878	7.11	0.0E+00	BE018293.1	EST_HUMAN	H.sapiens gene for Ig kappa light chain variable region "011"
11417	24361	37896	14.52	0.0E+00	X59314.1	NT	H.sapiens gene for Ig kappa light chain variable region "011"
11421	24365	37900	2.3	0.0E+00	AU121677.1	EST_HUMAN	AU121677 MAMMA1 Homo sapiens cDNA clone MAMMA1000731 5'
11430	24374	37913	4.14	0.0E+00	BE897953.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
11431	24375	37914	1.58	0.0E+00	AI459545.1	EST_HUMAN	aa86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11431	24375	37915	1.58	0.0E+00	AI459545.1	EST_HUMAN	aa86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11441	24384	37924	4.83	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
11446	24389	37931	4.18	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12
11446	24389	37932	4.18	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12
11474	24417	37897	2.85	0.0E+00	4758927	NT	Homo sapiens neurexin III (NRXN3) mRNA
11475	24418	37868	3.38	0.0E+00	BF206561.1	EST_HUMAN	601870802F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
11478	24421	37970	12.88	0.0E+00	AW207734.1	EST_HUMAN	U1-H-B12-age-h-01-Q.U1.s1 NCI_OGAP_Sub8 Homo sapiens cDNA clone IMAGE:2724312 3'
11479	24422	37971	5.09	0.0E+00	AW604975.1	EST_HUMAN	RCO-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
11479	24422	37972	5.09	0.0E+00	AW604975.1	EST_HUMAN	RCO-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
11483	24426	37975	2.91	0.0E+00	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11483	24426	37976	2.91	0.0E+00	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11484	24427	37977	3.54	0.0E+00	BE206846.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-59KDA-ASSOCIATED PROTEIN.;
11484	24427	37978	3.54	0.0E+00	BE206846.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-59KDA-ASSOCIATED PROTEIN.;
11508	24448	37898	2.13	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11509	20670	34037	1.92	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11513	24454	38003	3.74	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-H04 HT0230 Homo sapiens cDNA
11513	24454	38004	3.74	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-H04 HT0230 Homo sapiens cDNA
11523	24484	38017	7.64	0.0E+00	AA195905.1	EST_HUMAN	z995b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
11531	24472	38023	1.51	0.0E+00	AW673469.1	EST_HUMAN	ba54408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0622 PROTEIN.;
11531	24472	38024	1.51	0.0E+00	AW673469.1	EST_HUMAN	ba54408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0622 PROTEIN.;
11549	24490	38046	5.23	0.0E+00	BF507876.1	EST_HUMAN	U1-H-B14-aok-b-10-Q.U1.e1 NCI_OGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11549	24490	38047	5.23	0.0E+00	BF507876.1	EST_HUMAN	U1-H-B14-aok-b-10-Q.U1.e1 NCI_OGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11556	24496	38052	3.54	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5'
11560	24500	38056	1.84	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11560	24500	38057	1.84	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11561	24501	38058	17.24	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11561	24501	38059	17.24	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11567	24507	38064	2.8	0.0E+00	D87682.1	NT	Human mRNA for KIAA0241 gene, partial cds

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11571	24510		5.42	0.0E+00	BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
11582	24520	38076	1.69	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11582	24520	38076	1.68	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11588	24524	38079	3.41	0.0E+00	11430888	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11588	24524	38080	3.41	0.0E+00	11430888	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11590	24528	38085	2.06	0.0E+00	BE122764.1	EST_HUMAN	23_08 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 23_08 5' similar to Homo sapiens cyclin B2 (CCNB2)
11591	24529	38086	3.23	0.0E+00	BE017860.1	EST_HUMAN	bb73h05.v1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048057 5' similar to SW:CD97_HUMAN
11595	24533	38089	2.69	0.0E+00	AA772837.1	EST_HUMAN	P48960 LEUCOCYTE ANTIGEN CD97 PRECURSOR. [1];
11605	24543	38103	6.4	0.0E+00	4603644	NT	ae74g04.st Stragatene schizo brain S11 Homo sapiens cDNA clone IMAGE:969942 3'
11612	24550	38110	2.25	0.0E+00	BF576287.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
11615	24553	38114	5.5	0.0E+00	AW328173.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11620	24558		83.29	0.0E+00	M65083.1	NT	dt04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11624	24562	38123	159.29	0.0E+00	AI660988.1	EST_HUMAN	Human gamma actin-like pseudogene, complete cds
11625	24563	38124	2.3	0.0E+00	BF308998.1	EST_HUMAN	wf20e11.x1 Scores Dieckgrafe, colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
11625	24563	38125	2.3	0.0E+00	BF308998.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11632	24569	38133	59.57	0.0E+00	BF362462.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11648	24585	38154	2.42	0.0E+00	U36284.1	NT	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
11648	24585	38155	2.42	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11654	24591		4.74	0.0E+00	BE697051.1	EST_HUMAN	Human beta-prime-adaptin (BAM22) gene, exon 16
11665	24601	38177	1.54	0.0E+00	8923698	NT	601439805F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11668	24604		2.24	0.0E+00	BF207692.1	EST_HUMAN	Homo sapiens golgin-like protein (GLP), mRNA
11668	24605		4.82	0.0E+00	BE257744.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11682	24648	38225	4.13	0.0E+00	BE208946.1	EST_HUMAN	601116705F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-1
11682	24648	38226	4.13	0.0E+00	BE208946.1	EST_HUMAN	ba04d07.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-1
11684	24650	38228	3.8	0.0E+00	AW753028.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN. ;
11689	24655		4.96	0.0E+00	AA558707.1	EST_HUMAN	QV0-C10225-101259-071-406 C10225 Homo sapiens cDNA
11660	18451	31322	3.12	0.0E+00	AI934954.1	EST_HUMAN	nl42c08.x1 NCI CGAP_P14 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11691	24656	38234	9.26	0.0E+00	AW327895.1	EST_HUMAN	wp06g08.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
							df02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11711	25706	38254	1.63	0.0E+00	AW292776.1	EST_HUMAN	U1H.BWG-aj-d-07-0.U1.s1 NCI_CGAP_SubB Homo sapiens cDNA clone IMAGE:2729509 3'
11718	23916	37432	2.09	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11724	24610	38186	2.43	0.0E+00	BE965909.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11724	24610	38187	2.43	0.0E+00	BE965909.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11725	24611	38188	3.67	0.0E+00	BE165656.1	EST_HUMAN	IL5-H70731-020500-077-705 HT0731 Homo sapiens cDNA
11739	24624	38202	5.4	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11739	24624	38203	5.4	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
11746	24631	38211	2.29	0.0E+00	BF082504.1	EST_HUMAN	MR4-BT0358-130900-016-a04 BT0358 Homo sapiens cDNA
11760	24635	38214	19.22	0.0E+00	A1923116.1	EST_HUMAN	wn83g03.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11753	24681	38259	8.71	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287488 3' similar to TR:Q13686
11753	24681	38260	8.71	0.0E+00	AA760913.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN.;
11758	24688	38266	3.51	0.0E+00	BE910546.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287488 3' similar to TR:Q13686
11758	24688	38266	3.51	0.0E+00	BE910546.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN.;
11766	23921	37440	5.45	0.0E+00	BE676347.1	EST_HUMAN	601601090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5'
11769	23924	37443	2.02	0.0E+00	BE615966.1	EST_HUMAN	727112.x1 NCI_CGAP_CLI1 Homo sapiens cDNA clone IMAGE:3295919 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1.;
11769	23924	37444	2.02	0.0E+00	BE615966.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3811144 5'
11777	23932	37453	2.13	0.0E+00	AV757420.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3811144 5'
11808	24693	38273	5.01	0.0E+00	L39891.1	NT	AV757420 BM Homo sapiens cDNA clone BMFAGH03 5'
11808	24693	38274	5.01	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11822	24705	38287	3.67	0.0E+00	AU138211.1	EST_HUMAN	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11835	24718	38304	5.91	0.0E+00	BE622317.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
11880	24742	38326	2.22	0.0E+00	A1939534.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11889	24750	38332	14.23	0.0E+00	BE748899.1	EST_HUMAN	tn94c10.x5 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2165778 3'
11889	24750	38333	14.23	0.0E+00	BE748899.1	EST_HUMAN	601572186F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11877	24759	38343	2.54	0.0E+00	AU141882.1	EST_HUMAN	601572186F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11877	24759	38344	2.54	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11880	24762	38347	1.97	0.0E+00	AW006022.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11882	25707	38349	2.38	0.0E+00	BF002333.1	EST_HUMAN	wz91h01.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2 CE11040 ZINC FINGER, C2H2 TYPE ;
11896	24790	38366	1.48	0.0E+00	AL043705.1	EST_HUMAN	7h2b10.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO.;
11896	24790	38366	1.48	0.0E+00	AL043705.1	EST_HUMAN	DKFZp434L1227.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1227 5'

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11899	24780	38367	1.48	0.0E+00	AL043705.1	EST_HUMAN	DKFZp434L1227_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L1227 5'
11904	24785	38374	3.36	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-503 ST0118 Homo sapiens cDNA
11904	24785	38375	3.36	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-503 ST0118 Homo sapiens cDNA
11916	24787		2.43	0.0E+00	AW863777.1	EST_HUMAN	MR3-SN0010-310300-107-h03 SN0010 Homo sapiens cDNA
11927	24808	38402	4.22	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11927	24808	38403	4.22	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11932	24813	38409	5.01	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
11934	24815	38411	2.03	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11934	24815	38412	2.03	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11946	20655	34019	2.41	0.0E+00	AA211663.1	EST_HUMAN	zn5602.1 Strategic muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740
11947	24826	38421	2.36	0.0E+00	AA48894.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
11952	24831	38427	2.35	0.0E+00	BE794758.1	EST_HUMAN	aa55g11.81 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824900 3' similar to gb:M37766 B-
11953	24832	38428	160.92	0.0E+00	BE796933.1	EST_HUMAN	LYMPHOCYTE ACTIVATION MARKER BLAST-1 PRECURSOR (HUMAN);
11965	24844	38439	12.66	0.0E+00	BE406983.1	EST_HUMAN	601590388F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11966	24845	38440	2.25	0.0E+00	AF223391.1	NT	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11966	24845	38441	2.25	0.0E+00	AF223391.1	NT	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
11968	24846	38443	4.01	0.0E+00	BF681641.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11974	18348	31294	1.51	0.0E+00	AF272663.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11976	24853	38451	1.57	0.0E+00	AL132940.1	EST_HUMAN	Homo sapiens gephyrin mRNA, complete cds
11979	24856	38453	4.83	0.0E+00	BE903372.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP400929 5'
11992	24859	38464	3.47	0.0E+00	BF312552.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
11992	24859	38465	3.47	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11994	24871	38467	34.13	0.0E+00	X51755.1	NT	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11994	24871	38468	34.13	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12006	24883		3.04	0.0E+00	BE906402.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
12007	24884	38479	1.52	0.0E+00	BE892690.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
12035	25708		58.85	0.0E+00	BF309120.1	EST_HUMAN	601433908F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919321 5'
							601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12037	24912	38506	2.38	0.0E+00	BE698881.1	EST_HUMAN	RC4-NN0025-120600-016-607 NN0025 Homo sapiens cDNA
12037	24912	38506	2.38	0.0E+00	BE698881.1	EST_HUMAN	RC4-NN0025-120600-016-607 NN0025 Homo sapiens cDNA
12040	24915	38509	60.15	0.0E+00	BE297175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532988 5'
12048	24921	38517	1.81	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12048	24921	38518	1.81	0.0E+00	BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12062	24935	38531	1.81	0.0E+00	7689505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
12062	24935	38532	1.81	0.0E+00	7689505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
12087	24940	38535	1.68	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
12071	24944	38537	2.41	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12
12071	24944	38538	2.41	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12
12077	24949	38544	6.46	0.0E+00	BE545535.1	EST_HUMAN	601070391F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456407 5'
12080	24952	38547	3.24	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
12080	24952	38548	3.24	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
12118	24998	38590	2.15	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
12124	24993	38595	2.27	0.0E+00	BE284998.1	EST_HUMAN	601193827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
12124	24993	38596	2.27	0.0E+00	BE284998.1	EST_HUMAN	601193827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
12131	25000	38605	6.45	0.0E+00	11419020	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA
12131	25000	38606	6.45	0.0E+00	11419020	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA
12146	25972	31299	1.81	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
12161	25919		1.43	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12163	25828		6.62	0.0E+00	AI180993.1	EST_HUMAN	qel7b12.x1 Scores_fetal_jung_Nbhl19W Homo sapiens cDNA clone IMAGE:1739231 3'
12173	25022		1.33	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12192	25037		2.28	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12201	25044		5.82	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12218	25056		3.47	0.0E+00	5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
12251	25786	31523	2.06	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12265	25798		4.42	0.0E+00	AL041931.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5'
12291	25940		3.76	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
12289	25110		5.96	0.0E+00	AL046544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12314	25834		1.98	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
12357	25962		1.82	0.0E+00	N54484.1	EST_HUMAN	yy40e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEYM P10272 POL POLYPROTEIN ;
12371	25167		5.99	0.0E+00	AF106566.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
12374	13900	26857	3.44	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12374	13900	26858	3.44	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12383	25837		2.56	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
12411	13620		2.52	0.0E+00	AF003528.1	NT	Homo sapiens X-linked arylidrolitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12504	25787	31521	3.54	0.0E+00	AW590082.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
12534	25787		1.41	0.0E+00	L20493.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
12581	25831		2.82	0.0E+00	AF088767.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12587	25300		2.72	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12635	25823		1.47	0.0E+00	AI204914.1	EST_HUMAN	an05h04.x1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12683	15027	28034	1.88	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12683	15027	28035	1.88	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12701	25361	31787	1.52	0.0E+00	AF053365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12712	14723	27705	4.49	0.0E+00	H30132.1	EST_HUMAN	yc58e08.r1 Soares breast 3N6IBst Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M64099
12712	14723	27706	4.49	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12724	25377		52.99	0.0E+00	D50559.1	NT	Human gamma-cytoplasmic actin (ACTGP6) pseudogene
12726	25378	31743	3.63	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12725	25378	31744	3.63	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12739	15120	28141	2.42	0.0E+00	4768489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12780	25415		1.39	0.0E+00	AW684999.1	EST_HUMAN	hi89e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979154 3'
12818	25440	31721	1.51	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
12827	25446		1.55	0.0E+00	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12849	18338	31287	3.07	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12858	18346	31292	1.68	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12863	25468		2.17	0.0E+00	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12902	25488	31733	2.53	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
12927	25984		3.32	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
12935	13692	26809	2.65	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12988	14499	27473	1.32	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13018	25568		3.02	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
13051	25590	31885	1.36	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
13082	26613		1.63	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHIE.1 (ERV9)
13103	14203	27156	1.4	0.0E+00	8986844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

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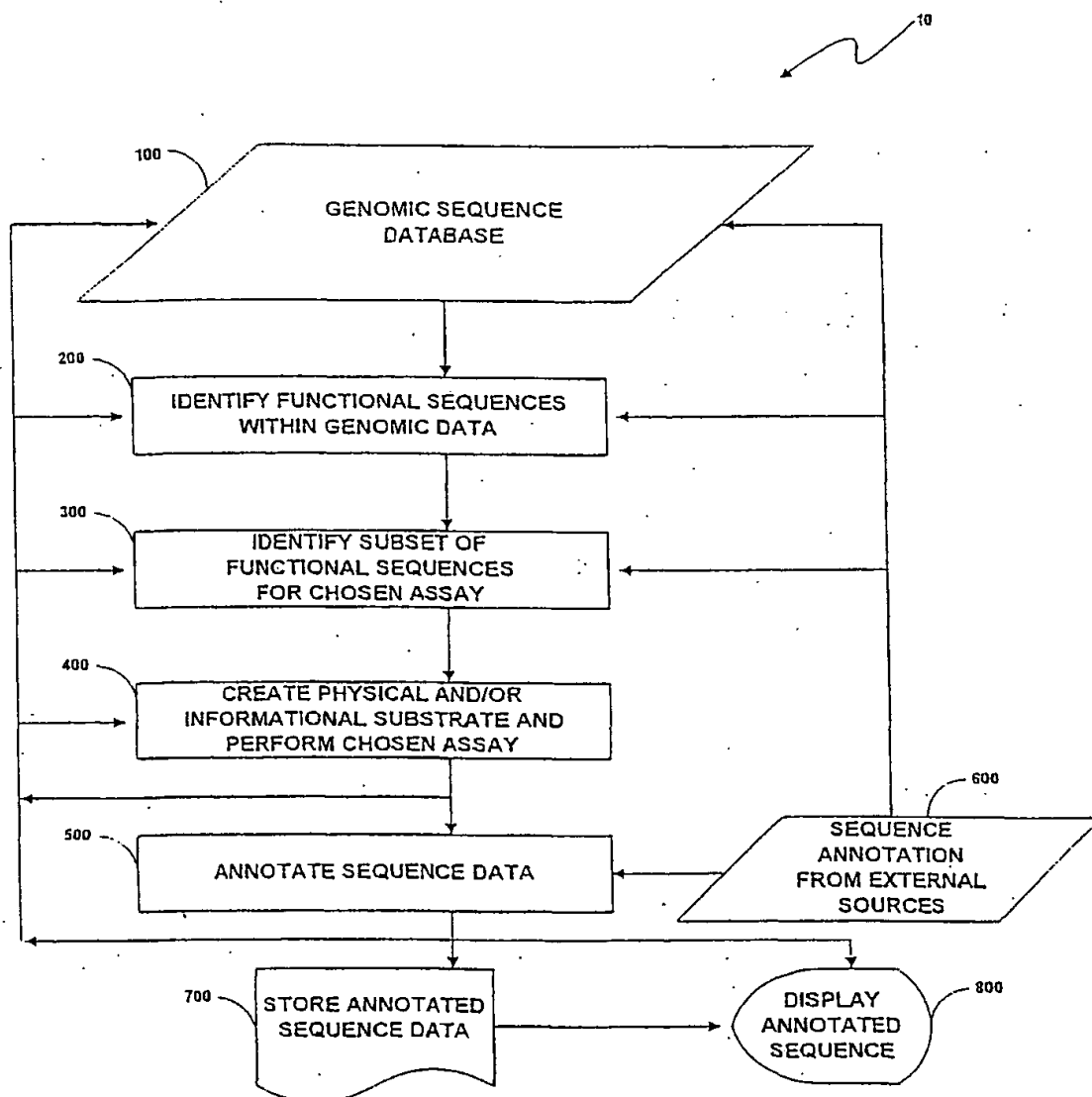


Fig. 1

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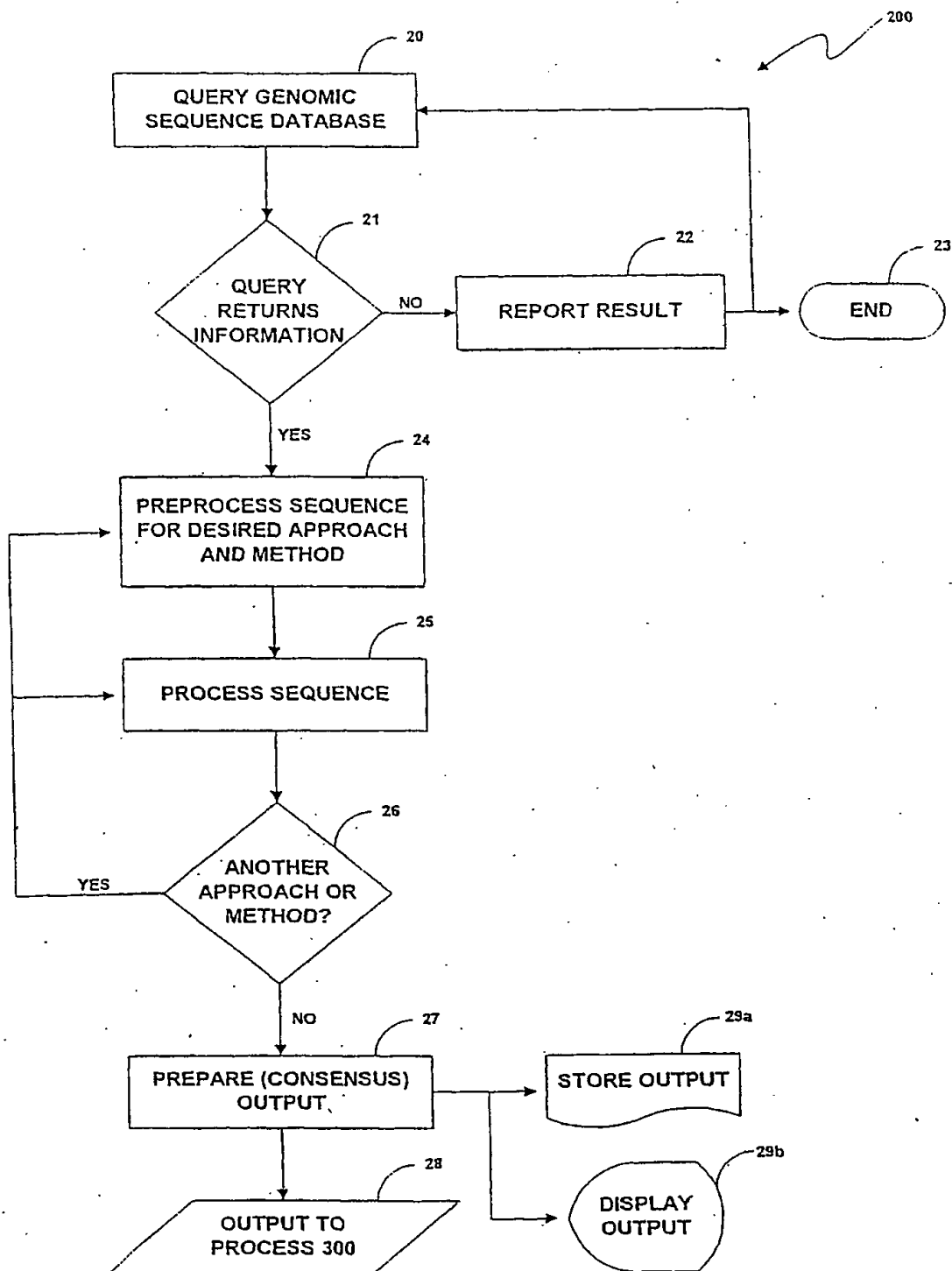


Fig. 2

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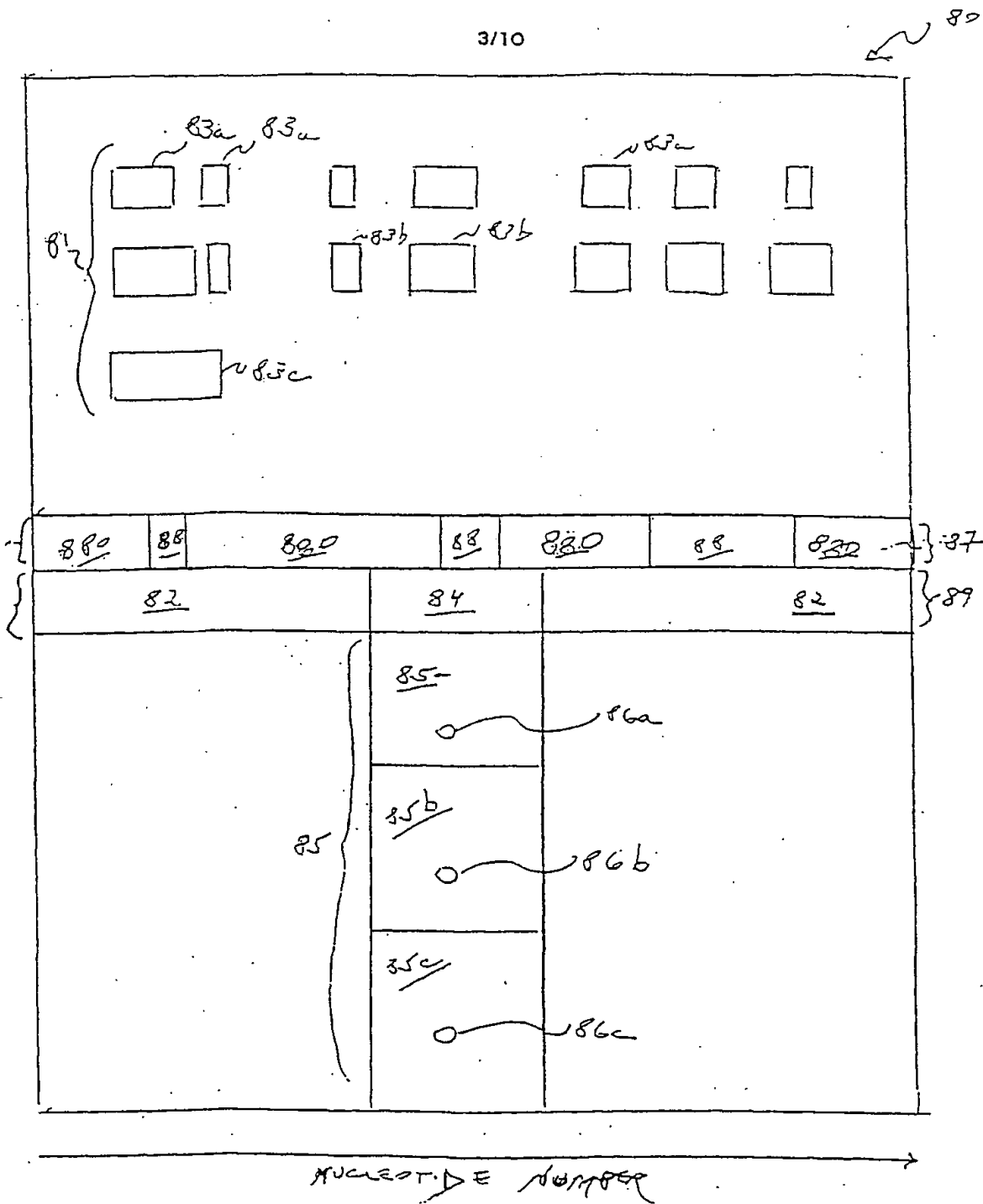


Fig. 3

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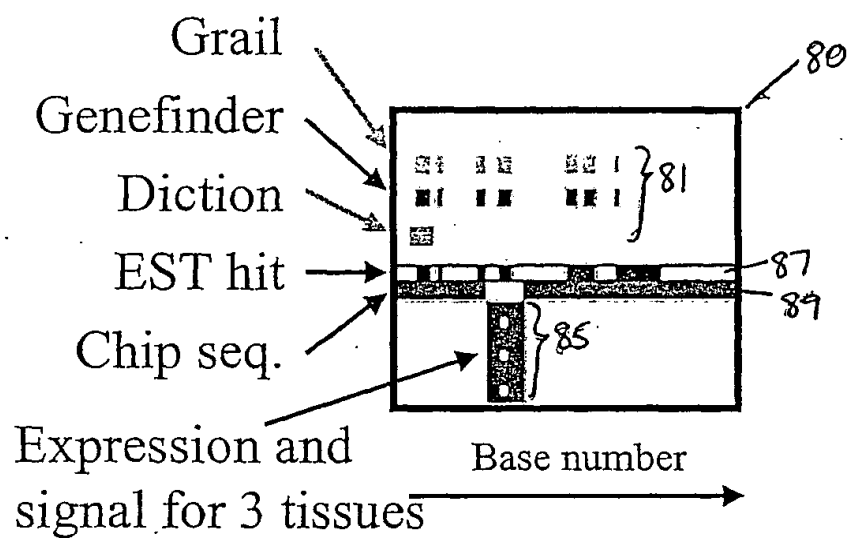


Fig. 4

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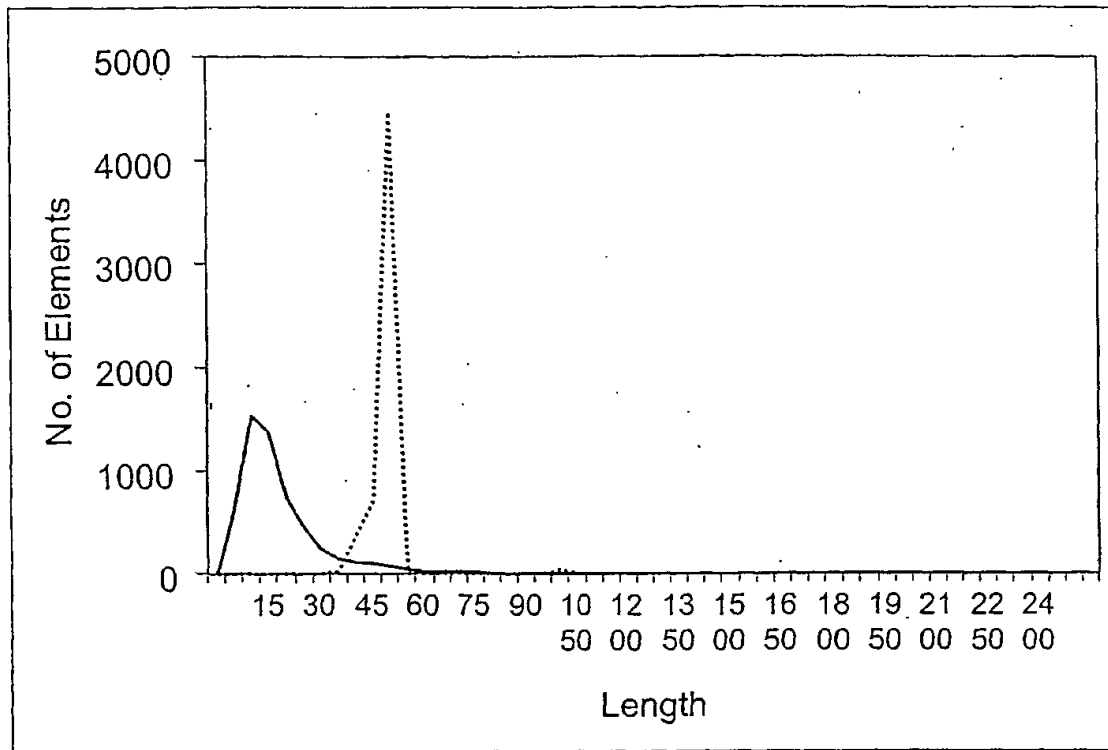


Fig. 5

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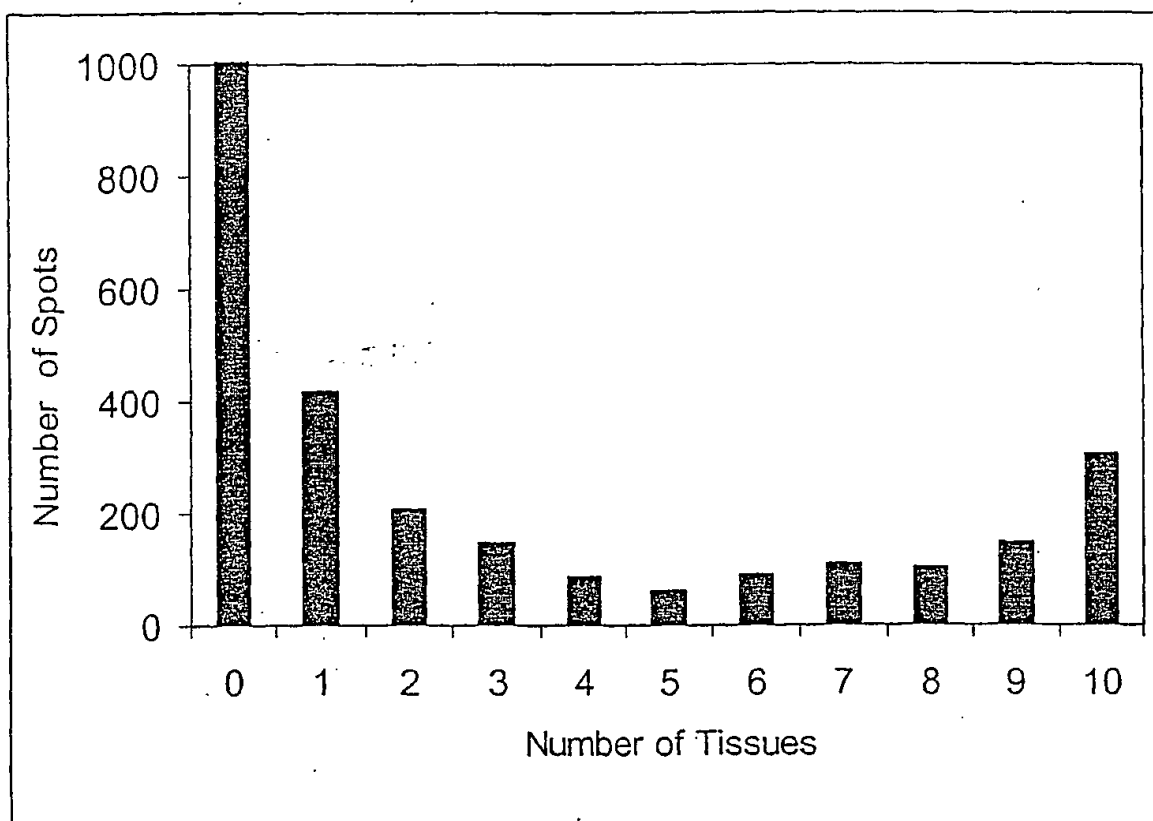


Fig. 6

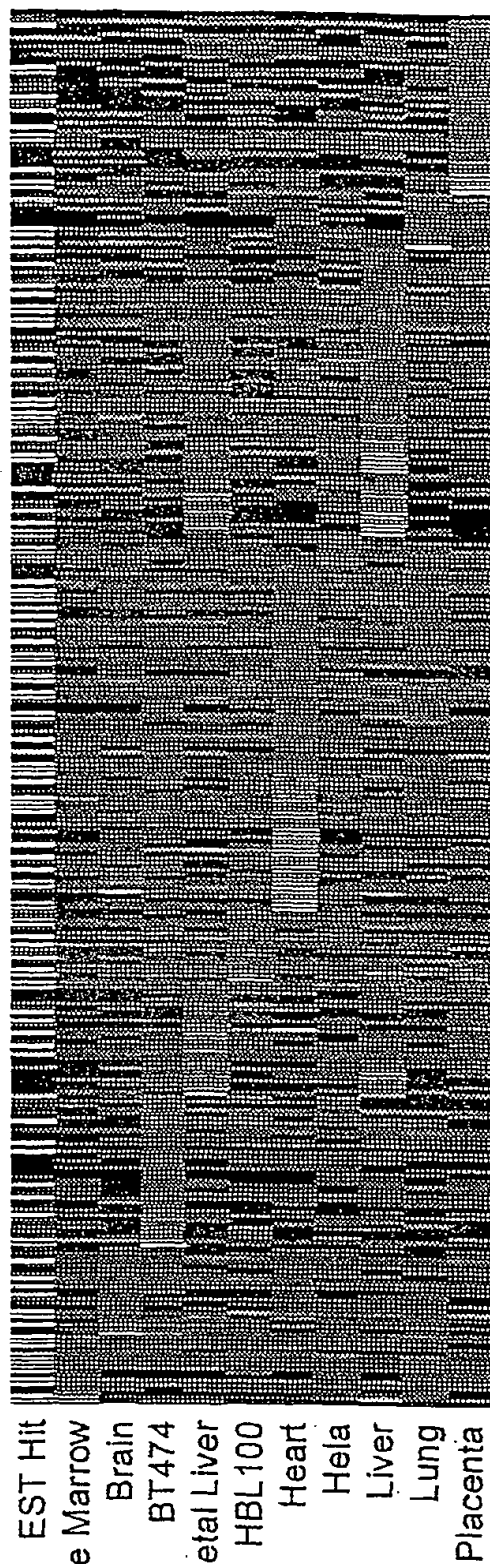


Fig. 7a

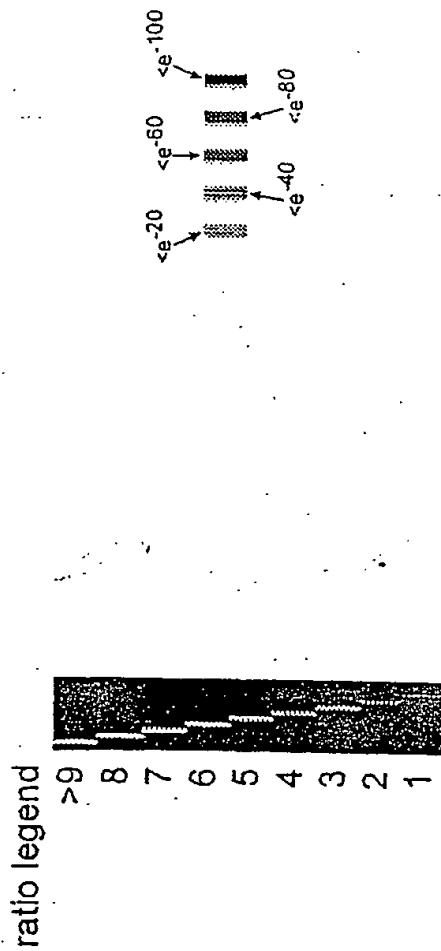


Fig. 7b

Fig. 7c

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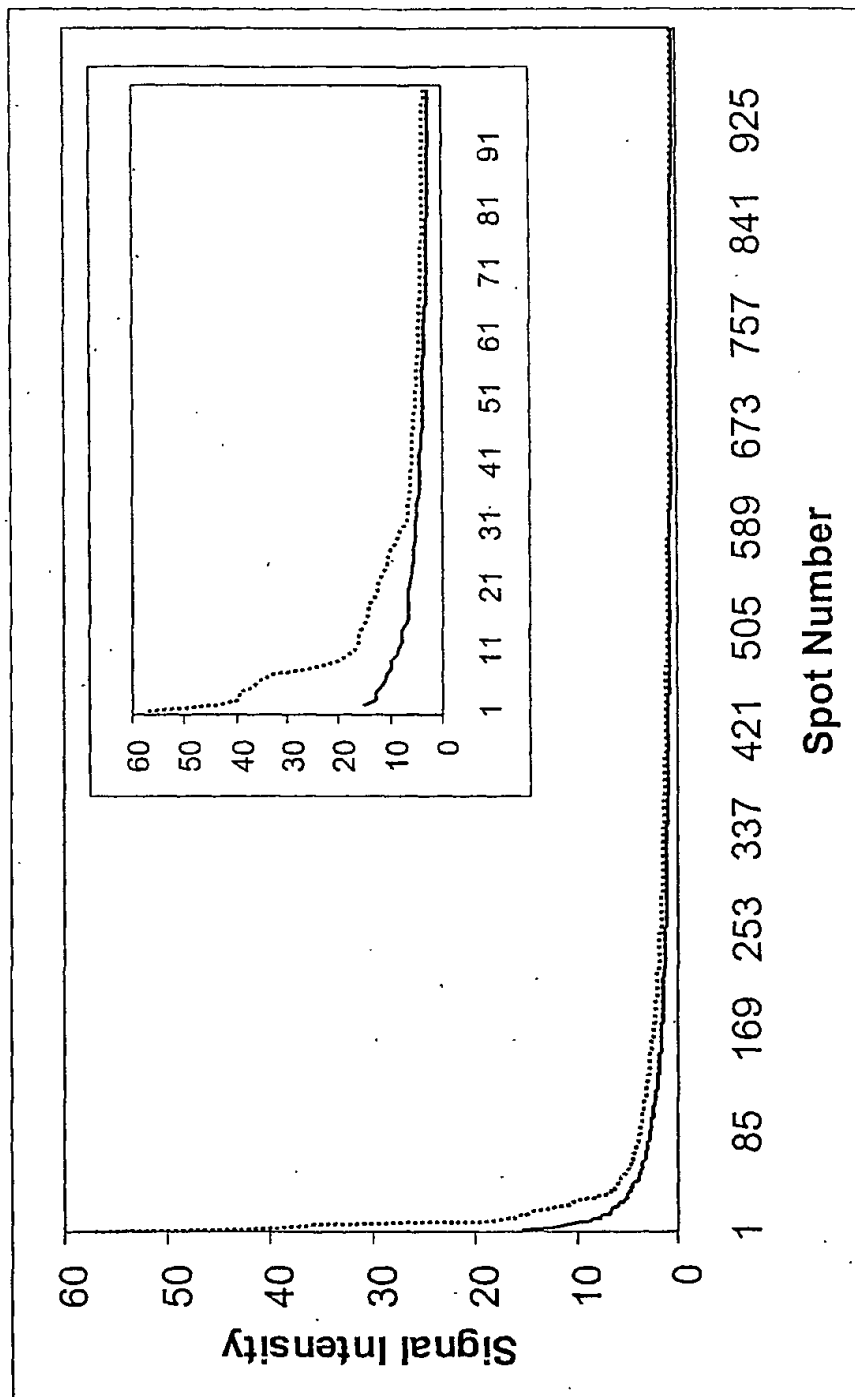


Fig. 8

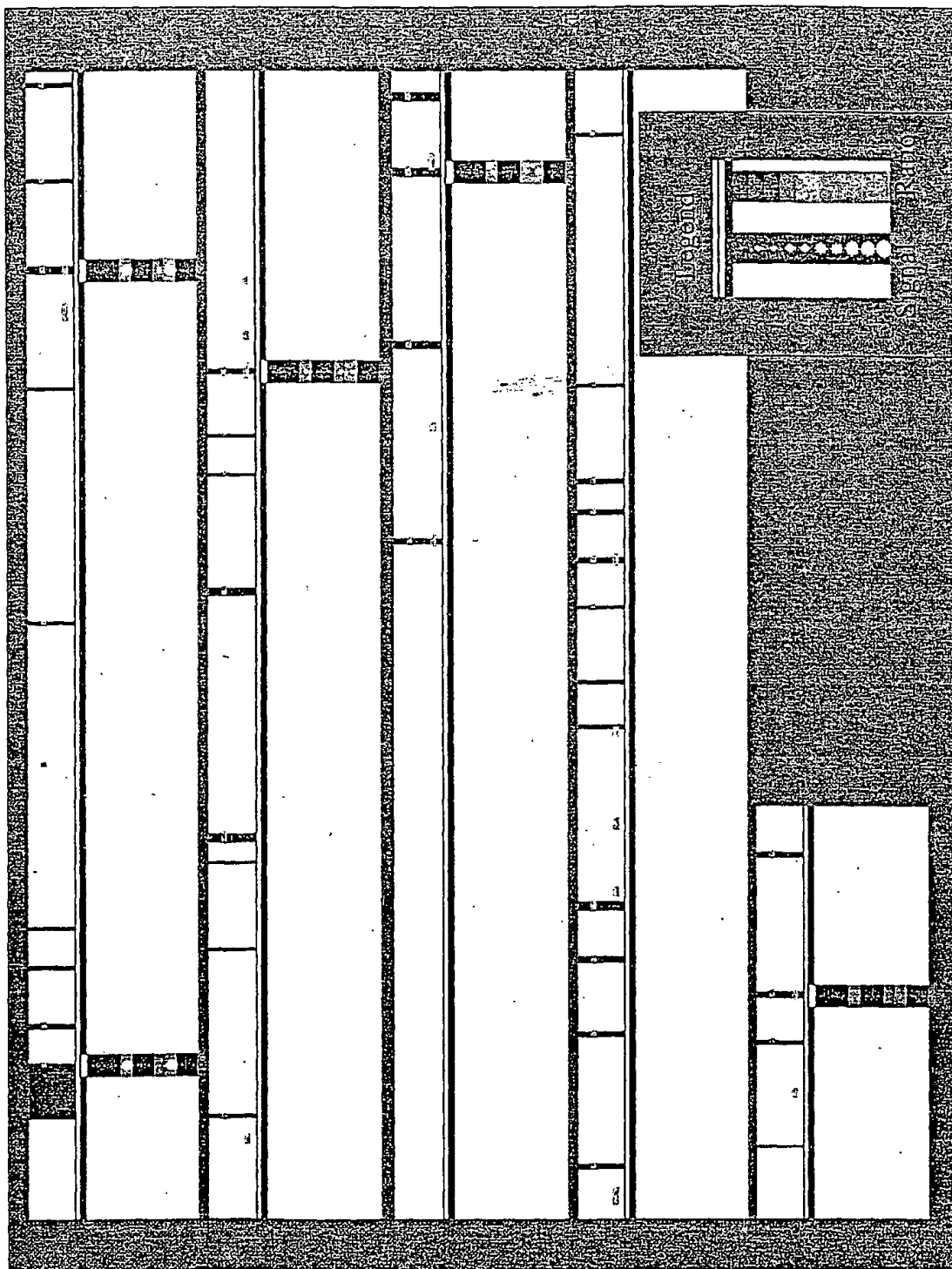
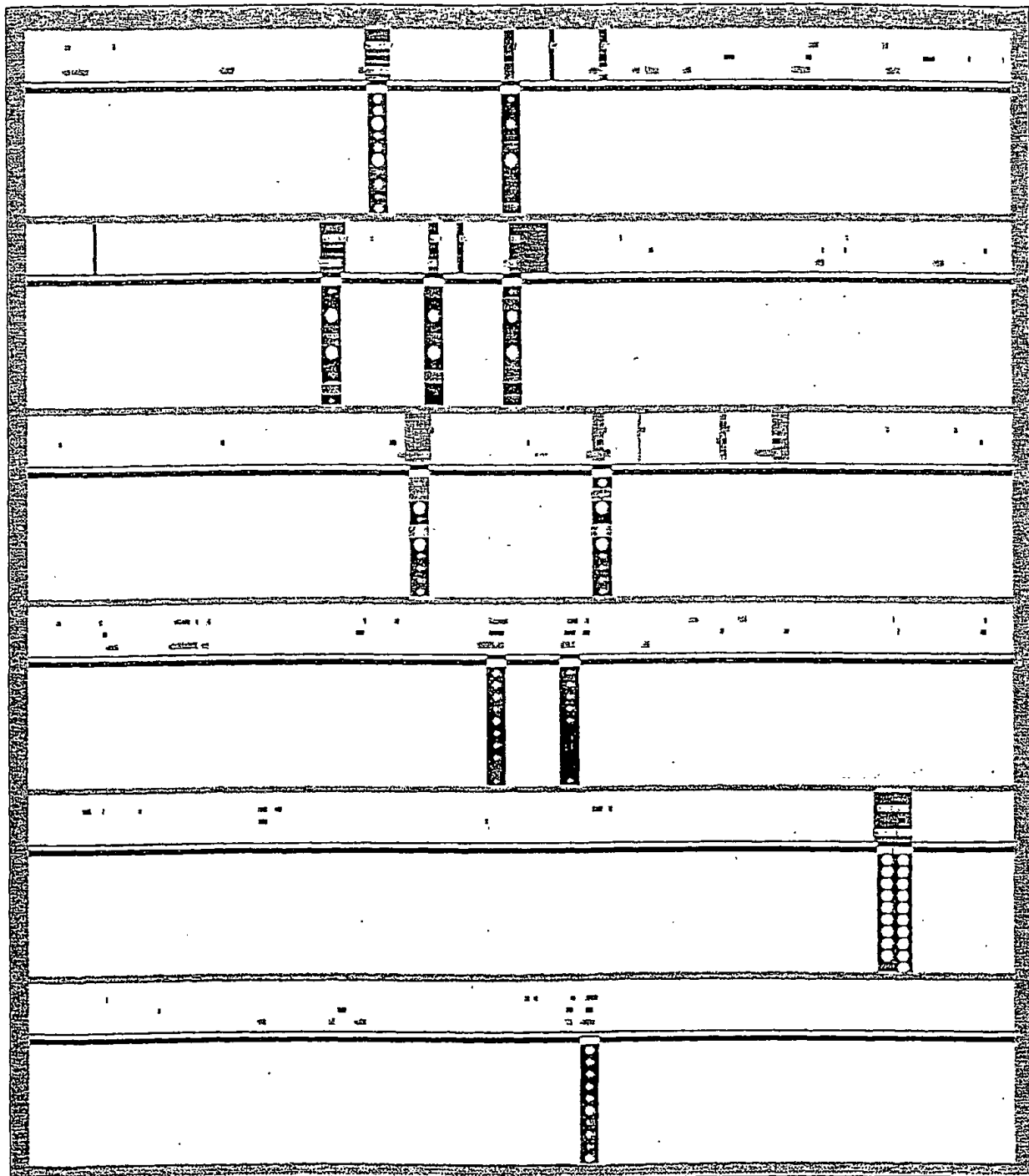


Fig. 9

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Fig. 10



(19) World Intellectual Property Organization
International Bureau



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- (74) Agent: **RONNING, Royal, N., Jr.**; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).
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- (71) Applicant (*for all designated States except US*): **AEOM-ICA, INC.** [US/US]; 928 East Arques Avenue, Sunnyvale, CA 94085 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): **PENN, Sharron, G.** [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). **HANZEL, David, K.** [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). **CHEN, Wen-sheng** [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). **RANK, David, R.** [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).
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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow is described. Also described are single exon nucleic acid probes expressed in the bone marrow and their use in methods for detecting gene expression.



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INTERNATIONAL SEARCH REPORT

In ☐ national Application No
PCT/US 01/00668

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, EPO-Internal, MEDLINE, EMBASE, CHEM ABS Data, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>STAUDER R ET AL: "Different CD44 splicing patterns define prognostic subgroups in multiple myeloma." BLOOD, (1996). VOL. 88, NO. 8, PP. 3101-8. JOURNAL CODE: A86. ISSN: 0006-4971., XP002182129 Basel Institute for Immunology, Switzerland. the whole document</p> <p style="text-align: center;">--- -/-</p>	13

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

2 August 2002

Date of mailing of the international search report

05.09.02

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INTERNATIONAL SEARCH REPORT

In Application No
PCT/US 01/00668

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X	SCREATON G R ET AL: "GENOMIC STRUCTURE OF DNA ENCODING THE LYMPHOCYTE HOMING RECEPTOR CD44 REVEALS AT LEAST 12 ALTERNATIVELY SPLICED EXONS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 89, no. 24, 15 December 1989 (1989-12-15), pages 12160-12164, XP000470187 ISSN: 0027-8424 abstract; table 1	13
X	DATABASE EBI 'Online! EMBL; Accession Number HSPA10C6 (Z77862), 5 August 1996 (1996-08-05) MUNGALL AJ ET AL.: "H. sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10C6" XP002182130 abstract	13
X	O'CONNOR H E ET AL: "Abnormalities of the ETV6 gene occur in the majority of patients with aberrations of the short arm of chromosome 12: a combined PCR and Southern blotting analysis." LEUKEMIA, (1998 JUL) 12 (7) 1099-106., XP001022502 p. 1099, col. 2, last par.-p. 1101, col. 2, 1st full par. column 2; figure 1	13
X	DATABASE EBI 'Online! EMBL; Accession Number AC007372, 27 April 1999 (1999-04-27) XP002182131 abstract	13
A	WO 99 33979 A (CHIRON CORP) 8 July 1999 (1999-07-08) page 1, line 19 -page 8, line 26; claims 19-21	1,12

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 Int I Application No
 PCT/US 01/00668

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A	EISEN M B ET AL: "Cluster analysis and display of genome-wide expression patterns" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 95, December 1998 (1998-12), pages 14863-14868, XP002140966 ISSN: 0027-8424 the whole document ----	1,12
A	WO 92 13075 A (GENETICS INST) 6 August 1992 (1992-08-06) page 28, line 4 - line 6; claims ----	1,12,13
A	SOLOVYEV V V ET AL: "PREDICTING INTERNAL EXONS BY OLIGONUCLEOTIDE COMPOSITION AND DISCRIMINANT ANALYSIS OF SPLICEABLE OPEN READING FRAMES" NUCLEIC ACIDS RESEARCH, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 22, no. 24, 1994, pages 5156-5163, XP002915964 ISSN: 0305-1048 the whole document ----	1-27
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INTERNATIONAL SEARCH REPORT

Int. Application No
PCT/US 01/00668

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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EBI 'Online! 9 May 1997 (1997-05-09) MARRA M. ET AL.: "The WashU-HHMI mouse EST project; vc72c02.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 780098" Database accession no. AA414703 XP002208274 abstract	13,14, 18,20,21
X	DATABASE EBI 'Online! 16 October 1997 (1997-10-16) MARRA M. ET AL.: "The WashU_HHMI mouse EST project; v160c06.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 976618" XP002208275 abstract	13,14, 16,18, 20,21
A	DATABASE EBI 'Online! 27 April 1999 (1999-04-27) DICKHOFF R. ET AL.: "Sequencing of human chromosome 14q31 region" XP002208276 abstract	13,14,18

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/00668

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 1 (see claim 13), or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 13115 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 1), spatially addressable set of probes comprising the said sequence (claim 1), microarrays comprising said sequence (claim 12), a method for measuring gene expression (claim 22), a method for identifying exons (claim 23) and a method for assigning exons to a single gene (claim 24) comprising using the said arrays, a peptide encoded by SEQ ID 1 or 13115 (claims 26-27), in particular having the sequence SEQ ID 26013, which is the translation from SEQ ID 13115 (see p. 74 of the description).

2. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 2, or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 13116 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 2), spatially addressable arrays comprising the said sequence, a method for measuring gene expression, a method for identifying exons and a method for assigning exons to a single gene comprising using the said arrays, a peptide encoded by SEQ ID 2 or 13116, in particular having the sequence SEQ ID 26014, which is the translation from SEQ ID 13116 (see p. 74 of the description).

...Inventions 3-13114: similar subject-matter as above related to SEQ IDs 3-13114.

Continuation of Box I.2

The following statements concerning the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject-matter for which a search has been performed and which has been identified as inventions 1 and 2 in PCT form 206.

1) Claims 1-3, 5, 6, 8-15 and 18-24 relate to fragments of undisclosed length or characteristics which cannot therefore be meaningfully searched. These claims have thus been searched only insofar as related to fragments having a length of at least 15 nt (see claim 15 and description pages 10, 1. 15-22).

2) Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising SEQ ID 1 or 2 and microarrays comprising the said sets. Therefore, the claims lack clarity and conciseness (Art. 6 PCT) to such an extent as to render a meaningful search over their whole scope impossible. Consequently, with respect to the said sets and microarrays the search has been carried out only insofar as related to the SEQ ID 1 and 2 as such.

3) In view of the absence of any indication as to which other peptides could be encoded by SEQ ID 1 and 2, the search with respect to claim 26 has been limited to the peptide sequences actually disclosed in the application, i.e. 26013 and 26014 (Art. 6 PCT).

4) Claims 15-21 relate to nucleic probes, solely defined in that they code for a polypeptide having the sequence SEQ ID 26013 or 26014. However, a peptide is potentially coded by an extremely large number of nucleic acid sequences. Hence, claims 15-21 lack clarity and conciseness to such an extent as to render a meaningful search over their whole scope impossible. The search has thus been limited to SEQ ID 1, 2, 13115 and 13116.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

 Int
 national Application No
 PCT/US 01/00668

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